# medigan Documentation

***Release 0.0.2***

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# DESCRIPTION

Let's install *medigan* and generate a few synthetic images.

```
pip install medigan
```

```
from medigan import Generators

# model 1 is "00001_DCGAN_MMG_CALC_ROI"
Generators().generate(model_id=1, install_dependencies=True)
```

CHAPTER

# ONE

# OVERVIEW

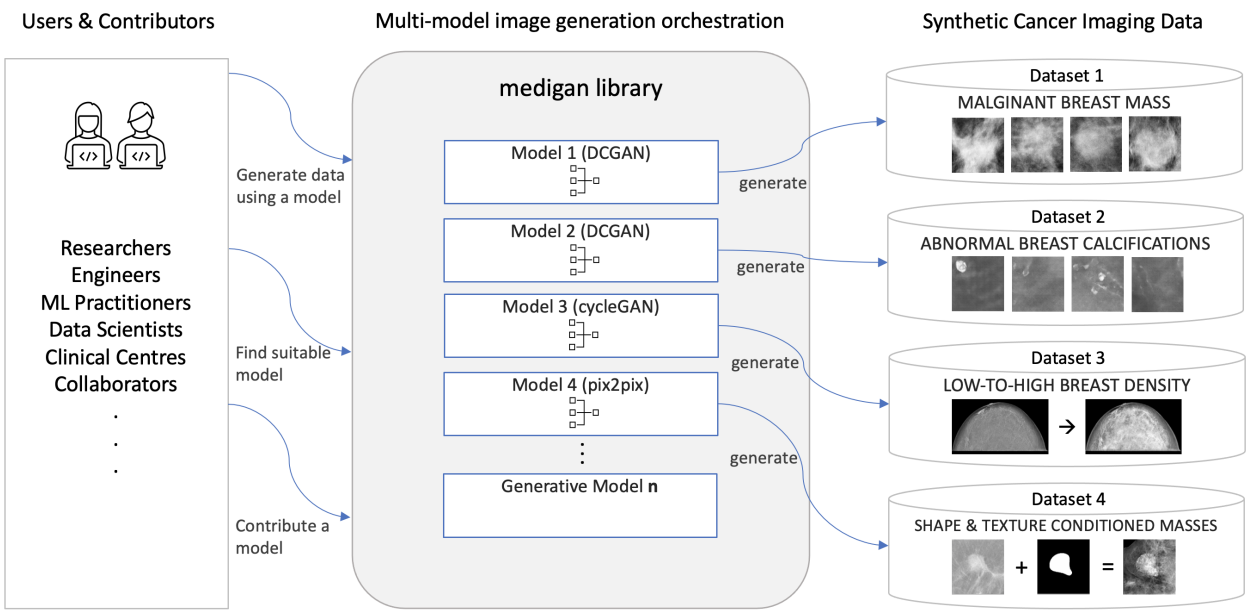



Fig. 1: Overview of *medigan* users, library, and models on the example of mammography cancer image dataset generation.

## 1.1 Description

**Table of Contents**

### 1.1.1 Aim and Scope

*medigan* focuses on automating medical image dataset synthesis using GANs.

These datasets can again be used to train diagnostic or prognostic clinical models such as disease classification, detection and segmentation models.

Despite this current focus, medigan, is readily extendable to any type of modality and any type of generative model.

### 1.1.2 Core Features

- Researchers and ML-practitioners can conveniently use an existing model in *medigan* for synthetic data augmentation instead of having to train their own generative model each time.
- Users can search and find a model using search terms (e.g. "Mammography, 128x128, DCGAN") or key value pairs (e.g. *key* = "modality", *value* = "Mammography")
- Users can explore the config and information (metrics, use-cases, modalities, etc) of each model in *medigan*
- Users can generate samples using a model
- Users can also get the generate_method of a model that they may want to use dynamically inside their dataloaders
- Model contributors can share and disseminate their generative models thereby augmenting their reach.

### 1.1.3 Architecture and Workflows

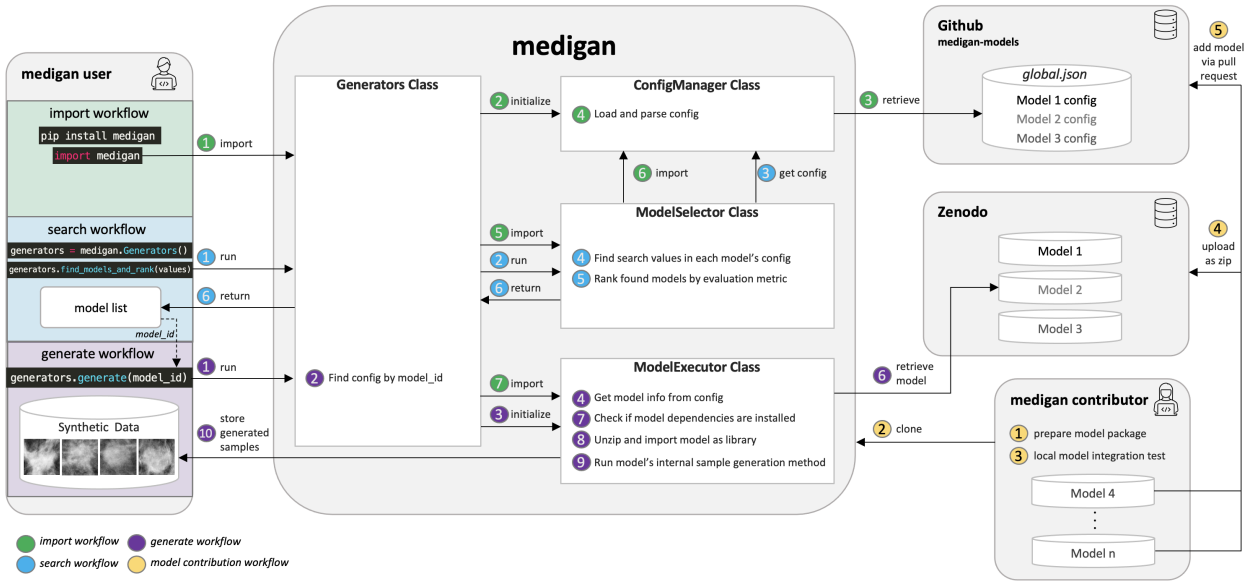



Fig. 2: Architectural overview including main workflows consisting of (a) library import and initialisation, (b) generative model search and ranking, (c) sample generation, and (d) generative model contribution.

### 1.1.4 Notes

- Each model in *medigan* has its own dependencies listed in the global.json model metadata/config file. Setting `install_dependencies=True`, in the `generate()` and related methods, triggers an automatic installation of the respective model's python dependencies (e.g. numpy. torch, etc), i.e., to the user's active python environment.
- Running the `generate()` and related methods for synthetic data generation will trigger the download of the respective generative model to the user's local directory from where the code is run (i.e. the current CLI path).

### 1.1.5 Issues

In case you encounter problems while using *medigan* or would like to request additional features, please create a new issue and we will try to help.

### 1.1.6 Links

- Github (medigan library)
- Test Pypi (medigan library)

## 1.2 Generative Models

This section provides an overview of the generative models in *medigan*.

Find in the tables below for each model:

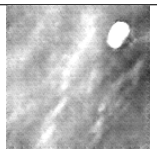
1. A **model_id**
2. A link to detailed documentation on **Zenodo**

Further model information can be found in the global.json metadata.

**Warning:** Some of the model internal checkpoint loading functions may implicitly use the pickle module (e.g. torch.load()), Pickle is insecure: It is possible to construct malicious pickle data which will execute arbitrary code during unpickling (example video). While we do our best to analyse and test each model before Zenodo upload and *medigan* integration, we cannot provide a security guarantee. Be aware and run only models you trust. To further mitigate risks, we plan to integrate a malware scanning tool into medigan's CI pipeline.

### 1.2.1 00001_DCGAN_MMG_CALC_ROI

DCGAN Model for Mammogram Calcification Region of Interest Generation (Trained on INbreast).
**Note:** A deep convolutional generative adversarial network (DCGAN) that generates regions of interest (ROI) of mammograms containing benign and/or malignant calcifications. Pixel dimensions are 128x128. The DCGAN was trained on ROIs from the INbreast dataset (Moreira et al, 2012). The uploaded ZIP file contains the files dcgan.pt (model weights), **init**.py (image generation method and utils), a README.md, and the GAN model architecture (in pytorch) below the /src folder. Kernel size=6 used in DCGAN discriminator.

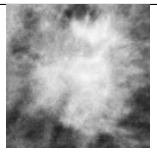
| Output type | Modality | Model type | Output size | Base dataset | Output examples | model_id | Hosted on | Reference |
|---|---|---|---|---|---|---|---|---|
| Breast Calcification | mammography | dcgan | 128x128 | Inbreast |  | 00001_DCGAN_MMG_CALC_ROI | Zenodo (5187714) | |

```
# create samples with this model
from medigan import Generators
Generators().generate(model_id="00001_DCGAN_MMG_CALC_ROI", image_size=128)

# model specific parameters
inputs= ["image_size: default=128, help=128 is the image size that works with the␣
↪supplied checkpoint."]
```

### 1.2.2 00002_DCGAN_MMG_MASS_ROI

DCGAN Model for Mammogram Mass Region of Interest Generation (Trained on OPTIMAM)
**Note:** A deep convolutional generative adversarial network (DCGAN) that generates regions of interest (ROI) of mammograms containing benign and/or malignant masses. Pixel dimensions are 128x128. The DCGAN was trained on ROIs from the Optimam dataset (Halling-Brown et al, 2014). The uploaded ZIP file contains the files malign_mass_gen (model weights), and **init**.py (image generation method and pytorch GAN model architecture). Kernel size=6 used in DCGAN discriminator.

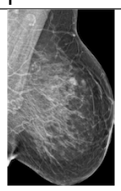
| Output type | Modality | Model type | Output size | Base dataset | Output examples | model_id | Hosted on | Reference |
|---|---|---|---|---|---|---|---|---|
| Breast Mass | mammography | dcgan | 128x128 | Optimam |  | 00002_DCGAN_MMG_MASS_ROI | Zenodo (5188557) | Alyafi et al (2019) |

```
# create samples with this model
from medigan import Generators
Generators().generate(model_id="00002_DCGAN_MMG_MASS_ROI")

# model specific parameters
inputs= []
```

### 1.2.3 00003_CYCLEGAN_MMG_DENSITY_FULL

CycleGAN Model for Low-to-High Brest Density Mammograms Translation (Trained on BCDR)
**Note:** A cycle generative adversarial network (CycleGAN) that generates mammograms with high breast density from an original mammogram e.g. with low-breast density. The CycleGAN was trained using normal (without pathologies) digital mammograms from BCDR dataset (Lopez, M. G., et al. 2012). The uploaded ZIP file contains the files CycleGAN_high_density.pth (model weights), **init**.py (image generation method and utils) and the GAN model architecture (in pytorch) below the /src folder.

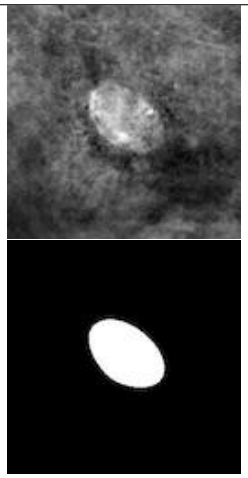
| Output type | Modality | Model type | Output size | Base dataset | Output examples | model_id | Hosted on | Reference |
|---|---|---|---|---|---|---|---|---|
| Breast Density Transfer | mammography | cyclegan | 1332x800 | BCDR |  | 00003_CYCLEGAN_MMG_DENSITY_FULL | Zenodo (5547263) | |

```
# create samples with this model
from medigan import Generators
Generators().generate(
    model_id="00003_CYCLEGAN_MMG_DENSITY_FULL",
    input_path="models/00003_CYCLEGAN_MMG_DENSITY_FULL/images",
    image_size=[1332, 800],
    gpu_id=0,
)

# model specific parameters
inputs= [
    "input_path: default=models/00003_CYCLEGAN_MMG_DENSITY_FULL/images, help=the path to␣
↪.png mammogram images that are translated from low to high breast density or vice versa
↪",
    "image_size: default=[1332, 800], help=list with image height and width. Images are␣
↪rescaled to these pixel dimensions.",
    "gpu_id: default=0, help=the gpu to run the model on.",
    "translate_all_images: default=False, help=flag to override num_samples in case the␣
↪user wishes to translate all images in the specified input_path folder."
]
```

### 1.2.4 00004_PIX2PIX_MMG_MASSES_W_MASKS

Generates synthetic patches given a random mask tiled with texture patches extracted from real images (Trained on BCDR)
**Note:** Generates synthetic patches given a random mask tiled with texture patches extracted from real images. The texture patches should be extracted from within the mass an outside the mass of a real image. Hence, some real ROIs are required to start with and its ideal for data augmentation purposes for mass segmentation.

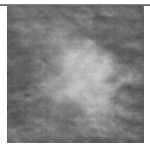
| Output type | Modality | Model type | Output size | Base dataset | Output examples | model_id | Hosted on | Reference |
|---|---|---|---|---|---|---|---|---|
| Breast Mass with Mask | mammography | pix2pix | 256x256 | BCDR |  | 00004_PIX2PIX_MMG_MASSES_W_MASKS | Zenodo (7093759) | |

```
# create samples with this model
from medigan import Generators
Generators().generate(
    model_id="00004_PIX2PIX_MMG_MASSES_W_MASKS",
    input_path="models/00004_PIX2PIX_MMG_MASSES_W_MASKS/images",
    image_size=[256, 256],
    patch_size=[32, 32],
    shapes=['oval', 'lobulated'],
    ssim_threshold=0.2,
    gpu_id=0,
)

# model specific parameters
inputs= [
    "input_path: default=models/00004_PIX2PIX_MMG_MASSES_W_MASKS/images help=inputs that␣
↪are used in the pix2pix input image pool (e.g. for tiled image generation) ",
    "image_size: default=[256, 256] help=height and width of images.",
    "patch_size: default=[32, 32] help=height and width of patches (annotation size on␣
↪image).",
    "shapes: default=['oval', 'lobulated'] help=the type of the mask curve shapes␣
↪generated via bezier curves.",
    "ssim_threshold: default=0.2, help=the SSIM threshold that images must surpass to be␣
↪output.",
    "gpu_id: default=0 help=the gpu to run the model.",
]
```

### 1.2.5 00005_DCGAN_MMG_MASS_ROI

DCGAN Model for Mammogram MASS Patch Generation (Trained on BCDR)
**Note:** A deep convolutional generative adversarial network (DCGAN) that generates mass patches of mammograms. Pixel dimensions are 128x128. The DCGAN was trained on MMG patches from the BCDR dataset (Lopez et al, 2012). The uploaded ZIP file contains the files 500.pt (model weight), **init**.py (image generation method and utils), a requirements.txt, and the GAN model architecture (in pytorch) below the /src folder.

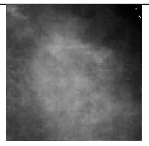
| Output type | Modality | Model type | Output size | Base dataset | Output examples | model_id | Hosted on | Reference |
|---|---|---|---|---|---|---|---|---|
| Breast Mass | mammography | dcgan | 128x128 | BCDR |  | 00005_DCGAN_MMG_MASS_ROI | Zenodo (6555188) | Szafranowska et al (2022) |

```
# create samples with this model
from medigan import Generators
Generators().generate(model_id="00005_DCGAN_MMG_MASS_ROI")

# model specific parameters
inputs= []
```

### 1.2.6 00006_WGANGP_MMG_MASS_ROI

WGAN-GP Model for Mammogram MASS Patch Generation (Trained on BCDR)
**Note:** A wasserstein generative adversarial network with gradient penalty (WGAN-GP) that generates mass patches of mammograms. Pixel dimensions are 128x128. The DCGAN was trained on MMG patches from the BCDR dataset (Lopez et al, 2012). The uploaded ZIP file contains the files 10000.pt (model weight), **init**.py (image generation method and utils), a requirements.txt, and the GAN model architecture (in pytorch) below the /src folder.

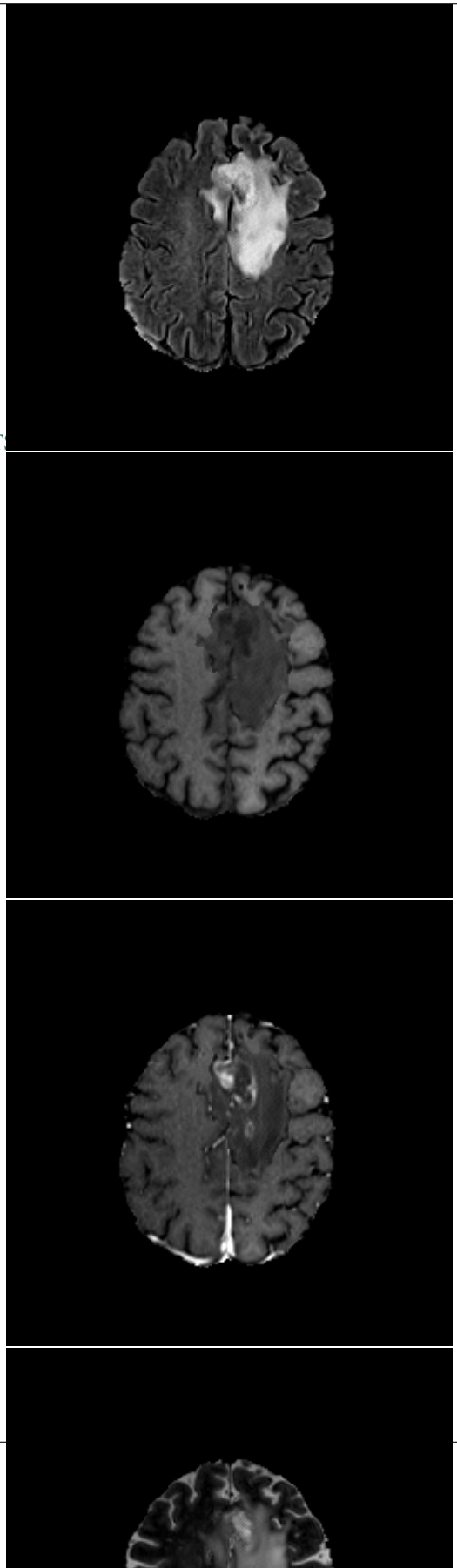
| Output type | Modality | Model type | Output size | Base dataset | Output examples | model_id | Hosted on | Reference |
|---|---|---|---|---|---|---|---|---|
| Breast Mass | mammography | wgan-gp | 128x128 | BCDR |  | 00006_WGANGP_MMG_MASS_ROI | Zenodo (6554713) | Szafranowska et al (2022) |

```
# create samples with this model
from medigan import Generators
Generators().generate(model_id="00006_WGANGP_MMG_MASS_ROI")

# model specific parameters
inputs= []
```

### 1.2.7 00007_INPAINT_BRAIN_MRI

Tumor Inpainting Model for Generation of Flair, T1, T1c, T2 Brain MRI Images (Trained on BRATS)
**Note:** A Generative adversarial network (GAN) for Inpainting tumors (based on concentric circle-based tumor grade masks) into multi-modal MRI images (Flair, T1, T1c, T2) with dimensions 256x256. Model was trained on BRATS MRI Dataset (Menze et al). For more information, see publication (https://doi.org/10.1002/mp.14701). Model comes with example input image folders. Apart from that, the uploaded ZIP file contains the model checkpoint files .pth (model weight), **init**.py (image generation method and utils), a requirements.txt, the MEDIGAN metadata.json. The proposed method synthesizes brain tumor images from normal brain images and concentric circles that are simplified tumor masks. The tumor masks are defined by complex features, such as grade, appearance, size, and location. Thus, these features of the tumor masks are condensed and simplified to concentric circles. In the proposed method, the user-defined concentric circles are converted to various tumor masks through deep neural networks. The normal brain images are masked by the tumor mask, and the masked region is inpainted with the tumor images synthesized by the deep neural networks. Also see original repository at: https://github.com/KSH0660/BrainTumor"

| Output type | Modality | Model type | Output size | Base dataset | Output examples | model_id | Hosted on | Reference |
|---|---|---|---|---|---|---|---|---|
| Brain Tumors on Flair, T1, T1c, T2 with Masks | brain MRI | in-paint GAN | 256x256 | BRATS 2018 |  | 00007_INPAINT_BRAIN_MRI | Zenodo (7041737) | Kim et al. (2020) |

```
# create samples with this model
from medigan import Generators
Generators().generate(
    model_id="00007_INPAINT_BRAIN_MRI",
    image_size=256,
    num_inpaints_per_sample=2,
    randomize_input_image_order=True,
    F_img_path=None,
    T1_img_path=None,
    T1c_img_path=None,
    T2_img_path=None,
    add_variations_to_mask=True,
    x_center=130,
    y_center=130,
    radius_1=10,
    radius_2=15,
    radius_3=30,
)

# model specific parameters
inputs= [
    "image_size: default=256, help=the size if height and width of the generated images.
↪",
    "num_inpaints_per_sample: default=2, help=the number of tumor inpaint images per MRI␣
↪modality that is generated from the same input sample",
    "randomize_input_image_order: default=True, help=input image order is randomized.␣
↪This helps to not exclude input images if batch generation is used.",
    "F_img_path: default=None, help=The path to the folder were the input Flair MRI␣
↪images are stored.",
    "T1_img_path: default=None, help=The path to the folder were the input T1 MRI images␣
↪are stored.",
    "T1c_img_path: default=None, help=The path to the folder were the input T1c MRI␣
↪images are stored.",
    "T2_img_path: default=None, help=The path to the folder were the input T2 MRI images␣
↪are stored.",
    "add_variations_to_mask: default=True, help=This slightly varies the values of x_
↪center, y_center, radius_1, radius_2, radius_3. If True, the same segmentation masks␣
↪is still used to generate each of the 4 modality images. This is recommended as it␣
↪results in higher image diversity.",
    "x_center: default=130, help=the x coordinate of the concentric circle upon which␣
↪the binary mask, the tumor grade mask, and, ultimately, the generated images are based.
↪",
    "y_center: default=130, help=the y coordinate of the concentric circle upon which␣
↪the binary mask, the tumor grade mask, and, ultimately, the generated images are based.
↪",
    "radius_1: default=10, help=the radius of the first (inside second) of three␣
↪concentric circles (necrotic and non-enhancing tumor) upon which the binary mask, the␣
↪tumor grade mask, and, ultimately, the generated images are based.",
    "radius_2: default=15, help=the radius of the second (inside third) of three␣
↪concentric circles (enhancing tumor) upon which the binary mask, the tumor grade mask,␣
↪and, ultimately, the generated images are based.",
    "radius_3: default=30, help=the radius of the third of three concentric circles␣
↪(edema) upon which the binary mask, the tumor grade mask, and, ultimately, the␣
↪generated images are based."
```

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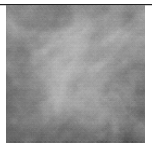
```
]
```

### 1.2.8 00008_C-DCGAN_MMG_MASSES

Conditional DCGAN Model for Patch Generation of Mammogram Masses Conditioned on Biopsy Proven Malignancy Status (Trained on CBIS-DDSM)
**Note:** A class-conditional deep convolutional generative adversarial network that generates mass patches of mammograms that are conditioned to either be benign (1) or malignant (0). Pixel dimensions are 128x128. The Cond-DCGAN was trained on MMG patches from the CBIS-DDSM (Sawyer Lee et al, 2016). The uploaded ZIP file contains the files 1750.pt (model weight), **init**.py (image generation method and utils), a requirements.txt, a LICENSE file, the MEDIGAN metadata, the used GAN training config file, a test.sh file to run the model, and two folders with a few generated images.

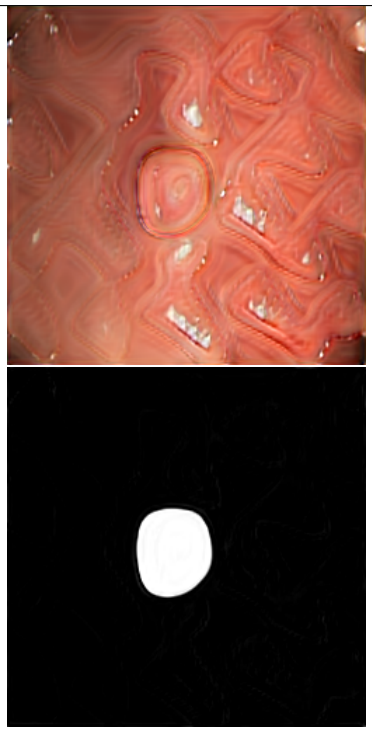
| Output type | Modality | Model type | Output size | Base dataset | Output examples | model_id | Hosted on | Reference |
|---|---|---|---|---|---|---|---|---|
| Breast Mass (Mal/Benign) | mammography | c-dcgan | 128x128 | CBIS-DDSM |  | 00008_C-DCGAN_MMG_MASSES | Zenodo (6647349) | |

```
# create samples with this model
from medigan import Generators
Generators().generate(
    model_id="00008_C-DCGAN_MMG_MASSES",
    condition=None,
    z=None,
)

# model specific parameters
inputs= [
    "condition: default=None, help=Either 0, 1 or None. Condition indicates whether a␣
↪generated mass is malignant (0) or benign (1). If None, a balanced set of malignant␣
↪and benign tumor images is created.",
    "z: default=None, help=the input noise torch tensor for the generator. If None, this␣
↪option is ignored (e.g. random input vector generation)"
]
```

### 1.2.9 00009_PGGAN_POLYP_PATCHES_W_MASKS

PGGAN Model for Patch Generation of Polyps with Corresponding Segmentation Masks (Trained on HyperKvasir)
**Note:** A Progressively-growing generative adversarial network that generates a 4 dimensional output containing an RGB image (channels 1-3) and a segmentation mask (channel 4). The RGB images are images of polyps and the segmentation mask indicates the location and shape of the polyp on the image. Pixel dimensions are 256x256. The model was trained on gastrointestinal endoscopy imaging data from the HyperKvasir dataset by Borgli et al (2020, 'https://doi.org/10.1038/s41597-020-00622-y'). The uploaded ZIP file contains the files ProGAN_300000_g.model (model weight), **init**.py (image generation method and utils), a requirements.txt, a LICENSE file, the MEDIGAN metadata, the source code from the official repository ('https://github.com/vlbthambawita/singan-seg-polyp'), and a test.sh file to run the model, and a folder 'examples/' with a few generated images.

| Output type | Modality | Model type | Output size | Base dataset | Output examples | model_id | Hosted on | Reference |
|---|---|---|---|---|---|---|---|---|
| Polyp with Mask | endoscopy | pggan | 256x256 | HyperKvasir |  | 00009_PGGAN_POLYP_PATCHES_W_MASKS | Zenodo (6653743) | Thambawita et al (2022) |

```
# create samples with this model
Generators().generate(
    model_id="00009_PGGAN_POLYP_PATCHES_W_MASKS",
    gpu_id=None,
    channel=128,
    z_dim=128,
    pixel_norm=False,
    img_channels=4,
    tanh=False,
    step=6,
    alpha=1,
    save_option="image_only",
    num_fakes=1000,
```

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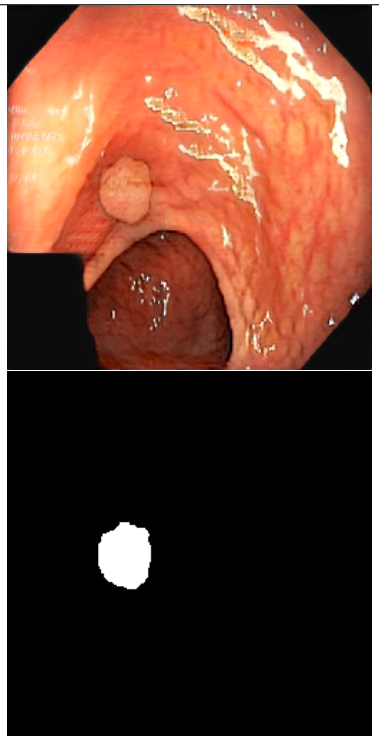
```
)

# model specific parameters
inputs=[
    "gpu_id: type=int, default=None, help=0 is the first gpu, 1 is the second gpu, etc.",
    "channel: type=int, default=128, help=determines how big the model is, smaller value␣
↪means faster training, but less capacity of the model",
    "z_dim: type=int, default=128, help=the initial latent vectors dimension, can be␣
↪smaller such as 64, if the dataset is not diverse",
    "pixel_norm: default=False, action=store_true, help=a normalization method inside␣
↪the model, you can try use it or not depends on the dataset",
    "img_channels: default=4, help=Number of channels in input data., for rgb images=3,␣
↪gray=1 etc.",
    "tanh: default=False, action=store_true, help=an output non-linearity on the output␣
↪of Generator, you can try use it or not depends on the dataset",
    "step: default=6, help=step to generate fake data. # can be 1 = 8, 2 = 16, 3 = 32, 4␣
↪= 64, 5 = 128, 6 = 256",
    "alpha: default=1, help=Progressive gan parameter to set, 0 or 1",
    "save_option: default=image_only, help=Options to save output, image_only, mask_only,
↪ image_and_mask, choices=[image_only,mask_only, image_and_mask]",
    "num_fakes: default=1000, help=Number of fakes to generate, type=int"
]
```

### 1.2.10 00010_FASTGAN_POLYP_PATCHES_W_MASKS

FastGAN Model for Patch Generation of Polyps with Corresponding Segmentation Masks (Trained on HyperKvasir) **Note:** A Fast generative adversarial network (FastGAN) that generates a 4 dimensional output containing an RGB image (channels 1-3) and a segmentation mask (channel 4). FASTGAN is from the paper 'Towards Faster and Stabilized GAN Training for High-fidelity Few-shot Image Synthesis' in ICLR 2021. The RGB images are images of polyps and the segmentation mask indicates the location and shape of the polyp on the image. Pixel dimensions are 256x256. The model was trained on gastrointestinal endoscopy imaging data from the HyperKvasir dataset by Borgli et al (2020, 'https://doi.org/10.1038/s41597-020-00622-y'). The uploaded ZIP file contains the files FastGAN_all_50000.pth (model weight), **init**.py (image generation method and utils), a requirements.txt, a LICENSE file, the MEDIGAN metadata, the source code from the repository ('https://github.com/vlbthambawita/singan-seg-polyp'), and a test.sh file to run the model, and a folder 'examples/' with a few generated images.

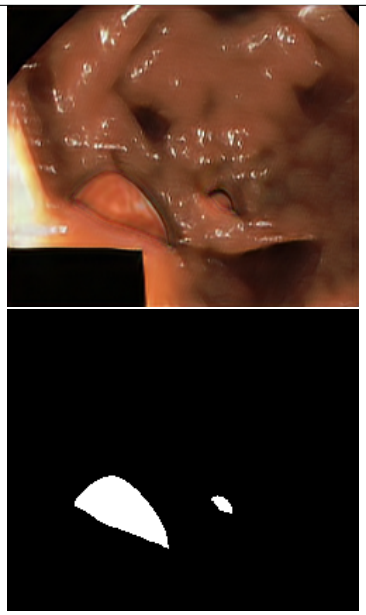
| Output type | Modality | Model type | Output size | Base dataset | Output examples | model_id | Hosted on | Reference |
|---|---|---|---|---|---|---|---|---|
| Polyp with Mask | endoscopy | fastgan | 256x256 | HyperK-vasir |  | 00010_FASTGAN_POLYP_PATCHES_W_MASKS | Zenodo (6660711) | Ghebawita et al (2022) |

```
# create samples with this model
from medigan import Generators
Generators().generate(
    model_id="00010_FASTGAN_POLYP_PATCHES_W_MASKS",
    gpu_id=None,
    save_option="image_and_mask",
)

# model specific parameters
inputs=[
    "gpu_id: type=int, default=None, help=0 is the first gpu, 1 is the second gpu, etc.",
    "save_option: default=image_only, help=Options to save output, image_only, mask_only,
↪ image_and_mask, choices=[image_only,mask_only, image_and_mask]"
]
```

### 1.2.11 00011_SINGAN_POLYP_PATCHES_W_MASKS

SinGAN Model for Patch Generation of Polyps with Corresponding Segmentation Masks (Trained on HyperKvasir)
**Note:** A SinGAN generative adversarial network that generates a 2dimensional output image tuple containing a 3-channel RGB image and a 3-channel segmentation mask. SinGAN is from the paper 'SinGAN: Learning a Generative Model from a Single Natural Image' in ICCV 2019. The width of the outputted images varies depending on the corresponding original image. The RGB images are images of polyps and the segmentation mask indicates the location and shape of the polyp on the image. Pixel dimensions are 213x256. The model was trained on gastrointestinal endoscopy imaging data from the HyperKvasir dataset by Borgli et al (2020, 'https://doi.org/10.1038/s41597-020-00622-y'). The uploaded ZIP file contains the checkpoints in folder 'SinGAN-Generated' (model weights), **init**.py (image generation method and utils), a requirements.txt, a LICENSE file, the MEDIGAN metadata, the source code from the repository ('https://github.com/vlbthambawita/singan-seg-polyp'), and a test.sh file to run the model, and a folder 'examples/' with a few generated images.

| Output type | Modality | Model type | Output size | Base dataset | Output examples | model_id | Hosted on | Reference |
|---|---|---|---|---|---|---|---|---|
| Polyp with Mask | endoscopy | singan | 250x250 | HyperKvasir |  | 00011_SINGAN_POLYP_PATCHES_W_MASKS | Zenodo (6667944) | Thambawita et al (2022) |

```
# create samples with this model
from medigan import Generators
Generators().generate(
    model_id="00011_SINGAN_POLYP_PATCHES_W_MASKS",
    model_files="models/00011_SINGAN_POLYP_PATCHES_W_MASKS/singan_seg_polyp/SinGAN-
↪Generated",
    gen_start_scale=0,
    checkpoint_ids=None,
    multiple_checkpoints=False
)

# model specific parameters
inputs= [
    "model_files: default=models/00011_SINGAN_POLYP_PATCHES_W_MASKS/singan_seg_polyp/
↪SinGAN-Generated help=the folder where the checkpoints are stored | ",
```

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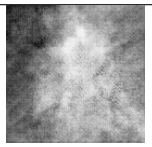
```
    "gen_start_scale: default=0 help=The start for scaling (progressively increasing␣
↪generator input size) in SinGAN.",
    "checkpoint_ids: default=None help=A list of checkpoint ids that will be used for␣
↪polyp generation. If None, all available checkpoints (i.e. 1000) or one random one␣
↪(depending on 'multiple_checkpoints' arg) will be used.",
    "multiple_checkpoints: default=False help=A boolean indicating if all checkpoint_ids␣
↪or one random one is used for generating images, but only in case 'checkpoint_ids
↪'==None"
]
```

### 1.2.12 00012_C-DCGAN_MMG_MASSES

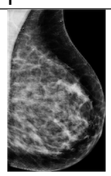
Conditional DCGAN Model for Patch Generation of Mammogram Masses Conditioned on Biopsy Proven Malignancy Status (Trained on BCDR)
**Note:** A class-conditional deep convolutional generative adversarial network that generates mass patches of mammograms that are conditioned to either be benign (1) or malignant (0). Pixel dimensions are 128x128. The Cond-DCGAN was trained on MMG patches from the BCDR dataset (Lopez et al, 2012). The uploaded ZIP file contains the files 1250.pt (model weight), **init**.py (image generation method and utils), a requirements.txt, a LICENSE file, the MEDIGAN metadata, the used GAN training config file, a test.sh file to run the model, and two folders with a few generated images.

| Output type | Modality | Model type | Output size | Base dataset | Output examples | model_id | Hosted on | Reference |
|---|---|---|---|---|---|---|---|---|
| Breast Mass (Mal/Benign) | mammography | c-dcgan | 128x128 | BCDR |  | 00012_C-DCGAN_MMG_MASSES | Zenodo (6755693) | |

```
# create samples with this model
from medigan import Generators
Generators().generate(
    model_id="00012_C-DCGAN_MMG_MASSES",
    condition=None,
    z=None,
)

# model specific parameters
inputs= [
    "condition: default=None, help=Either 0, 1 or None. Condition indicates whether a␣
↪generated mass is malignant (0) or benign (1). If None, a balanced set of malignant␣
↪and benign tumor images is created.",
    "z: default=None, help=the input noise torch tensor for the generator. If None, this␣
↪option is ignored (e.g. random input vector generation)"
]
```

### 1.2.13 00013_CYCLEGAN_MMG_DENSITY_OPTIMAM_MLO

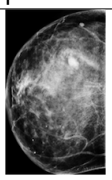
CycleGAN Model for Low-to-High Brest Density Mammograms Translation of MLO VIEW (Trained on OPTIMAM) **Note:** A cycle generative adversarial network (CycleGAN) that generates mammograms with high breast density from an original mammogram e.g. with low-breast density. The CycleGAN was trained using normal (without pathologies) digital mammograms from OPTIMAM dataset (Halling-Brown et al, 2014). The uploaded ZIP file contains the files CycleGAN_high_density.pth (model weights), **init**.py (image generation method and utils) and the GAN model architecture (in pytorch) below the /src folder.

| Output type | Modality | Model type | Output size | Base dataset | Output examples | model_id | Hosted on | Reference |
|---|---|---|---|---|---|---|---|---|
| Breast Density Transfer MLO | mammography | cyclegan | 1332x800 | OPTIMAM |  | 00013_CYCLEGAN_MMG_DENSITY_OPTIMAM_MLO | Zenodo (6818095) | |

```
# create samples with this model
from medigan import Generators
Generators().generate(
    model_id="00013_CYCLEGAN_MMG_DENSITY_OPTIMAM_MLO",
    input_path="models/00013_CYCLEGAN_MMG_DENSITY_OPTIMAM_MLO/images",
    image_size=[1332, 800],
    gpu_id=0,
    translate_all_images=False,
    low_to_high=True,
)

# model specific parameters
inputs= [
    "input_path: default=models/00013_CYCLEGAN_MMG_DENSITY_OPTIMAM_MLO/images, help=the␣
↪path to .png mammogram images that are translated from low to high breast density or␣
↪vice versa",
    "image_size: default=[1332, 800], help=list with image height and width. Images are␣
↪rescaled to these pixel dimensions.",
    "gpu_id: default=0, help=the gpu to run the model on.",
    "translate_all_images: default=False, help=flag to override num_samples in case the␣
↪user wishes to translate all images in the specified input_path folder.",
    "low_to_high: default=True, help=if true, breast density is added. If false, it is␣
↪removed from the input image. A different generator of the cycleGAN is used based no␣
↪this flag."
]
```

### 1.2.14 00014_CYCLEGAN_MMG_DENSITY_OPTIMAM_CC

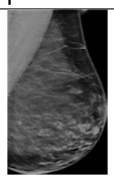
CycleGAN Model for Low-to-High Brest Density Mammograms Translation of CC VIEW (Trained on OPTIMAM)
**Note:** A cycle generative adversarial network (CycleGAN) that generates mammograms with high breast density from an original mammogram e.g. with low-breast density. The CycleGAN was trained using normal (without pathologies) digital mammograms from OPTIMAM dataset (Halling-Brown et al, 2014). The uploaded ZIP file contains the files CycleGAN_high_density.pth (model weights), **init**.py (image generation method and utils) and the GAN model architecture (in pytorch) below the /src folder.

| Output type | Modality | Model type | Output size | Base dataset | Output examples | model_id | Hosted on | Reference |
|---|---|---|---|---|---|---|---|---|
| Breast Density Transfer CC | mammography | cyclegan | 1332x800 | OPTIMAM |  | 00014_CYCLEGAN_MMG_DENSITY_OPTIMAM_CC | Zenodo (6818103) | |

```
# create samples with this model
from medigan import Generators
Generators().generate(
    model_id="00014_CYCLEGAN_MMG_DENSITY_OPTIMAM_CC",
    input_path="models/00014_CYCLEGAN_MMG_DENSITY_OPTIMAM_CC/images",
    image_size=[1332, 800],
    gpu_id=0,
    translate_all_images=False,
    low_to_high=True,
)

# model specific parameters
inputs= [
    "input_path: default=models/00013_CYCLEGAN_MMG_DENSITY_OPTIMAM_MLO/images, help=the␣
↪path to .png mammogram images that are translated from low to high breast density or␣
↪vice versa",
    "image_size: default=[1332, 800], help=list with image height and width. Images are␣
↪rescaled to these pixel dimensions.",
    "gpu_id: default=0, help=the gpu to run the model on.",
    "translate_all_images: default=False, help=flag to override num_samples in case the␣
↪user wishes to translate all images in the specified input_path folder.",
    "low_to_high: default=True, help=if true, breast density is added. If false, it is␣
↪removed from the input image. A different generator of the cycleGAN is used based no␣
↪this flag."
]
```

### 1.2.15 00015_CYCLEGAN_MMG_DENSITY_CSAW_MLO

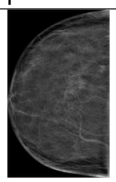
CycleGAN Model for Low-to-High Brest Density Mammograms Translation of MLO VIEW (Trained on CSAW)
**Note:** A cycle generative adversarial network (CycleGAN) that generates mammograms with high breast density from an original mammogram e.g. with low-breast density. The CycleGAN was trained using normal (without pathologies) digital mammograms from CSAW dataset (Dembrower et al., 2020, https://doi.org/10.1007/s10278-019-00278-0). The uploaded ZIP file contains the files CycleGAN_high_density.pth (model weights), **init**.py (image generation method and utils) and the GAN model architecture (in pytorch) below the /src folder.

| Output type | Modality | Model type | Output size | Base dataset | Output examples | model_id | Hosted on | Reference |
|---|---|---|---|---|---|---|---|---|
| Breast Density Transfer MLO | mammography | cycle-gan | 1332x800 | CSAW |  | 00015_CYCLEGAN_MMG_DENSITY_CSAW_MLO | Zenodo (6818105) | |

```
# create samples with this model
from medigan import Generators
Generators().generate(
    model_id="00015_CYCLEGAN_MMG_DENSITY_CSAW_MLO",
    input_path="models/00015_CYCLEGAN_MMG_DENSITY_CSAW_MLO/images",
    image_size=[1332, 800],
    gpu_id=0,
    translate_all_images=False,
    low_to_high=True,
)

# model specific parameters
inputs= [
    "input_path: default=models/00013_CYCLEGAN_MMG_DENSITY_OPTIMAM_MLO/images, help=the␣
↪path to .png mammogram images that are translated from low to high breast density or␣
↪vice versa",
    "image_size: default=[1332, 800], help=list with image height and width. Images are␣
↪rescaled to these pixel dimensions.",
    "gpu_id: default=0, help=the gpu to run the model on.",
    "translate_all_images: default=False, help=flag to override num_samples in case the␣
↪user wishes to translate all images in the specified input_path folder.",
    "low_to_high: default=True, help=if true, breast density is added. If false, it is␣
↪removed from the input image. A different generator of the cycleGAN is used based no␣
↪this flag."
]
```

### 1.2.16 00016_CYCLEGAN_MMG_DENSITY_CSAW_CC

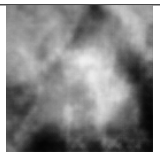
CycleGAN Model for Low-to-High Brest Density Mammograms Translation of CC VIEW (Trained on CSAW)
**Note:** A cycle generative adversarial network (CycleGAN) that generates mammograms with high breast density from an original mammogram e.g. with low-breast density. The CycleGAN was trained using normal (without pathologies) digital mammograms from CSAW dataset (Dembrower et al., 2020, https://doi.org/10.1007/s10278-019-00278-0). The uploaded ZIP file contains the files CycleGAN_high_density.pth (model weights), **init**.py (image generation method and utils) and the GAN model architecture (in pytorch) below the /src folder.

| Output type | Modality | Model type | Output size | Base dataset | Output examples | model_id | Hosted on | Reference |
|---|---|---|---|---|---|---|---|---|
| Breast Density Transfer CC | mammography | cycle-gan | 1332x800 | CSAW |  | 00016_CYCLEGAN_MMG_DENSITY_CSAW_CC | Zenodo (6818107) | |

```
# create samples with this model
from medigan import Generators
Generators().generate(
    model_id="00016_CYCLEGAN_MMG_DENSITY_CSAW_CC",
    input_path="models/00016_CYCLEGAN_MMG_DENSITY_CSAW_CC/images",
    image_size=[1332, 800],
    gpu_id=0,
    translate_all_images=False,
    low_to_high=True,
)

# model specific parameters
inputs= [
    "input_path: default=models/00013_CYCLEGAN_MMG_DENSITY_OPTIMAM_MLO/images, help=the␣
↪path to .png mammogram images that are translated from low to high breast density or␣
↪vice versa",
    "image_size: default=[1332, 800], help=list with image height and width. Images are␣
↪rescaled to these pixel dimensions.",
    "gpu_id: default=0, help=the gpu to run the model on.",
    "translate_all_images: default=False, help=flag to override num_samples in case the␣
↪user wishes to translate all images in the specified input_path folder.",
    "low_to_high: default=True, help=if true, breast density is added. If false, it is␣
↪removed from the input image. A different generator of the cycleGAN is used based no␣
↪this flag."
]
```

### 1.2.17 00017_DCGAN_XRAY_LUNG_NODULES

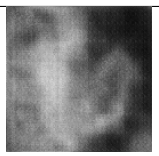
DCGAN Model for Patch Generation of Lung Nodules (Trained on Node21)
**Note:** An unconditional deep convolutional generative adversarial network (DCGAN) that generates lung nodule regions-of-interest patches based on chest xray (CXR) images. The pixel dimension of the generated patches is 128x128. The WGANGP was trained on cropped patches from CXR images from the NODE21 dataset (Sogancioglu et al, 2021). The uploaded ZIP file contains the files model.pt (model weight), **init**.py (image generation method and utils), a requirements.txt, a LICENSE file, the MEDIGAN metadata.json file, the used GAN training config file, a test.sh file to run the model, and an /image folder with a few generated example images.

| Output type | Modality | Model type | Output size | Base dataset | Output examples | model_id | Hosted on | Reference |
|---|---|---|---|---|---|---|---|---|
| Lung Nodules | chest x-ray | dcgan | 128x128 | NODE21 |  | 00017_DCGAN_XRAY_LUNG_NODULES | Zenodo (6943691) | |

```
# create samples with this model
from medigan import Generators
Generators().generate(model_id="00017_DCGAN_XRAY_LUNG_NODULES")

# model specific parameters
inputs= []
```

### 1.2.18 00018_WGANGP_XRAY_LUNG_NODULES

WGANGP Model for Patch Generation of Lung Nodules (Trained on Node21)
**Note:** An unconditional wasserstein generative adversarial network with gradient penalty (WGAN_GP) that generates lung nodule regions-of-interest patches based on chest xray (CXR) images. The pixel dimension of the generated patches is 128x128. The WGANGP was trained on cropped patches from CXR images from the NODE21 dataset (Sogancioglu et al, 2021). The uploaded ZIP file contains the files model.pt (model weight), **init**.py (image generation method and utils), a requirements.txt, a LICENSE file, the MEDIGAN metadata.json file, the used GAN training config file, a test.sh file to run the model, and an /image folder with a few generated example images.

| Output type | Modality | Model type | Output size | Base dataset | Output examples | model_id | Hosted on | Reference |
|---|---|---|---|---|---|---|---|---|
| Lung Nodules | chest x-ray | wgan-gp | 128x128 | NODE21 |  | 00018_WGANGP_XRAY_LUNG_NODULES | Zenodo (6943761) | |

```
# create samples with this model
from medigan import Generators
Generators().generate(model_id="00018_WGANGP_XRAY_LUNG_NODULES")

# model specific parameters
inputs= []
```

### 1.2.19 00019_PGGAN_CHEST_XRAY

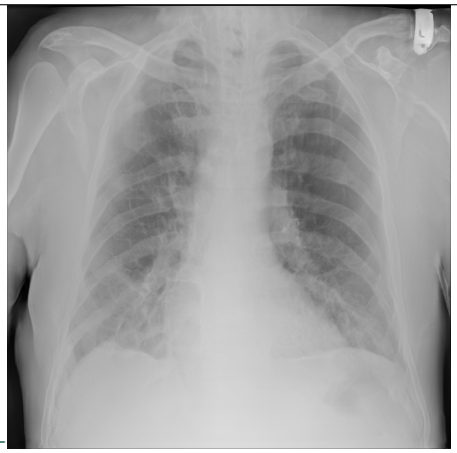
PGGAN Model for Generation of Chest XRAY (CXR) Images (Trained on ChestX-ray14 Dataset)
**Note:** An unconditional Progressively-growing generative adversarial network (PGGAN) that generates chest xray (CXR) images with pixel dimensions 1024x1024. The PGGAN was trained on CXR images from the ChestX-ray14 Dataset (Wang et al., 2017, Paper: https://arxiv.org/pdf/1705.02315.pdf, Data: https://nihcc.app.box.com/v/ChestXray-NIHCC). The uploaded ZIP file contains the files model.pt (model weight), **init**.py (image generation method and utils), a requirements.txt, a LICENSE file, the MEDIGAN metadata.json file, the used GAN training config file, a test.sh file to run the model, and an /image folder with a few generated example images.

| Output type | Modality | Model type | Output size | Base dataset | Output examples | model_id | Hosted on | Reference |
|---|---|---|---|---|---|---|---|---|
| Chest Xray Images | chest x-ray | pggan | 1024x1024 | ChestX-ray14 |  | 00019_PGGAN_CHEST_XRAY | Zenodo (6943803) | |

```
# create samples with this model
from medigan import Generators
Generators().generate(model_id="00019_PGGAN_CHEST_XRAY")

# model specific parameters
inputs= []
```

### 1.2.20 00020_PGGAN_CHEST_XRAY

PGGAN Model for Generation of Chest XRAY (CXR) Images (Trained on ChestX-ray14 Dataset)
**Note:** An unconditional Progressively-growing generative adversarial network (PGGAN) that generates chest xray (CXR) images with pixel dimensions 1024x1024. The PGGAN was trained on CXR images from the ChestX-ray14 Dataset (Wang et al., 2017, Paper: https://arxiv.org/pdf/1705.02315.pdf, Data: https://nihcc.app.box.com/v/ChestXray-NIHCC). The uploaded ZIP file contains the model weights checkpoint file, **init**.py (image generation method and utils), a requirements.txt, the MEDIGAN metadata.json file, a test.sh file to run the model, and an /image folder with a few generated example images.

| Output type | Modality | Model type | Output size | Base dataset | Output examples | model_id | Hosted on | Reference |
|---|---|---|---|---|---|---|---|---|
| Chest Xray Images | chest x-ray | pg-gan | 1024x1024 | ChestX-ray14 |  | 00020_PGGAN_CHEST_XRAY | Zenodo (7046280) | Singh et al (2021) |

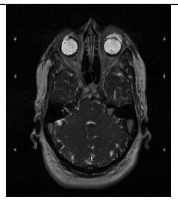
```
# create samples with this model
from medigan import Generators
Generators().generate(
    model_id="00020_PGGAN_CHEST_XRAY",
    image_size=1024,
    resize_pixel_dim=None,
)

# model specific parameters
inputs = [
    "image_size: default=1024, help=the size if height and width of the generated images
↪",
    "resize_pixel_dim: default=None, help=Resizing of generated images via the pillow␣
↪PIL image library."
]
```

### 1.2.21 00021_CYCLEGAN_BRAIN_MRI_T1_T2

CycleGAN Brain MRI T1-T2 translation (trained on CrossMoDA 2021 dataset)

**Note:** In recent years, deep learning models have considerably advanced the performance of segmentation tasks on Brain Magnetic Resonance Imaging (MRI). However, these models show a considerable performance drop when they are evaluated on unseen data from a different distribution. Since annotation is often a hard and costly task requiring expert supervision, it is necessary to develop ways in which existing models can be adapted to the unseen domains without any additional labelled information. In this work, we explore one such technique which extends the CycleGAN [2] architecture to generate label-preserving data in the target domain. The synthetic target domain data is used to train the nn-UNet [3] framework for the task of multi-label segmentation. The experiments are conducted and evaluated on the dataset [1] provided in the 'Cross-Modality Domain Adaptation for Medical Image Segmentation' challenge [23] for segmentation of vestibular schwannoma (VS) tumour and cochlea on contrast enhanced (ceT1) and high resolution (hrT2) MRI scans. In the proposed approach, our model obtains dice scores (DSC) 0.73 and 0.49 for tumour and cochlea respectively on the validation set of the dataset. This indicates the applicability of the proposed technique to

real-world problems where data may be obtained by different acquisition protocols as in [1] where hrT2 images are more reliable, safer, and lower-cost alternative to ceT1.

| Output type | Modality | Model type | Output size | Base dataset | Output examples | model_id | Hosted on | Reference |
|---|---|---|---|---|---|---|---|---|
| Brain T1-T2 MRI Modality Transfer | brain MRI | cyclegan | 224x192 | Cross-MoDA 2021 |  | 00021_CYCLEGAN_BRAIN_MRI_T1_T2 | Zenodo (7074555) | Jiahui et al (2022) |

```
# create samples with this model
from medigan import Generators
Generators().generate(
    model_id="00021_CYCLEGAN_BRAIN_MRI_T1_T2",
    input_path= "models/00021_CYCLEGAN_BRAIN_MRI_T1_T2/inputs/T1", # or /T2
    image_size=[224, 192],
    gpu_id=0,
    translate_all_images=True,
    T1_to_T2=True,
)

# model specific parameters
inputs = [
    "input_path: default=models/00021_CYCLEGAN_BRAIN_MRI_T1_T2/inputs/T1, help=the path␣
↪to .png brain MRI images that are translated from T1 to T2 or vice versa. ",
    "image_size: default=[224, 192], help=list with image height and width. ",
    "gpu_id: default=0, help=the gpu to run the model on.",
    "translate_all_images: default=False, help=flag to override num_samples in case the␣
↪user wishes to translate all images in the specified input_path folder.",
    "T1_to_T2: default=True, help=if true, generator for T1 to T2 translation is used.␣
↪If false, the translation is done from T2 to T1 instead. Need to adjust input path in␣
↪this case e.g. models/00021_CYCLEGAN_BRAIN_MRI_T1_T2/inputs/T2 instead of models/00021_
↪CYCLEGAN_BRAIN_MRI_T1_T2/inputs/T1. A different generator of the cycleGAN is used␣
↪based on this flag."
]
```

## 1.3 Code Examples

**Table of Contents**

### 1.3.1 Install

Install *medigan* library from pypi (or github).

```
pip install medigan
```

Import *medigan* and initialize Generators

```
from medigan import Generators
generators = Generators()
```

### 1.3.2 Generate Images

Generate 10 samples using one (model 1 is *00001_DCGAN_MMG_CALC_ROI*) of the medigan models from the config.

*install_dependencies* signals to medigan that the user wishes to automatically install all the python dependencies (e.g. numpy. torch, etc) required to run this model (i.e. to the user's active python environment).

```
generators.generate(model_id=1, num_samples=10, install_dependencies=True)
```

Get the model's generate method and run it to generate 3 samples

```
# model 1 is "00001_DCGAN_MMG_CALC_ROI"
gen_function = generators.get_generate_function(model_id=1, num_samples=3)
gen_function()
```

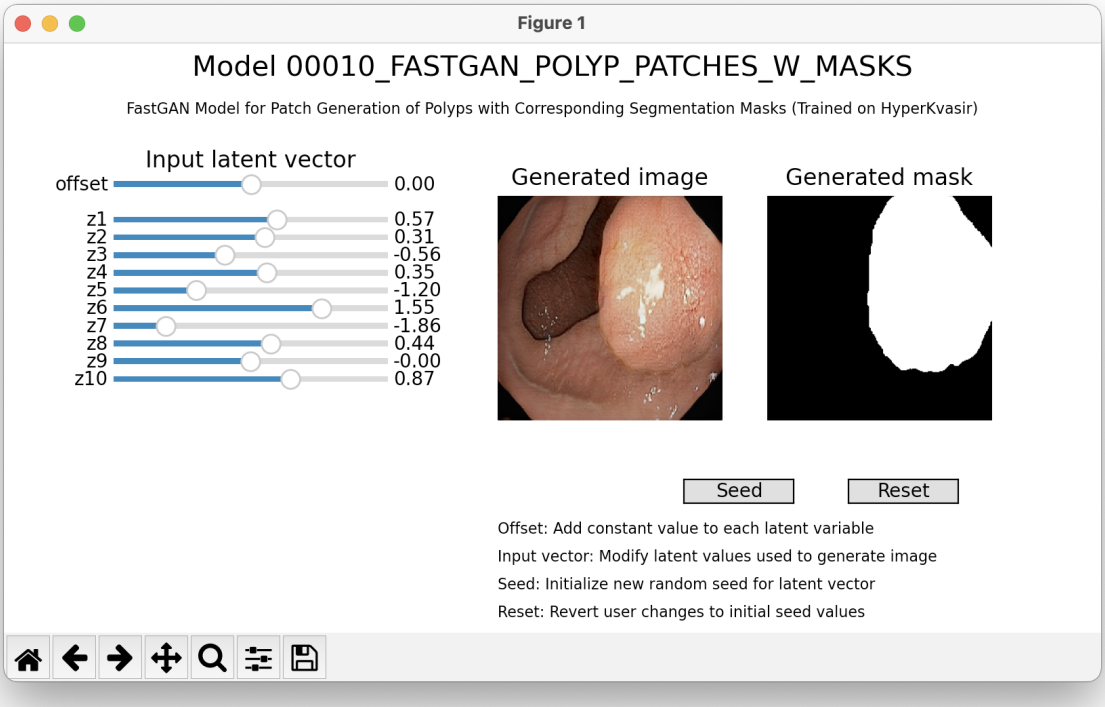
Get the model's synthetic data as torch dataloader with 3 samples

```
# model 4 is "00004_PIX2PIX_MMG_MASSES_W_MASKS"
dataloader = generators.get_as_torch_dataloader(model_id=4, num_samples=3)
```

### 1.3.3 Visualize Generative Model

Displays an interactive visual interface for exploration of applicable models.

```
# model 10 is "00010_FASTGAN_POLYP_PATCHES_W_MASKS"
generators.visualize(10)
```




### 1.3.4 Search for Generative Models

Find all models that contain a specific key-value pair in their model config.

```
key = "modality"
value = "Full-Field Mammography"
found_models = generators.get_models_by_key_value_pair(key1=key, value1=value, is_case_
↪sensitive=False)
print(found_models)
```

Create a list of search terms and find the models that have these terms in their config.

```
values_list = ['dcgan', 'Mammography', 'inbreast']
models = generators.find_matching_models_by_values(values=values_list, target_values_
↪operator='AND', are_keys_also_matched=True, is_case_sensitive=False)
print(f'Found models: {models}')
```

Create a list of search terms, find a model and generate

```
values_list = ['dcgan', 'mMg', 'ClF', 'modalities', 'inbreast']
generators.find_model_and_generate(values=values_list, target_values_operator='AND', are_
↪keys_also_matched=True, is_case_sensitive=False, num_samples=5)
```

### 1.3.5 Rank Generative Models

Rank the models by a performance metric and return ranked list of models

```
ranked_models = generators.rank_models_by_performance(metric="SSIM", order="asc")
print(ranked_models)
```

Find the models, then rank them by a performance metric and return ranked list of models

```
ranked_models = generators.find_models_and_rank(values=values_list, target_values_
↪operator='AND', are_keys_also_matched=True, is_case_sensitive=False, metric="SSIM",␣
↪order="asc")
print(ranked_models)
```

Find the models, then rank them, and then generate samples with the best ranked model.

```
generators.find_models_rank_and_generate(values=values_list, target_values_operator='AND
↪', are_keys_also_matched=True, is_case_sensitive=False, metric="SSIM", order="asc",␣
↪num_samples=5)
```

## 1.4 Modules Overview

**Table of Contents**



### 1.4.1 Generators

#### medigan.generators Module

Base class providing user-library interaction methods for config management, and model selection and execution.

## Classes

| | |
|---|---|
| ConfigManager([config_dict, ...]) | *ConfigManager* class: Downloads, loads and parses medigan's config json as dictionary. |
| DataLoader(dataset[, batch_size, shuffle, ...]) | Data loader. |
| Dataset(*args, **kwds) | An abstract class representing a Dataset. |
| Generators([config_manager, model_selector, ...]) | *Generators* class: Contains medigan's public methods to facilitate users' automated sample generation workflows. |
| ModelContributor(model_id, init_py_path) | *ModelContributor* class: Contributes a user's local model to the public medigan library |
| ModelExecutor(model_id, execution_config[, ...]) | *ModelExecutor* class: Find config links to download models, init models as python packages, run generate methods. |
| ModelSelector([config_manager]) | *ModelSelector* class: Given a config dict, gets, searches, and ranks matching models. |
| ModelVisualizer(model_executor, config) | *ModelVisualizer* class: Visualises synthetic data through a user interface. |
| SyntheticDataset(samples[, masks, ...]) | A synthetic dataset containing data generated by a model of medigan |
| Utils() | Utils class containing reusable static methods. |

## Generators

**class** medigan.generators.**Generators**(*config_manager: Optional[*medigan.config_manager.ConfigManager*] = None*, *model_selector: Optional[*medigan.select_model.model_selector.ModelSelector*] = None*, *model_executors: Optional[list] = None*, *model_contributors: Optional[list] = None*, *initialize_all_models: bool = False*)

Bases: object

*Generators* class: Contains medigan's public methods to facilitate users' automated sample generation workflows.

**Parameters**

- **config_manager** (ConfigManager) – Provides the config dictionary, based on which *model_ids* are retrieved and models are selected and executed
- **model_selector** (ModelSelector) – Provides model comparison, search, and selection based on keys/values in the selection part of the config dict
- **model_executors** (*list*) – List of initialized *ModelExecutor* instances that handle model package download, init, and sample generation
- **initialize_all_models** (*bool*) – Flag indicating, if True, that one *ModelExecutor* for each *model_id* in the config dict should be initialized triggered by creation of *Generators* class instance. Note that, if False, the *Generators* class will only initialize a *ModelExecutor* on the fly when need be i.e. when the generate method for the respective model is called.

**config_manager**

Provides the config dictionary, based on which model_ids are retrieved and models are selected and executed

**Type** *ConfigManager*

**model_selector**

Provides model comparison, search, and selection based on keys/values in the selection part of the config dict

**Type** *ModelSelector*

**model_executors**

List of initialized *ModelExecutor* instances that handle model package download, init, and sample generation

**Type** list

### Methods Summary

| | |
|---|---|
| add_all_model_executors() | Add *ModelExecutor* class instances for all models available in the config. |
| add_metadata_from_file(model_id, ...) | Read and parse the metadata of a local model, identified by *model_id*, from a metadata file in json format. |
| add_metadata_from_input(model_id, ...[, ...]) | Create a metadata dict for a local model, identified by *model_id*, given the necessary minimum metadata contents. |
| add_model_contributor(model_id[, init_py_path]) | Add a *ModelContributor* instance of this model_id to the *self.model_contributors* list. |
| add_model_executor(model_id[, ...]) | Add one *ModelExecutor* class instance corresponding to the specified *model_id*. |
| add_model_to_config(model_id, metadata[, ...]) | Adding or updating a model entry in the global metadata. |
| contribute(model_id, init_py_path, ...[, ...]) | Implements the full model contribution workflow including model metadata generation, model test, model Zenodo upload, and medigan github issue creation. |
| find_matching_models_by_values(values[, ...]) | Search for values (and keys) in model configs and return a list of each matching *ModelMatchCandidate*. |
| find_model_and_generate(values[, ...]) | Search for values (and keys) in model configs to generate samples with the found model. |
| find_model_executor_by_id(model_id) | Find and return the *ModelExecutor* instance of this model_id in the *self.model_executors* list. |
| find_models_and_rank(values[, ...]) | Search for values (and keys) in model configs, rank results and return sorted list of model dicts. |
| find_models_rank_and_generate(values[, ...]) | Search for values (and keys) in model configs, rank results to generate samples with highest ranked model. |
| generate(model_id[, num_samples, ...]) | Generate samples with the model corresponding to the *model_id* or return the model's generate function. |
| get_as_torch_dataloader([dataset, model_id, ...]) | Get torch Dataloader sampling synthetic data from medigan model. |
| get_as_torch_dataset(model_id[, ...]) | Get synthetic data in a torch Dataset for specified medigan model. |
| get_config_by_id(model_id[, config_key]) | Get and return the part of the config below a *config_key* for a specific *model_id*. |
| get_generate_function(model_id[, ...]) | Return the model's generate function. |

continues on next page

Table 1 – continued from previous page

| | |
|---|---|
| get_model_contributor_by_id(model_id) | Find and return the *ModelContributor* instance of this model_id in the *self.model_contributors* list. |
| get_model_executor(model_id[, ...]) | Add and return the *ModelExecutor* instance of this model_id from the *self.model_executors* list. |
| get_models_by_key_value_pair(key1, value1[, ...]) | Get and return a list of model_id dicts that contain the specified key value pair in their selection config. |
| get_selection_criteria_by_id(model_id[, ...]) | Get and return the selection config dict for a specific model_id. |
| get_selection_criteria_by_ids([model_ids, ...]) | Get and return a list of selection config dicts for each of the specified model_ids. |
| get_selection_keys([model_id]) | Get and return all first level keys from the selection config dict for a specific model_id. |
| get_selection_values_for_key(key[, model_id]) | Get and return the value of a specified key of the selection dict in the config for a specific model_id. |
| is_model_executor_already_added(model_id) | Check whether the *ModelExecutor* instance of this model_id is already in *self.model_executors* list. |
| is_model_metadata_valid(model_id, metadata) | Checking if a model's corresponding metadata is valid. |
| list_models() | Return the list of model_ids as strings based on config. |
| push_to_github(model_id, github_access_token) | Upload the model's metadata inside a github issue to the medigan github repository. |
| push_to_zenodo(model_id, zenodo_access_token) | Upload the model files as zip archive to a public Zenodo repository where the model will be persistently stored. |
| rank_models_by_performance([model_ids, ...]) | Rank model based on a provided metric and return sorted list of model dicts. |
| test_model(model_id[, is_local_model, ...]) | Test if a model generates and returns a specific number of samples in the correct format |
| visualize(model_id[, slider_grouper, ...]) | Initialize and run *ModelVisualizer* of this model_id if it is available. |

### Methods Documentation

**add_all_model_executors**()

Add *ModelExecutor* class instances for all models available in the config.

**Return type** None

**add_metadata_from_file**(*model_id: str*, *metadata_file_path: str*) → dict

Read and parse the metadata of a local model, identified by *model_id*, from a metadata file in json format.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **metadata_file_path** (*str*) – the path pointing to the metadata file

**Returns** Returns a dict containing the contents of parsed metadata json file.

**Return type** dict

**add_metadata_from_input**(*model_id: str*, *model_weights_name: str*, *model_weights_extension: str*, *generate_method_name: str*, *dependencies: list*, *fill_more_fields_interactively: bool = True*, *output_path: str = 'config'*) → dict

Create a metadata dict for a local model, identified by *model_id*, given the necessary minimum metadata contents.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **model_weights_name** (*str*) – the name of the checkpoint file containing the model's weights
- **model_weights_extension** (*str*) – the extension (e.g. .pt) of the checkpoint file containing the model's weights
- **generate_method_name** (*str*) – the name of the sample generation method inside the models __init__.py file
- **dependencies** (*list*) – the list of dependencies that need to be installed via pip to run the model
- **fill_more_fields_interactively** (*bool*) – flag indicating whether a user will be interactively asked via command line for further input to fill out missing metadata content
- **output_path** (*str*) – the path where the created metadata json file will be stored

**Returns** Returns a dict containing the contents of the metadata json file.

**Return type** dict

**add_model_contributor**(*model_id: str*, *init_py_path: Optional[str] = None*) → *medigan.contribute_model.model_contributor.ModelContributor*

Add a *ModelContributor* instance of this model_id to the *self.model_contributors* list.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **init_py_path** (*str*) – The path to the local model's __init__.py file needed for importing and running this model.

**Returns** *ModelContributor* class instance corresponding to the *model_id*

**Return type** *ModelContributor*

**add_model_executor**(*model_id: str*, *install_dependencies: bool = False*)

Add one *ModelExecutor* class instance corresponding to the specified *model_id*.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **install_dependencies** (*bool*) – flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.

**Return type** None

**add_model_to_config**(*model_id: str*, *metadata: dict*, *is_local_model: Optional[bool] = None*, *overwrite_existing_metadata: bool = False*, *store_new_config: bool = True*) → bool

Adding or updating a model entry in the global metadata.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **metadata** (*dict*) – The model's corresponding metadata

- **is_local_model** (*bool*) – flag indicating whether the tested model is a new local user model i.e not yet part of medigan's official models
- **overwrite_existing_metadata** (*bool*) – in case of *is_local_model*, flag indicating whether existing metadata for this model in medigan's *config/global.json* should be overwritten.
- **store_new_config** (*bool*) – flag indicating whether the current model metadata should be stored on disk i.e. in config/

**Returns** Flag indicating whether model metadata update was successfully concluded

**Return type** bool

**contribute**(*model_id: str*, *init_py_path: str*, *github_access_token: str*, *zenodo_access_token: str*, *metadata_file_path: Optional[str] = None*, *model_weights_name: Optional[str] = None*, *model_weights_extension: Optional[str] = None*, *generate_method_name: Optional[str] = None*, *dependencies: Optional[list] = None*, *fill_more_fields_interactively: bool = True*, *overwrite_existing_metadata: bool = False*, *output_path: str = 'config'*, *creator_name: str = 'unknown name'*, *creator_affiliation: str = 'unknown affiliation'*, *model_description: str = ''*, *install_dependencies: bool = False*)

Implements the full model contribution workflow including model metadata generation, model test, model Zenodo upload, and medigan github issue creation.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **init_py_path** (*str*) – The path to the local model's __init__.py file needed for importing and running this model.
- **github_access_token** (*str*) – a personal access token linked to your github user account, used as means of authentication
- **zenodo_access_token** (*str*) – a personal access token in Zenodo linked to a user account for authentication
- **metadata_file_path** (*str*) – the path pointing to the metadata file
- **model_weights_name** (*str*) – the name of the checkpoint file containing the model's weights
- **model_weights_extension** (*str*) – the extension (e.g. .pt) of the checkpoint file containing the model's weights
- **generate_method_name** (*str*) – the name of the sample generation method inside the models __init__.py file
- **dependencies** (*list*) – the list of dependencies that need to be installed via pip to run the model
- **fill_more_fields_interactively** (*bool*) – flag indicating whether a user will be interactively asked via command line for further input to fill out missing metadata content
- **overwrite_existing_metadata** (*bool*) – flag indicating whether existing metadata for this model in medigan's *config/global.json* should be overwritten.
- **output_path** (*str*) – the path where the created metadata json file will be stored
- **creator_name** (*str*) – the creator name that will appear on the corresponding github issue
- **creator_affiliation** (*str*) – the creator affiliation that will appear on the corresponding github issue

- **model_description** (*list*) – the model_description that will appear on the corresponding github issue
- **install_dependencies** (*bool*) – flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.

**Returns** Returns the url pointing to the corresponding issue on github

**Return type** str

**find_matching_models_by_values**(*values: list*, *target_values_operator: str = 'AND'*, *are_keys_also_matched: bool = False*, *is_case_sensitive: bool = False*) → list

Search for values (and keys) in model configs and return a list of each matching *ModelMatchCandidate*.

This function calls an identically named function in a *ModelSelector* instance.

**Parameters**

- **values** (*list*) – list of values used to search and find models corresponding to these *values*
- **target_values_operator** (*str*) – the operator indicating the relationship between *values* in the evaluation of model search results. Should be either "AND", "OR", or "XOR".
- **are_keys_also_matched** (*bool*) – flag indicating whether, apart from values, the keys in the model config should also be searchable
- **is_case_sensitive** (*bool*) – flag indicating whether the search for values (and) keys in the model config should be case-sensitive.

**Returns** a list of *ModelMatchCandidate* class instances each of which was successfully matched against the search values.

**Return type** list

**find_model_and_generate**(*values: list*, *target_values_operator: str = 'AND'*, *are_keys_also_matched: bool = False*, *is_case_sensitive: bool = False*, *num_samples: int = 30*, *output_path: Optional[str] = None*, *is_gen_function_returned: bool = False*, *install_dependencies: bool = False*, ***kwargs*)

Search for values (and keys) in model configs to generate samples with the found model.

Note that the number of found models should be ==1. Else no samples will be generated and a error is logged to console.

**Parameters**

- **values** (*list*) – list of values used to search and find models corresponding to these *values*
- **target_values_operator** (*str*) – the operator indicating the relationship between *values* in the evaluation of model search results. Should be either "AND", "OR", or "XOR".
- **are_keys_also_matched** (*bool*) – flag indicating whether, apart from values, the keys in the model config should also be searchable
- **is_case_sensitive** (*bool*) – flag indicating whether the search for values (and) keys in the model config should be case-sensitive.
- **num_samples** (*int*) – the number of samples that will be generated
- **output_path** (*str*) – the path as str to the output folder where the generated samples will be stored

- **is_gen_function_returned** (*bool*) – flag indicating whether, instead of generating samples, the sample generation function will be returned
- **install_dependencies** (*bool*) – flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.
- ****kwargs** – arbitrary number of keyword arguments passed to the model's sample generation function

**Returns** However, if *is_gen_function_returned* is True, it returns the internal generate function of the model.

**Return type** None

**find_model_executor_by_id**(*model_id: str*) → *medigan.execute_model.model_executor.ModelExecutor*

Find and return the *ModelExecutor* instance of this model_id in the *self.model_executors* list.

**Parameters** **model_id** (*str*) – The generative model's unique id

**Returns** *ModelExecutor* class instance corresponding to the *model_id*

**Return type** *ModelExecutor*

**find_models_and_rank**(*values: list*, *target_values_operator: str = 'AND'*, *are_keys_also_matched: bool = False*, *is_case_sensitive: bool = False*, *metric: str = 'SSIM'*, *order: str = 'asc'*) → list

Search for values (and keys) in model configs, rank results and return sorted list of model dicts.

This function calls an identically named function in a *ModelSelector* instance.

**Parameters**

- **values** (*list`*) – list of values used to search and find models corresponding to these *values*
- **target_values_operator** (*str*) – the operator indicating the relationship between *values* in the evaluation of model search results. Should be either "AND", "OR", or "XOR".
- **are_keys_also_matched** (*bool*) – flag indicating whether, apart from values, the keys in the model config should also be searchable
- **is_case_sensitive** (*bool*) – flag indicating whether the search for values (and) keys in the model config should be case-sensitive.
- **metric** (*str*) – The key in the selection dict that corresponds to the metric of interest
- **order** (*str*) – the sorting order of the ranked results. Should be either "asc" (ascending) or "desc" (descending)

**Returns** a list of the searched and matched model dictionaries containing metric and model_id, sorted by metric.

**Return type** list

**find_models_rank_and_generate**(*values: list*, *target_values_operator: str = 'AND'*, *are_keys_also_matched: bool = False*, *is_case_sensitive: bool = False*, *metric: str = 'SSIM'*, *order: str = 'asc'*, *num_samples: int = 30*, *output_path: Optional[str] = None*, *is_gen_function_returned: bool = False*, *install_dependencies: bool = False*, ***kwargs*)

Search for values (and keys) in model configs, rank results to generate samples with highest ranked model.

**Parameters**

- **values** (*list*) – list of values used to search and find models corresponding to these *values*
- **target_values_operator** (*str*) – the operator indicating the relationship between *values* in the evaluation of model search results. Should be either "AND", "OR", or "XOR".
- **are_keys_also_matched** (*bool*) – flag indicating whether, apart from values, the keys in the model config should also be searchable
- **is_case_sensitive** (*bool*) – flag indicating whether the search for values (and) keys in the model config should be case-sensitive.
- **metric** (*str*) – The key in the selection dict that corresponds to the metric of interest
- **order** (*str*) – the sorting order of the ranked results. Should be either "asc" (ascending) or "desc" (descending)
- **num_samples** (*int*) – the number of samples that will be generated
- **output_path** (*str*) – the path as str to the output folder where the generated samples will be stored
- **is_gen_function_returned** (*bool*) – flag indicating whether, instead of generating samples, the sample generation function will be returned
- **install_dependencies** (*bool*) – flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.
- ****kwargs** – arbitrary number of keyword arguments passed to the model's sample generation function

**Returns** However, if *is_gen_function_returned* is True, it returns the internal generate function of the model.

**Return type** None

**generate**(*model_id: str*, *num_samples: int = 30*, *output_path: Optional[str] = None*, *save_images: bool = True*, *is_gen_function_returned: bool = False*, *install_dependencies: bool = False*, ***kwargs*)

Generate samples with the model corresponding to the *model_id* or return the model's generate function.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **num_samples** (*int*) – the number of samples that will be generated
- **output_path** (*str*) – the path as str to the output folder where the generated samples will be stored
- **save_images** (*bool*) – flag indicating whether generated samples are returned (i.e. as list of numpy arrays) or rather stored in file system (i.e in *output_path*)
- **is_gen_function_returned** (*bool*) – flag indicating whether, instead of generating samples, the sample generation function will be returned
- **install_dependencies** (*bool*) – flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.
- ****kwargs** – arbitrary number of keyword arguments passed to the model's sample generation function

**Returns** Returns images as list of numpy arrays if *save_images* is False. However, if *is_gen_function_returned* is True, it returns the internal generate function of the model.

**Return type** list

**get_as_torch_dataloader**(*dataset=None*, *model_id: Optional[str] = None*, *num_samples: int = 1000*, *install_dependencies: bool = False*, *transform=None*, *batch_size=1*, *shuffle=False*, *sampler=None*, *batch_sampler=None*, *num_workers=0*, *collate_fn=None*, *pin_memory=False*, *drop_last=False*, *timeout=0*, *worker_init_fn=None*, *prefetch_factor=2*, *persistent_workers=False*, ***kwargs*) → torch.utils.data.dataloader.DataLoader

Get torch Dataloader sampling synthetic data from medigan model.

Dataloader combines a dataset and a sampler, and provides an iterable over the given torch dataset. Dataloader is created for synthetic data for the specified medigan model.

**Parameters**

- **dataset** (*Dataset*) – dataset from which to load the data.
- **model_id** – str The generative model's unique id
- **num_samples** – int the number of samples that will be generated
- **install_dependencies** – bool flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.
- ****kwargs** – arbitrary number of keyword arguments passed to the model's sample generation function (e.g. the input path for image-to-image translation models in medigan).
- **transform** – the torch data transformation functions to be applied to the data in the dataset.
- **batch_size** (*int, optional*) – how many samples per batch to load (default: 1).
- **shuffle** (*bool, optional*) – set to True to have the data reshuffled at every epoch (default: False).
- **sampler** (*Sampler or Iterable, optional*) – defines the strategy to draw samples from the dataset. Can be any Iterable with __len__ implemented. If specified, shuffle must not be specified.
- **batch_sampler** (*Sampler or Iterable, optional*) – like sampler, but returns a batch of indices at a time. Mutually exclusive with batch_size, shuffle, sampler, and drop_last.
- **num_workers** (*int, optional*) – how many subprocesses to use for data loading. 0 means that the data will be loaded in the main process. (default: 0)
- **collate_fn** (*callable, optional*) – merges a list of samples to form a mini-batch of Tensor(s). Used when using batched loading from a map-style dataset.
- **pin_memory** (*bool, optional*) – If True, the data loader will copy Tensors into CUDA pinned memory before returning them. If your data elements are a custom type, or your collate_fn returns a batch that is a custom type, see the example below.
- **drop_last** (*bool, optional*) – set to True to drop the last incomplete batch, if the dataset size is not divisible by the batch size. If False and the size of dataset is not divisible by the batch size, then the last batch will be smaller. (default: False)
- **timeout** (*numeric, optional*) – if positive, the timeout value for collecting a batch from workers. Should always be non-negative. (default: 0)
- **worker_init_fn** (*callable, optional*) – If not None, this will be called on each worker subprocess with the worker id (an int in [0, num_workers - 1]) as input, after seeding and before data loading. (default: None)

- **prefetch_factor** (*int, optional, keyword-only arg*) – Number of samples loaded in advance by each worker. 2 means there will be a total of 2 * num_workers samples prefetched across all workers. (default: 2)
- **persistent_workers** (*bool, optional*) – If True, the data loader will not shutdown the worker processes after a dataset has been consumed once. This allows to maintain the workers *Dataset* instances alive. (default: False)

**Returns** a torch.utils.data.DataLoader object with data generated by model corresponding to inputted *Dataset* or *model_id*.

**Return type** DataLoader

**get_as_torch_dataset**(*model_id: str*, *num_samples: int = 100*, *install_dependencies: bool = False*, *transform=None*, ***kwargs*) → torch.utils.data.dataset.Dataset

Get synthetic data in a torch Dataset for specified medigan model.

The dataset returns a dict with keys sample (== image), labels (== condition), and mask (== segmentation mask). While key 'sample' is mandatory, the other key value pairs are only returned if applicable to generative model.

**Parameters**

- **model_id** – str The generative model's unique id
- **num_samples** – int the number of samples that will be generated
- **install_dependencies** –

  **bool** flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.

  **transform** the torch data transformation functions to be applied to the data in the dataset.
- ****kwargs** – arbitrary number of keyword arguments passed to the model's sample generation function (e.g. the input path for image-to-image translation models in medigan).

**Returns** a torch.utils.data.Dataset object with data generated by model corresponding to *model_id*.

**Return type** Dataset

**get_config_by_id**(*model_id: str*, *config_key: Optional[str] = None*) → dict

Get and return the part of the config below a *config_key* for a specific *model_id*.

The config_key parameters can be separated by a '.' (dot) to allow for retrieval of nested config keys, e.g, 'execution.generator.name'

This function calls an identically named function in a *ConfigManager* instance.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **config_key** (*str*) – A key of interest present in the config dict

**Returns** a dictionary from the part of the config file corresponding to *model_id* and *config_key*.

**Return type** dict

**get_generate_function**(*model_id: str*, *num_samples: int = 30*, *output_path: Optional[str] = None*, *install_dependencies: bool = False*, ***kwargs*)

Return the model's generate function.

Relies on the *self.generate* function.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **num_samples** (*int*) – the number of samples that will be generated
- **output_path** (*str*) – the path as str to the output folder where the generated samples will be stored
- **install_dependencies** (*bool*) – flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.
- ****kwargs** – arbitrary number of keyword arguments passed to the model's sample generation function

**Returns** The internal reusable generate function of the generative model.

**Return type** function

**get_model_contributor_by_id**(*model_id: str*) → *medigan.contribute_model.model_contributor.ModelContributor*

Find and return the *ModelContributor* instance of this model_id in the *self.model_contributors* list.

**Parameters** **model_id** (*str*) – The generative model's unique id

**Returns** *ModelContributor* class instance corresponding to the *model_id*

**Return type** *ModelContributor*

**get_model_executor**(*model_id: str*, *install_dependencies: bool = False*) → *medigan.execute_model.model_executor.ModelExecutor*

Add and return the *ModelExecutor* instance of this model_id from the *self.model_executors* list.

Relies on *self.add_model_executor* and *self.find_model_executor_by_id* functions.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **install_dependencies** (*bool*) – flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.

**Returns** *ModelExecutor* class instance corresponding to the *model_id*

**Return type** *ModelExecutor*

**get_models_by_key_value_pair**(*key1: str*, *value1: str*, *is_case_sensitive: bool = False*) → list

Get and return a list of model_id dicts that contain the specified key value pair in their selection config.

The key param can contain '.' (dot) separations to allow for retrieval of nested config keys such as 'execution.generator.name'

This function calls an identically named function in a *ModelSelector* instance.

**Parameters**

- **key1** (*str*) – The key in the selection dict
- **value1** (*str*) – The value in the selection dict that corresponds to key1
- **is_case_sensitive** (*bool*) – flag to evaluate keys and values with case sensitivity if set to True

**Returns** a list of the dictionaries each containing a models id and the found key-value pair in the models config

**Return type** list

**get_selection_criteria_by_id**(*model_id: str*, *is_model_id_removed: bool = True*) → dict

Get and return the selection config dict for a specific model_id.

This function calls an identically named function in a *ModelSelector* instance.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **is_model_id_removed** (*bool*) – flag to to remove the model_ids from first level of dictionary.

**Returns** a dictionary corresponding to the selection config of a model

**Return type** dict

**get_selection_criteria_by_ids**(*model_ids: Optional[list] = None*, *are_model_ids_removed: bool = True*) → list

Get and return a list of selection config dicts for each of the specified model_ids.

This function calls an identically named function in a *ModelSelector* instance.

**Parameters**

- **model_ids** (*list*) – A list of generative models' unique ids or ids abbreviated as integers (e.g. 1, 2, .. 21)
- **are_model_ids_removed** (*bool*) – flag to remove the model_ids from first level of dictionary.

**Returns** a list of dictionaries each corresponding to the selection config of a model

**Return type** list

**get_selection_keys**(*model_id: Optional[str] = None*) → list

Get and return all first level keys from the selection config dict for a specific model_id.

This function calls an identically named function in a *ModelSelector* instance.

**Parameters** **model_id** (*str*) – The generative model's unique id

**Returns** a list containing the keys as strings of the selection config of the *model_id*.

**Return type** list

**get_selection_values_for_key**(*key: str*, *model_id: Optional[str] = None*) → list

Get and return the value of a specified key of the selection dict in the config for a specific model_id.

The key param can contain '.' (dot) separations to allow for retrieval of nested config keys such as 'execution.generator.name'

This function calls an identically named function in a *ModelSelector* instance.

**Parameters**

- **key** (*str*) – The key in the selection dict
- **model_id** (*str*) – The generative model's unique id

**Returns** a list of the values that correspond to the key in the selection config of the *model_id*.

**Return type** list

**is_model_executor_already_added**(*model_id*) → bool

Check whether the *ModelExecutor* instance of this model_id is already in *self.model_executors* list.

**Parameters** **model_id** (*str*) – The generative model's unique id

**Returns** indicating whether this *ModelExecutor* had been already previously added to *self.model_executors*

**Return type** bool

**is_model_metadata_valid**(*model_id: str*, *metadata: dict*, *is_local_model: bool = True*) → bool

Checking if a model's corresponding metadata is valid.

Specific fields in the model's metadata are mandatory. It is asserted if these key value pairs are present.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **metadata** (*dict*) – The model's corresponding metadata
- **is_local_model** (*bool*) – flag indicating whether the tested model is a new local user model i.e not yet part of medigan's official models

**Returns** Flag indicating whether the specific model's metadata format and fields are valid

**Return type** bool

**list_models**() → list

Return the list of model_ids as strings based on config.

**Return type** list

**push_to_github**(*model_id: str*, *github_access_token: str*, *package_link: Optional[str] = None*, *creator_name: str = ''*, *creator_affiliation: str = ''*, *model_description: str = ''*)

Upload the model's metadata inside a github issue to the medigan github repository.

To add your model to medigan, your metadata will be reviewed on Github and added to medigan's official model metadata

The medigan repository issues page: https://github.com/RichardObi/medigan/issues

Get your Github access token here: https://github.com/settings/tokens

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **github_access_token** (*str*) – a personal access token linked to your github user account, used as means of authentication
- **package_link** – a package link
- **creator_name** (*str*) – the creator name that will appear on the corresponding github issue
- **creator_affiliation** (*str*) – the creator affiliation that will appear on the corresponding github issue
- **model_description** (*list*) – the model_description that will appear on the corresponding github issue

**Returns** Returns the url pointing to the corresponding issue on github

**Return type** str

**push_to_zenodo**(*model_id: str*, *zenodo_access_token: str*, *creator_name: str = 'unknown name'*, *creator_affiliation: str = 'unknown affiliation'*, *model_description: str = ''*) → str

Upload the model files as zip archive to a public Zenodo repository where the model will be persistently stored.

Get your Zenodo access token here: https://zenodo.org/account/settings/applications/tokens/new/ (Enable scopes *deposit:actions* and *deposit:write*)

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **zenodo_access_token** (*str*) – a personal access token in Zenodo linked to a user account for authentication
- **creator_name** (*str*) – the creator name that will appear on the corresponding Zenodo model upload homepage
- **creator_affiliation** (*str*) – the creator affiliation that will appear on the corresponding Zenodo model upload homepage
- **model_description** (*list*) – the model_description that will appear on the corresponding Zenodo model upload homepage

**Returns** Returns the url pointing to the corresponding Zenodo model upload homepage

**Return type** str

**rank_models_by_performance**(*model_ids: Optional[list] = None*, *metric: str = 'SSIM'*, *order: str = 'asc'*) → list

Rank model based on a provided metric and return sorted list of model dicts.

The metric param can contain '.' (dot) separations to allow for retrieval of nested metric config keys such as 'downstream_task.CLF.accuracy'

This function calls an identically named function in a *ModelSelector* instance.

**Parameters**

- **model_ids** (*list*) – only evaluate the *model_ids* in this list. If none, evaluate all available *model_ids*
- **metric** (*str*) – The key in the selection dict that corresponds to the metric of interest
- **order** (*str*) – the sorting order of the ranked results. Should be either "asc" (ascending) or "desc" (descending)

**Returns** a list of model dictionaries containing metric and *model_id*, sorted by metric.

**Return type** list

**test_model**(*model_id: str*, *is_local_model: bool = True*, *overwrite_existing_metadata: bool = False*, *store_new_config: bool = True*, *num_samples: int = 3*, *install_dependencies: bool = False*)

Test if a model generates and returns a specific number of samples in the correct format

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **is_local_model** (*bool*) – flag indicating whether the tested model is a new local user model i.e not yet part of medigan's official models
- **overwrite_existing_metadata** (*bool*) – in case of *is_local_model*, flag indicating whether existing metadata for this model in medigan's *config/global.json* should be overwritten.

- **store_new_config** (*bool*) – flag indicating whether the current model metadata should be stored on disk i.e. in config/
- **num_samples** (*int*) – the number of samples that will be generated
- **install_dependencies** (*bool*) – flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.

**visualize**(*model_id: str*, *slider_grouper: int = 10*, *auto_close: bool = False*, *install_dependencies: bool = False*) → None

Initialize and run *ModelVisualizer* of this model_id if it is available. It allows to visualize a sample from the model's output. UI window will pop up allowing the user to control the generation parameters (conditional and unconditional ones).

**Parameters**

- **model_id** (*str*) – The generative model's unique id to visualize.
- **slider_grouper** (*int*) – Number of input parameters to group together within one slider.
- **auto_close** (*bool*) – Flag for closing the user interface automatically after time. Used while testing.
- **install_dependencies** (*bool*) – flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.

### 1.4.2 ModelExecutor

#### medigan.execute_model.model_executor Module

Model executor class that downloads models, loads them as python packages, and runs their generate functions.

#### Classes

| | |
|---|---|
| *ModelExecutor*(model_id, execution_config[, ...]) | *ModelExecutor* class: Find config links to download models, init models as python packages, run generate methods. |
| Path(*args, **kwargs) | PurePath subclass that can make system calls. |
| Utils() | Utils class containing reusable static methods. |
| tqdm(*_, **__) | Decorate an iterable object, returning an iterator which acts exactly like the original iterable, but prints a dynamically updating progressbar every time a value is requested. |

### ModelExecutor

class medigan.execute_model.model_executor.**ModelExecutor**(*model_id: str*, *execution_config: dict*, *download_package: bool = True*, *install_dependencies: bool = False*)

Bases: object

*ModelExecutor* class: Find config links to download models, init models as python packages, run generate methods.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **execution_config** (*dict*) – The part of the config below the 'execution' key
- **download_package** (*bool*) – Flag indicating, if True, that the model's package should be downloaded instead of using an existing one that was downloaded previously
- **install_dependencies** (*bool*) – flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.

**model_id**

The generative model's unique id

**Type** str

**execution_config**

The part of the config below the 'execution' key

**Type** dict

**download_package**

Flag indicating, if True, that the model's package should be downloaded instead of using an existing one that was downloaded previously

**Type** bool

**image_size**

Pixel dimension of the generated samples, where images are assumed to have the same width and height

**Type** int

**dependencies**

List of the dependencies of a models python package.

**Type** list

**model_name**

Name of the generative model

**Type** str

**model_extension**

File extension of the generative model's weights file.

**Type** str

**package_name**

Name of the model's python package i.e. the name of the model's zip file and unzipped package folder

**Type** str

**package_link**

The link to the zipped model package. Note: Convention is to host models on Zenodo (reason: static doi content)

**Type** str

**generate_method_name**

The name of the model's generate method inside the model package. This method is called to generate samples.

**Type** str

**generate_method_args**

The args of the model's generate method inside the model package

**Type** dict

**serialised_model_file_path**

Path as string to the generative model's weights file

**Type** str

**package_path**

Path as string to the generative model's python package containing an *__init__.py* file

**Type** str

**deserialized_model_as_lib**

The generative model's package imported as python library. Generate method inside this library can be called.

### Methods Summary

| | |
|---|---|
| *generate*([num_samples, output_path, ...]) | Generate samples using the generative model or return the model's generate function. |
| *is_model_already_unpacked*() | Check if a valid path to the model files exists and, if so, set the *package_path* |

### Methods Documentation

**generate**(*num_samples: int = 20*, *output_path: Optional[str] = None*, *save_images: bool = True*, *is_gen_function_returned: bool = False*, *batch_size: int = 32*, ***kwargs*)

Generate samples using the generative model or return the model's generate function.

The name amd additional parameters of the generate function of the respective generative model are retrieved from the model's *execution_config*.

**Parameters**

- **num_samples** (*int*) – the number of samples that will be generated
- **output_path** (*str*) – the path as str to the output folder where the generated samples will be stored
- **save_images** (*bool*) – flag indicating whether generated samples are returned (i.e. as list of numpy arrays) or rather stored in file system (i.e in *output_path*)

- **is_gen_function_returned** (*bool*) – flag indicating whether, instead of generating samples, the sample generation function will be returned
- **batch_size** (*int*) – the batch size for the sample generation function
- ****kwargs** – arbitrary number of keyword arguments passed to the model's sample generation function

**Returns** Returns images as list of numpy arrays if *save_images* is False. However, if *is_gen_function_returned* is True, it returns the internal generate function of the model.

**Return type** list

**Raises** **Exception** – If the generate method of the model does not exist, cannot be called, or is called with missing params, or if the sample generation inside the model package returns an exception.

**is_model_already_unpacked**() → bool

Check if a valid path to the model files exists and, if so, set the *package_path*

### 1.4.3 ModelVisualizer

#### medigan.model_visualizer Module

*ModelVisualizer* class providing visualizing corresponding model input and model output changes.

#### Classes

| | |
|---|---|
| Button(ax, label[, image, color, hovercolor]) | A GUI neutral button. |
| *ModelVisualizer*(model_executor, config) | *ModelVisualizer* class: Visualises synthetic data through a user interface. |
| Slider(ax, label, valmin, valmax[, valinit, ...]) | A slider representing a floating point range. |

#### ModelVisualizer

**class** medigan.model_visualizer.**ModelVisualizer**(*model_executor*, *config: None*)

Bases: object

*ModelVisualizer* class: Visualises synthetic data through a user interface. Depending on a model, it is possible to control the input latent vector values and conditional input.

**Parameters**

- **model_executor** (ModelExecutor) – The generative model's executor object
- **config** (*dict*) – The config dict containing the model metadata

**model_executor**

The generative model's executor object

**Type** *ModelExecutor*

**input_latent_vector_size**

Size of the latent vector used as an input for generation

**Type** int

**conditional**

Flag for models with conditional input

**Type** bool

**condition**

Value of the conditinal input to the model

**Type** Union[int, float]

**max_input_value**

Absolute value used for setting latent values input range

**Type** float

#### Methods Summary

| | |
|---|---|
| *visualize*([slider_grouper, auto_close]) | Visualize the model's output. |

#### Methods Documentation

**visualize**(*slider_grouper: int = 10*, *auto_close=False*)

Visualize the model's output. This method is called by the user. It opens up a user interface with available controls.

**Parameters**

- **slider_grouper** (*int*) – Number of input parameters to group together within one slider.
- **auto_close** (*bool*) – Flag for closing the user interface automatically after time. Used while testing.

**Return type** None

### 1.4.4 ModelSelector

#### medigan.select_model.model_selector Module

Model selection class that describes, finds, compares, and ranks generative models.

### Classes

| | |
|---|---|
| ConfigManager([config_dict, ...]) | *ConfigManager* class: Downloads, loads and parses medigan's config json as dictionary. |
| MatchedEntry(key, value[, matching_element]) | *MatchedEntry* class: One target key-value pair that matches with a model's selection config. |
| ModelMatchCandidate(model_id, target_values) | *ModelMatchCandidate* class: A prospectively matching model given the target values as model search params. |
| *ModelSelector*([config_manager]) | *ModelSelector* class: Given a config dict, gets, searches, and ranks matching models. |
| Utils() | Utils class containing reusable static methods. |

### ModelSelector

**class** medigan.select_model.model_selector.**ModelSelector**(*config_manager: Optional[*medigan.config_manager.ConfigManager*] = None*)

Bases: object

*ModelSelector* class: Given a config dict, gets, searches, and ranks matching models.

**Parameters** **config_manager** (ConfigManager) – Provides the config dictionary, based on which models are selected and compared.

**config_manager**

Provides the config dictionary, based on which models are selected and compared.

**Type** *ConfigManager*

**model_selection_dicts**

Contains a dictionary for each model id that consists of the *model_id* and the selection config of that model

**Type** list

### Methods Summary

| | |
|---|---|
| *find_matching_models_by_values*(values[, ...]) | Search for values (and keys) in model configs and return a list of each matching *ModelMatchCandidate*. |
| *find_models_and_rank*(values[, ...]) | Search for values (and keys) in model configs, rank results and return sorted list of model dicts. |
| *get_models_by_key_value_pair*(key1, value1[, ...]) | Get and return a list of *model_id* dicts that contain the specified key value pair in their selection config. |
| *get_selection_criteria_by_id*(model_id[, ...]) | Get and return the selection config dict for a specific *model_id*. |
| *get_selection_criteria_by_ids*([model_ids, ...]) | Get and return a list of selection config dicts for each of the specified *model_ids*. |
| *get_selection_keys*([model_id]) | Get and return all first level keys from the selection config dict for a specific *model_id*. |
| *get_selection_values_for_key*(key[, model_id]) | Get and return the value of a specified key of the selection dict in the config for a specific *model_id*. |
| *rank_models_by_performance*([model_ids, ...]) | Rank model based on a provided metric and return sorted list of model dicts. |
| *recursive_search_for_values*(search_dict, ...) | Do a recursive search to match values in the *search_dict* with values (and keys) in a model's config. |

### Methods Documentation

**find_matching_models_by_values**(*values: list*, *target_values_operator: str = 'AND'*, *are_keys_also_matched: bool = False*, *is_case_sensitive: bool = False*) → list

Search for values (and keys) in model configs and return a list of each matching *ModelMatchCandidate*.

Uses *self.recursive_search_for_values* to recursively populate each *ModelMatchCandidate* with *MatchedEntry* instances. After populating, each *ModelMatchCandidate* is evaluated based on the provided *target_values_operator* and *values* list using *ModelMatchCandidate.check_if_is_match*.

**Parameters**

- **values** (*list*) – list of values used to search and find models corresponding to these values
- **target_values_operator** (*str*) – the operator indicating the relationship between *values* in the evaluation of model search results. Should be either "AND", "OR", or "XOR".
- **are_keys_also_matched** (*bool*) – flag indicating whether, apart from values, the keys in the model config should also be searchable
- **is_case_sensitive** (*bool*) – flag indicating whether the search for values (and) keys in the model config should be case-sensitive.

**Returns** a list of *ModelMatchCandidate* class instances each of which was successfully matched against the search values.

**Return type** list

**find_models_and_rank**(*values: list*, *target_values_operator: str = 'AND'*, *are_keys_also_matched: bool = False*, *is_case_sensitive: bool = False*, *metric: str = 'SSIM'*, *order: str = 'asc'*) → list

Search for values (and keys) in model configs, rank results and return sorted list of model dicts.

**Parameters**

- **values** (*list*) – list of values used to search and find models corresponding to these *values*
- **target_values_operator** (*str*) – the operator indicating the relationship between *values* in the evaluation of model search results. Should be either "AND", "OR", or "XOR".
- **are_keys_also_matched** (*bool*) – flag indicating whether, apart from *values*, the keys in the model config should also be searchable
- **is_case_sensitive** (*bool*) – flag indicating whether the search for values (and) keys in the model config should be case-sensitive.
- **metric** (*str*) – The key in the selection dict that corresponds to the *metric* of interest
- **order** (*str*) – the sorting order of the ranked results. Should be either "asc" (ascending) or "desc" (descending)

**Returns** a list of the searched and matched model dictionaries containing *metric* and *model_id*, sorted by *metric*.

**Return type** list

**get_models_by_key_value_pair**(*key1: str*, *value1: str*, *is_case_sensitive: bool = False*) → list

Get and return a list of *model_id* dicts that contain the specified key value pair in their selection config.

The key param can contain '.' (dot) separations to allow for retrieval of nested config keys such as 'execution.generator.name'. If *key1* points to a list, any value in the list that matches value1` is accepted.

**Parameters**

- **key1** (*str*`) – The key in the selection dict
- **value1** (*str*) – The value in the selection dict that corresponds to key1
- **is_case_sensitive** (*bool*) – flag to evaluate keys and values with case sensitivity if set to True

**Returns** a list of the dictionaries each containing a model's *model_id* and the found key-value pair in the models config

**Return type** list

**get_selection_criteria_by_id**(*model_id: str*, *is_model_id_removed: bool = True*) → dict

Get and return the selection config dict for a specific *model_id*.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **is_model_id_removed** (*bool*) – flag to to remove the *model_id* from first level of each dictionary.

**Returns** a dictionary corresponding to the selection config of a model

**Return type** dict

**get_selection_criteria_by_ids**(*model_ids: Optional[list] = None*, *are_model_ids_removed: bool = True*) → list

Get and return a list of selection config dicts for each of the specified *model_ids*.

**Parameters**

- **model_ids** (*list*) – A list of generative models' unique ids

- **are_model_ids_removed** (*bool*) – flag to remove the *model_ids* from first level of dictionary.

**Returns** a list of dictionaries each corresponding to the selection config of a model

**Return type** list

**get_selection_keys**(*model_id: Optional[str] = None*) → list

Get and return all first level keys from the selection config dict for a specific *model_id*.

**Parameters** **model_id** (*str*) – The generative model's unique id

**Returns** a list containing the keys as strings of the selection config of the *model_id*.

**Return type** list

**get_selection_values_for_key**(*key: str*, *model_id: Optional[str] = None*) → list

Get and return the value of a specified key of the selection dict in the config for a specific *model_id*.

The key param can contain '.' (dot) separations to allow for retrieval of nested config keys such as 'execution.generator.name'

**Parameters**

- **key** (*str*) – The key in the selection dict
- **model_id** (*str*) – The generative model's unique id

**Returns** a list of the values that correspond to the key in the selection config of the *model_id*.

**Return type** list

**rank_models_by_performance**(*model_ids: Optional[list] = None*, *metric: str = 'SSIM'*, *order: str = 'asc'*) → list

Rank model based on a provided metric and return sorted list of model dicts.

The metric param can contain '.' (dot) separations to allow for retrieval via nested metric config keys such as 'downstream_task.CLF.accuracy'. If the value found for the metric key is of type list, then the largest value in the list is used for ranking if *order* is descending, while the smallest value is used if *order* is ascending.

**Parameters**

- **model_ids** (*list*) – only evaluate the model_ids in this list. If none, evaluate all available *model_ids*
- **metric** (*str*) – The key in the selection dict that corresponds to the metric of interest
- **order** (*str*) – the sorting order of the ranked results. Should be either "asc" (ascending) or "desc" (descending)

**Returns** a list of model dictionaries containing metric and *model_id*, sorted by *metric*.

**Return type** list

**recursive_search_for_values**(*search_dict: dict*, *model_match_candidate:* medigan.select_model.model_match_candidate.ModelMatchCandidate)

Do a recursive search to match values in the *search_dict* with values (and keys) in a model's config.

The provided *ModelMatchCandidate* instance is recursively populated with *MatchedEntry* instances. A *MatchedEntry* instance contains a key-value pair found in the model's config that matches with one search term of interest.

The search terms of interest are stored in *ModelMatchCandidate.target_values*. The model's selection config is provided in the 'search_dict'.

To traverse the *search_dict*, the value for each key in the *search_dict* is retrieved.

- If that value is of type dictionary, the function calls itself with that nested dictionary as new *search_dict*.
- If that value is of type list, each value in the list is compared with each search term of interest in *ModelMatchCandidate.target_values*.
- If the value of the *search_dict* is of another type (i.e. str), it is compared with each search term of interest in *ModelMatchCandidate.target_values*.

**Parameters**

- **search_dict** (*dict*) – contains keys and values from a model's config that are matched against a set of search values.
- **model_match_candidate** (ModelMatchCandidate) – a class instance representing a model to be prepared for evaluation (populated with *MatchedEntry* objects), as to whether it is a match given its search values (*self.target_values*).

**Returns** a *ModelMatchCandidate* class instance that has been populated with *MatchedEntry* class instances.

**Return type** list

### 1.4.5 ModelContributor

#### medigan.contribute_model.model_contributor Module

Model contributor class that tests models, creates metadata entries, uploads and contributes them to medigan.

#### Classes

| | |
|---|---|
| GithubModelUploader(model_id, access_token) | *GithubModelUploader* class: Pushes the metadata of a user's model to the medigan repo, where it creates a dedicated github issue. |
| *ModelContributor*(model_id, init_py_path) | *ModelContributor* class: Contributes a user's local model to the public medigan library |
| Path(*args, **kwargs) | PurePath subclass that can make system calls. |
| Utils() | Utils class containing reusable static methods. |
| ZenodoModelUploader(model_id, access_token) | *ZenodoModelUploader* class: Uploads a user's model via API to Zenodo, here it is permanently stored with DOI. |

### ModelContributor

class medigan.contribute_model.model_contributor.**ModelContributor**(*model_id: str*, *init_py_path: str*)

Bases: object

*ModelContributor* class: Contributes a user's local model to the public medigan library

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **init_py_path** (*str*) – The path to the local model's *__init__.py* file needed for importing and running this model.

**model_id**

The generative model's unique id

**Type** str

**init_py_path**

The path to the local model's __init__.py file needed for importing and running this model.

**Type** str

**package_path**

Path as string to the generative model's python package

**Type** str

**package_name**

Name of the model's python package i.e. the name of the model's zip file and unzipped package folder

**Type** str

**metadata_file_path**

Path as string to the generative model's metadata file e.g. default is relative path to package root.

**Type** str

**zenodo_model_uploader**

An instance of the *ZenodoModelUploader* class

**Type** str

**github_model_uploader**

An instance of the *GithubModelUploader* class.

**Type** str

### Methods Summary

| | |
|---|---|
| *add_metadata_from_file*(metadata_file_path) | Read and parse the metadata of a local model, identified by *model_id*, from a metadata file in json format. |
| *add_metadata_from_input*([...]) | Create a metadata dict for a local model, identified by *model_id*, given the necessary minimum metadata contents. |
| *is_value_for_key_already_set*(key, metadata, ...) | Check if the value of a *key* in a *metadata* dictionary is already set and e.g. |
| *load_metadata_template*() | Loads and parses (json to dict) a default medigan metadata template. |
| *push_to_github*(access_token[, package_link, ...]) | Upload the model's metadata inside a github issue to the medigan github repository. |
| *push_to_zenodo*(access_token, creator_name, ...) | Upload the model files as zip archive to a public Zenodo repository where the model will be persistently stored. |
| *validate_and_update_model_weights_path*() | Check if the model files can be found in the *package_path* or based on the *path_to_metadata*. |
| *validate_init_py_path*(init_py_path) | Asserts whether the *init_py_path* exists and points to a valid *__init__.py* correct file. |
| *validate_local_model_import*() | Check if the model package in the *package_path* can be imported as python library using importlib. |
| *validate_model_id*(model_id[, max_chars, ...]) | Asserts if the *model_id* is in the correct format and has a valid length |

### Methods Documentation

**add_metadata_from_file**(*metadata_file_path*) → dict

Read and parse the metadata of a local model, identified by *model_id*, from a metadata file in json format.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **metadata_file_path** (*str*) – the path pointing to the metadata file

**Returns** Returns a dict containing the contents of parsed metadata json file.

**Return type** dict

**add_metadata_from_input**(*model_weights_name: Optional[str] = None*, *model_weights_extension: Optional[str] = None*, *generate_method_name: Optional[str] = None*, *dependencies: list = []*, *fill_more_fields_interactively: bool = True*, *output_path: str = 'config'*)

Create a metadata dict for a local model, identified by *model_id*, given the necessary minimum metadata contents.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **model_weights_name** (*str*) – the name of the checkpoint file containing the model's weights
- **model_weights_extension** (*str*) – the extension (e.g. .pt) of the checkpoint file containing the model's weights

- **generate_method_name** (*str*) – the name of the sample generation method inside the models __init__.py file
- **dependencies** (*list*) – the list of dependencies that need to be installed via pip to run the model.
- **fill_more_fields_interactively** (*bool*) – flag indicating whether a user will be interactively asked via command line for further input to fill out missing metadata content
- **output_path** (*str*) – the path where the created metadata json file will be stored.

**Returns** Returns a dict containing the contents of the metadata json file.

**Return type** dict

**is_value_for_key_already_set**(*key: str*, *metadata: dict*, *nested_key*) → bool

Check if the value of a *key* in a *metadata* dictionary is already set and e.g. not an empty string, dict or list.

**Parameters**

- **key** (*str*) – The key in the currently traversed part of the model's metadata dictionary
- **metadata** (*dict*) – The currently traversed part of the model's metadata dictionary
- **nested_key** (*str*) – the *nested_key* indicates which subpart of the model's metadata we are currently traversing

**Returns** Flag indicating whether a value exists for the *key* in the dict

**Return type** bool

**load_metadata_template**() → dict

Loads and parses (json to dict) a default medigan metadata template.

**Returns** Returns the metadata template as dict

**Return type** dict

**push_to_github**(*access_token: str*, *package_link: Optional[str] = None*, *creator_name: str = ''*, *creator_affiliation: str = ''*, *model_description: str = ''*)

Upload the model's metadata inside a github issue to the medigan github repository.

To add your model to medigan, your metadata will be reviewed on Github and added to medigan's official model metadata

The medigan repository issues page: https://github.com/RichardObi/medigan/issues

Get your Github access token here: https://github.com/settings/tokens

**Parameters**

- **access_token** (*str*) – a personal access token linked to your github user account, used as means of authentication
- **package_link** – a package link
- **creator_name** (*str*) – the creator name that will appear on the corresponding github issue
- **creator_affiliation** (*str*) – the creator affiliation that will appear on the corresponding github issue
- **model_description** (*list*) – the model_description that will appear on the corresponding github issue

**Returns** Returns the url pointing to the corresponding issue on github

**Return type** str

**push_to_zenodo**(*access_token: str*, *creator_name: str*, *creator_affiliation: str*, *model_description: str = ''*)

Upload the model files as zip archive to a public Zenodo repository where the model will be persistently stored.

Get your Zenodo access token here: https://zenodo.org/account/settings/applications/tokens/new/ (Enable scopes *deposit:actions* and *deposit:write*)

**Parameters**

- **access_token** (*str*) – a personal access token in Zenodo linked to a user account for authentication
- **creator_name** (*str*) – the creator name that will appear on the corresponding Zenodo model upload homepage
- **creator_affiliation** (*str*) – the creator affiliation that will appear on the corresponding Zenodo model upload homepage
- **model_description** (*list*) – the model_description that will appear on the corresponding Zenodo model upload homepage

**Returns** Returns the url pointing to the corresponding Zenodo model upload homepage

**Return type** str

**validate_and_update_model_weights_path**() → dict

Check if the model files can be found in the *package_path* or based on the *path_to_metadata*.

Ideally, the user provided *package_path* and the *path_to_metadata* should both point to the same model package containing weights, config, license, etc. Here we check both of these paths to find the model weights.

**Returns** Returns the metadata after updating the path to the model's checkpoint's weights

**Return type** dict

**validate_init_py_path**(*init_py_path*) → bool

Asserts whether the *init_py_path* exists and points to a valid *__init__.py* correct file.

**Parameters** **init_py_path** (*str*) – The path to the local model's __init__.py file needed for importing and running this model.

**validate_local_model_import**()

Check if the model package in the *package_path* can be imported as python library using importlib.

**validate_model_id**(*model_id: str*, *max_chars: int = 30*, *min_chars: int = 13*) → bool

Asserts if the *model_id* is in the correct format and has a valid length

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **max_chars** (*int*) – the maximum of chars allowed in the model_id
- **min_chars** (*int*) – the minimum of chars allowed in the model_id

**Returns** Returns flag indicating whether the *model_id* is correctly formatted.

**Return type** bool

### 1.4.6 ConfigManager

#### medigan.config_manager Module

Config manager class that downloads, ingests, parses, and prepares the config information for all models.

#### Classes

| | |
|---|---|
| ConfigManager([config_dict, ...]) | *ConfigManager* class: Downloads, loads and parses medigan's config json as dictionary. |
| Path(*args, **kwargs) | PurePath subclass that can make system calls. |
| Utils() | Utils class containing reusable static methods. |

#### ConfigManager

class medigan.config_manager.**ConfigManager**(*config_dict: Optional[dict] = None*, *is_new_download_forced: bool = False*)

Bases: object

*ConfigManager* class: Downloads, loads and parses medigan's config json as dictionary.

**Parameters**

- **config_dict** (*dict*) – Optionally provides the config dictionary if already loaded and parsed in a previous process.
- **is_new_download_forced** (*bool*) – Flags, if True, that a new config file should be downloaded from the config link instead of parsing an existing file.

**config_dict**

Optionally provides the config dictionary if already loaded and parsed in a previous process.

**Type** dict

**is_new_download_forced**

Flags, if True, that a new config file should be downloaded from the config link instead of parsing an existing file.

**Type** bool

**model_ids**

Lists the unique id's of the generative models specified in the *config_dict*

**Type** list

**is_config_loaded**

Flags if the loading and parsing of the config file was successful (True) or not (False).

**Type** bool

### Methods Summary

| | |
|---|---|
| *add_model_to_config*(model_id, metadata[, ...]) | Adding or updating a model entry in the global metadata. |
| *get_config_by_id*(model_id[, config_key]) | From *config_manager*, get and return the part of the config below a config_key for a specific *model_id*. |
| *is_model_in_config*(model_id) | Checking if a *model_id* is present in the global model metadata file |
| *is_model_metadata_valid*(model_id, metadata) | Checking if a model's corresponding metadata is valid. |
| *load_config_file*([is_new_download_forced]) | Load a config file and return boolean flag indicating success of loading process. |

### Methods Documentation

**add_model_to_config**(*model_id: str*, *metadata: dict*, *is_local_model: bool = True*, *overwrite_existing_metadata: bool = False*, *store_new_config: bool = True*) → bool

Adding or updating a model entry in the global metadata.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **metadata** (*dict*) – The model's corresponding metadata
- **is_local_model** (*bool*) – flag indicating whether the tested model is a new local user model i.e not yet part of medigan's official models
- **overwrite_existing_metadata** (*bool*) – in case of *is_local_model*, flag indicating whether existing metadata for this model in medigan's *config/global.json* should be overwritten.
- **store_new_config** (*bool*) – flag indicating whether the current model metadata should be stored on disk i.e. in config/

**Returns** Flag indicating whether model metadata update was successfully concluded

**Return type** bool

**get_config_by_id**(*model_id: str*, *config_key: Optional[str] = None*) → dict

From *config_manager*, get and return the part of the config below a config_key for a specific *model_id*.

The key param can contain '.' (dot) separations to allow for retrieval of nested config keys such as 'execution.generator.name'

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **config_key** (*str*) – A key of interest present in the config dict

**Returns** a dictionary from the part of the config file corresponding to *model_id* and *config_key*.

**Return type** dict

**is_model_in_config**(*model_id: str*) → bool

Checking if a *model_id* is present in the global model metadata file

**Parameters** **model_id** (*str*) – The generative model's unique id

**Returns** Flag indicating whether a *model_id* is present in global model metadata

**Return type** bool

`is_model_metadata_valid`(*model_id: str*, *metadata: dict*, *is_local_model: bool = True*) → bool

Checking if a model's corresponding metadata is valid.

Specific fields in the model's metadata are mandatory. It is asserted if these key value pairs are present.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **metadata** (*dict*) – The model's corresponding metadata
- **is_local_model** (*bool*) – flag indicating whether the tested model is a new local user model i.e not yet part of medigan's official models

**Returns** Flag indicating whether the specific model's metadata format and fields are valid

**Return type** bool

`load_config_file`(*is_new_download_forced: bool = False*) → bool

Load a config file and return boolean flag indicating success of loading process.

If the config file is not present in *medigan.CONSTANTS.CONFIG_FILE_FOLDER*, it is per default downloaded from the web resource specified in *medigan.CONSTANTS.CONFIG_FILE_URL*.

**Parameters** **is_new_download_forced** (*bool*) – Forces new download of config file even if the file has been downloaded before.

**Returns** a boolean flag indicating true only if the config file was loaded successfully.

**Return type** bool

## 1.5 Full Code Documentation

### 1.5.1 medigan package

#### Subpackages

#### medigan.contribute_model package

#### Submodules

#### medigan.contribute_model.base_model_uploader module

Base Model uploader class that uploads models to medigan associated data storage services.

`class medigan.contribute_model.base_model_uploader.BaseModelUploader`(*model_id: str*, *metadata: dict*)

Bases: `object`

*BaseModelUploader* class: Uploads a user's model and metadata to third party storage to allow its inclusion into the medigan library.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **metadata** (*dict*) – The model's corresponding metadata

**model_id**

The generative model's unique id

**Type** str

**metadata**

The model's corresponding metadata

**Type** dict

**push**()

### medigan.contribute_model.github_model_uploader module

Github Model uploader class that uploads the metadata of a new model to the medigan github repository.

**class** medigan.contribute_model.github_model_uploader.**GithubModelUploader**(*model_id: str*, *access_token: str*)

Bases: *medigan.contribute_model.base_model_uploader.BaseModelUploader*

*GithubModelUploader* class: Pushes the metadata of a user's model to the medigan repo, where it creates a dedicated github issue.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **access_token** (*str*) – a personal access token linked to your github user account, used as means of authentication

**model_id**

The generative model's unique id

**Type** str

**access_token**

a personal access token linked to your github user account, used as means of authentication

**Type** str

**add_package_link_to_metadata**(*metadata: dict*, *package_link: Optional[str] = None*, *is_update_forced: bool = False*) → dict

Update *package_link* in the model's metadata if current *package_link* does not containing a valid url.

**Parameters**

- **metadata** (*dict*) – The model's corresponding metadata
- **package_link** (*str*) – the new package link to used to replace the old one
- **is_update_forced** (*bool*) – flag to update metadata even though metadata already contains a valid url in its *package_link*

**Returns** Returns the updated metadata dict with replaced *package_link* if replacement was applicable.

**Return type** dict

**push**(*metadata: dict*, *package_link: Optional[str] = None*, *creator_name: str = 'n.a.'*, *creator_affiliation: str = 'n.a.'*, *model_description: str = 'n.a.'*)

Upload the model's metadata inside a github issue to the medigan github repository.

To add your model to medigan, your metadata will be reviewed on Github and added to medigan's official model metadata

The medigan repository issues page: https://github.com/RichardObi/medigan/issues

Get your Github access token here: https://github.com/settings/tokens

**Parameters**

- **metadata** (*dict*) – The model's corresponding metadata
- **package_link** – a package link
- **creator_name** (*str*) – the creator name that will appear on the corresponding github issue
- **creator_affiliation** (*str*) – the creator affiliation that will appear on the corresponding github issue
- **model_description** (*list*) – the model_description that will appear on the corresponding github issue

**Returns** Returns the url pointing to the corresponding issue on github

**Return type** str

### medigan.contribute_model.model_contributor module

Model contributor class that tests models, creates metadata entries, uploads and contributes them to medigan.

**class** medigan.contribute_model.model_contributor.**ModelContributor**(*model_id: str*, *init_py_path: str*)

Bases: object

*ModelContributor* class: Contributes a user's local model to the public medigan library

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **init_py_path** (*str*) – The path to the local model's *__init__.py* file needed for importing and running this model.

**model_id**

The generative model's unique id

**Type** str

**init_py_path**

The path to the local model's __init__.py file needed for importing and running this model.

**Type** str

**package_path**

Path as string to the generative model's python package

**Type** str

**package_name**

Name of the model's python package i.e. the name of the model's zip file and unzipped package folder

**Type** str

**metadata_file_path**

Path as string to the generative model's metadata file e.g. default is relative path to package root.

**Type** str

**zenodo_model_uploader**

An instance of the *ZenodoModelUploader* class

**Type** str

**github_model_uploader**

An instance of the *GithubModelUploader* class.

**Type** str

**add_metadata_from_file**(*metadata_file_path*) → dict

Read and parse the metadata of a local model, identified by *model_id*, from a metadata file in json format.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **metadata_file_path** (*str*) – the path pointing to the metadata file

**Returns** Returns a dict containing the contents of parsed metadata json file.

**Return type** dict

**add_metadata_from_input**(*model_weights_name: Optional[str] = None*, *model_weights_extension: Optional[str] = None*, *generate_method_name: Optional[str] = None*, *dependencies: list = []*, *fill_more_fields_interactively: bool = True*, *output_path: str = 'config'*)

Create a metadata dict for a local model, identified by *model_id*, given the necessary minimum metadata contents.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **model_weights_name** (*str*) – the name of the checkpoint file containing the model's weights
- **model_weights_extension** (*str*) – the extension (e.g. .pt) of the checkpoint file containing the model's weights
- **generate_method_name** (*str*) – the name of the sample generation method inside the models __init__.py file
- **dependencies** (*list*) – the list of dependencies that need to be installed via pip to run the model.
- **fill_more_fields_interactively** (*bool*) – flag indicating whether a user will be interactively asked via command line for further input to fill out missing metadata content
- **output_path** (*str*) – the path where the created metadata json file will be stored.

**Returns** Returns a dict containing the contents of the metadata json file.

**Return type** dict

**is_value_for_key_already_set**(*key: str*, *metadata: dict*, *nested_key*) → bool

Check if the value of a *key* in a *metadata* dictionary is already set and e.g. not an empty string, dict or list.

**Parameters**

- **key** (*str*) – The key in the currently traversed part of the model's metadata dictionary
- **metadata** (*dict*) – The currently traversed part of the model's metadata dictionary
- **nested_key** (*str*) – the *nested_key* indicates which subpart of the model's metadata we are currently traversing

**Returns** Flag indicating whether a value exists for the *key* in the dict

**Return type** bool

**load_metadata_template**() → dict

Loads and parses (json to dict) a default medigan metadata template.

**Returns** Returns the metadata template as dict

**Return type** dict

**push_to_github**(*access_token: str*, *package_link: Optional[str] = None*, *creator_name: str = ''*, *creator_affiliation: str = ''*, *model_description: str = ''*)

Upload the model's metadata inside a github issue to the medigan github repository.

To add your model to medigan, your metadata will be reviewed on Github and added to medigan's official model metadata

The medigan repository issues page: https://github.com/RichardObi/medigan/issues

Get your Github access token here: https://github.com/settings/tokens

**Parameters**

- **access_token** (*str*) – a personal access token linked to your github user account, used as means of authentication
- **package_link** – a package link
- **creator_name** (*str*) – the creator name that will appear on the corresponding github issue
- **creator_affiliation** (*str*) – the creator affiliation that will appear on the corresponding github issue
- **model_description** (*list*) – the model_description that will appear on the corresponding github issue

**Returns** Returns the url pointing to the corresponding issue on github

**Return type** str

**push_to_zenodo**(*access_token: str*, *creator_name: str*, *creator_affiliation: str*, *model_description: str = ''*)

Upload the model files as zip archive to a public Zenodo repository where the model will be persistently stored.

Get your Zenodo access token here: https://zenodo.org/account/settings/applications/tokens/new/ (Enable scopes *deposit:actions* and *deposit:write*)

**Parameters**

- **access_token** (*str*) – a personal access token in Zenodo linked to a user account for authentication

- **creator_name** (*str*) – the creator name that will appear on the corresponding Zenodo model upload homepage
- **creator_affiliation** (*str*) – the creator affiliation that will appear on the corresponding Zenodo model upload homepage
- **model_description** (*list*) – the model_description that will appear on the corresponding Zenodo model upload homepage

**Returns** Returns the url pointing to the corresponding Zenodo model upload homepage

**Return type** str

**validate_and_update_model_weights_path**() → dict

Check if the model files can be found in the *package_path* or based on the *path_to_metadata*.

Ideally, the user provided *package_path* and the *path_to_metadata* should both point to the same model package containing weights, config, license, etc. Here we check both of these paths to find the model weights.

**Returns** Returns the metadata after updating the path to the model's checkpoint's weights

**Return type** dict

**validate_init_py_path**(*init_py_path*) → bool

Asserts whether the *init_py_path* exists and points to a valid *__init__.py* correct file.

**Parameters** **init_py_path** (*str*) – The path to the local model's __init__.py file needed for importing and running this model.

**validate_local_model_import**()

Check if the model package in the *package_path* can be imported as python library using importlib.

**validate_model_id**(*model_id: str*, *max_chars: int = 30*, *min_chars: int = 13*) → bool

Asserts if the *model_id* is in the correct format and has a valid length

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **max_chars** (*int*) – the maximum of chars allowed in the model_id
- **min_chars** (*int*) – the minimum of chars allowed in the model_id

**Returns** Returns flag indicating whether the *model_id* is correctly formatted.

**Return type** bool

### medigan.contribute_model.zenodo_model_uploader module

Zenodo Model uploader class that uploads models to medigan associated data storage on Zenodo.

**class** medigan.contribute_model.zenodo_model_uploader.**ZenodoModelUploader**(*model_id*, *access_token*)

Bases: *medigan.contribute_model.base_model_uploader.BaseModelUploader*

*ZenodoModelUploader* class: Uploads a user's model via API to Zenodo, here it is permanently stored with DOI.

**Parameters**

- **model_id** (*str*) – The generative model's unique id

- **access_token** (*str*) – a personal access token in Zenodo linked to a user account for authentication

**model_id**

The generative model's unique id

**Type** str

**access_token**

a personal access token in Zenodo linked to a user account for authentication

**Type** str

**create_upload_description**(*metadata: dict*, *model_description: str = ''*) → str

Create a string containing the textual description that will accompany the upload model files.

The string contains tags and a text retrieved from the description subsection of the model metadata.

**Parameters**

- **metadata** (*dict*) – The model's corresponding metadata
- **model_description** (*str*) – the model_description that will appear on the corresponding Zenodo model upload homepage

**Returns** Returns the textual description of the model upload

**Return type** str

**create_upload_json_data**(*creator_name: str*, *creator_affiliation: str*, *description: str = ''*) → dict

Create some descriptive data in dict format to be uploaded and stored alongside the model files.

**Parameters**

- **creator_name** (*str*) – the creator name that will appear on the corresponding Zenodo model upload homepage
- **creator_affiliation** (*str*) – the creator affiliation that will appear on the corresponding Zenodo model upload homepage
- **description** (*str*) – the model_description that will appear on the corresponding Zenodo model upload homepage

**Returns** Returns the descriptive data in dictionary structure describing the model upload.

**Return type** dict

**empty_upload**() → dict

Upload an empty placeholder entry to Zenodo as is required to retrieve a *deposition_id* and *bucket_url*.

deposition_id and bucket_url aare needed for file upload and publishing in the subsequent upload steps.

**Returns** Returns the response retrieved via the Zenodo API

**Return type** dict

**locate_or_create_model_zip_file**(*package_path: str*, *package_name: str) -> (<class 'str'>*, *<class 'str'>*)

If not possible to locate, create a zipped python package of the model.

**Parameters**

- **package_path** (*str*) – Path as string to the generative model's python package containing an *__init__.py* file

- **package_name** (*str*) – Name of the model's python package i.e. the name of the model's zip file and unzipped package folder

**Returns** Returns a tuple containing two strings: The *filename* and the *file_path* of and to the zipped python package

**Return type** tuple

**publish**(*deposition_id: str*) → dict

Publish a zenodo upload.

This makes the upload official, as it will then be publicly accessible and persistently stored on Zenodo with associated DOI.

**Parameters** **deposition_id** (*str*) – The deposition id assigned by Zenodo to the uploaded model file

**Returns** Returns the response retrieved via the Zenodo API

**Return type** dict

**push**(*metadata: dict*, *package_path: str*, *package_name: str*, *creator_name: str*, *creator_affiliation: str*, *model_description: str = ''*)

Upload the model files as zip archive to a public Zenodo repository where the model will be persistently stored.

Get your Zenodo access token here: https://zenodo.org/account/settings/applications/tokens/new/ (Enable scopes *deposit:actions* and *deposit:write*)

**Parameters**

- **metadata** (*dict*) – The model's corresponding metadata
- **package_path** (*dict*) – The path to the packaged model files
- **package_name** (*dict*) – The name of the packaged model files
- **creator_name** (*str*) – the creator name that will appear on the corresponding Zenodo model upload homepage
- **creator_affiliation** (*str*) – the creator affiliation that will appear on the corresponding Zenodo model upload homepage
- **model_description** (*list*) – the model_description that will appear on the corresponding Zenodo model upload homepage

**Returns** Returns the url pointing to the corresponding Zenodo model upload homepage

**Return type** str

**upload**(*file_path: str*, *filename: str*, *bucket_url: str*) → dict

Upload a file to Zenodo entry of the uploaded model files.

**Parameters**

- **file_path** (*str*) – The path of the file that is uploaded to Zenodo
- **filename** (*str*) – The name of the file that is uploaded to Zenodo
- **bucket_url** (*str*) – The bucket url used in the PUT request to upload the data file.

**Returns** Returns the response retrieved via the Zenodo API

**Return type** dict

**upload_descriptive_data**(*deposition_id: str*, *data: dict*) → dict

Upload textual descriptive data to be associated and added to the Zenodo entry of the uploaded model files.

**Parameters**

- **deposition_id** (*str*) – The deposition id assigned by Zenodo to the uploaded model file
- **data** (*dict*) – The descriptive information that will to be uploaded to Zenodo and associated with the desposition_id

**Returns** Returns the response retrieved via the Zenodo API

**Return type** dict

### Module contents

### medigan.execute_model package

### Submodules

### medigan.execute_model.install_model_dependencies module

Functionality for automated installation of a model's python package dependencies.

medigan.execute_model.install_model_dependencies.**install_model**(*model_id: str*, *config_manager: Optional[*medigan.config_manager.ConfigManager*] = None*, *execution_config: Optional[dict] = None*)

installing the dependencies required for this model as stated in config

medigan.execute_model.install_model_dependencies.**parse_args**() → argparse.Namespace

### medigan.execute_model.model_executor module

Model executor class that downloads models, loads them as python packages, and runs their generate functions.

**class** medigan.execute_model.model_executor.**ModelExecutor**(*model_id: str*, *execution_config: dict*, *download_package: bool = True*, *install_dependencies: bool = False*)

Bases: object

*ModelExecutor* class: Find config links to download models, init models as python packages, run generate methods.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **execution_config** (*dict*) – The part of the config below the 'execution' key
- **download_package** (*bool*) – Flag indicating, if True, that the model's package should be downloaded instead of using an existing one that was downloaded previously
- **install_dependencies** (*bool*) – flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.

**model_id**

The generative model's unique id

**Type** str

**execution_config**

The part of the config below the 'execution' key

**Type** dict

**download_package**

Flag indicating, if True, that the model's package should be downloaded instead of using an existing one that was downloaded previously

**Type** bool

**image_size**

Pixel dimension of the generated samples, where images are assumed to have the same width and height

**Type** int

**dependencies**

List of the dependencies of a models python package.

**Type** list

**model_name**

Name of the generative model

**Type** str

**model_extension**

File extension of the generative model's weights file.

**Type** str

**package_name**

Name of the model's python package i.e. the name of the model's zip file and unzipped package folder

**Type** str

**package_link**

The link to the zipped model package. Note: Convention is to host models on Zenodo (reason: static doi content)

**Type** str

**generate_method_name**

The name of the model's generate method inside the model package. This method is called to generate samples.

**Type** str

**generate_method_args**

The args of the model's generate method inside the model package

**Type** dict

**serialised_model_file_path**

Path as string to the generative model's weights file

**Type** str

**package_path**

Path as string to the generative model's python package containing an *__init__.py* file

**Type** str

**deserialized_model_as_lib**

The generative model's package imported as python library. Generate method inside this library can be called.

**generate**(*num_samples: int = 20*, *output_path: Optional[str] = None*, *save_images: bool = True*, *is_gen_function_returned: bool = False*, *batch_size: int = 32*, ***kwargs*)

Generate samples using the generative model or return the model's generate function.

The name amd additional parameters of the generate function of the respective generative model are retrieved from the model's *execution_config*.

**Parameters**

- **num_samples** (*int*) – the number of samples that will be generated
- **output_path** (*str*) – the path as str to the output folder where the generated samples will be stored
- **save_images** (*bool*) – flag indicating whether generated samples are returned (i.e. as list of numpy arrays) or rather stored in file system (i.e in *output_path*)
- **is_gen_function_returned** (*bool*) – flag indicating whether, instead of generating samples, the sample generation function will be returned
- **batch_size** (*int*) – the batch size for the sample generation function
- ****kwargs** – arbitrary number of keyword arguments passed to the model's sample generation function

**Returns** Returns images as list of numpy arrays if *save_images* is False. However, if *is_gen_function_returned* is True, it returns the internal generate function of the model.

**Return type** list

**Raises** **Exception** – If the generate method of the model does not exist, cannot be called, or is called with missing params, or if the sample generation inside the model package returns an exception.

**is_model_already_unpacked**() → bool

Check if a valid path to the model files exists and, if so, set the *package_path*

### medigan.execute_model.synthetic_dataset module

*SyntheticDataset* allows to return a generative model as torch dataset.

**class** medigan.execute_model.synthetic_dataset.**SyntheticDataset**(*samples*, *masks=None*, *other_imaging_output=None*, *labels=None*, *transform=None*)

Bases: torch.utils.data.dataset.Dataset

A synthetic dataset containing data generated by a model of medigan

**Parameters**

- **samples** (*list*) – List of data points in the dataset e.g. generated images as numpy array.
- **masks** (*list*) – List of segmentation masks, if applicable, pertaining to the *samples* items

- **other_imaging_output** (*list*) – List of other imaging output produced by the generative model (e.g. specific types of other masks/modalities)
- **labels** (*list*) – list of labels, if applicable, pertaining to the *samples* items
- **transform** – torch compose transform functions that are applied to the torch dataset.

**samples**

List of data points in the dataset e.g. generated images as numpy array.

**Type** list

**masks**

List of segmentation masks, if applicable, pertaining to the *samples* items

**Type** list

**other_imaging_output**

List of other imaging output produced by the generative model (e.g. specific types of other masks/modalities)

**Type** list

**labels**

list of labels, if applicable, pertaining to the *samples* items

**Type** list

**transform**

torch compose transform functions that are applied to the torch dataset.

### Module contents

### medigan.select_model package

### Submodules

### medigan.select_model.matched_entry module

MatchedEntry class that represents one match of a key value pair of a model's config against a search query.

**class** medigan.select_model.matched_entry.**MatchedEntry**(*key: str*, *value*, *matching_element: Optional[str] = None*)

Bases: object

*MatchedEntry* class: One target key-value pair that matches with a model's selection config.

**Parameters**

- **key** (*str*) – string that represents the matched key in model selection dict
- **value** – represents the key's matched value in the model selection dict
- **matching_element** (*str*) – string that was used to match the search value

**key**

string that represents the matched key in model selection dict

**Type** str

**value**

represents the key's matched value in the model selection dict

**matching_element**

string that was used to match the search value

**Type** str

### medigan.select_model.model_match_candidate module

ModelMatchCandidate class that holds data to evaluate if a generative model matches against a search query.

**class** medigan.select_model.model_match_candidate.**ModelMatchCandidate**(*model_id: str*, *target_values: list*, *target_values_operator: str = 'AND'*, *is_case_sensitive: bool = False*, *are_keys_also_matched: bool = False*, *is_match: bool = False*)

Bases: `object`

*ModelMatchCandidate* class: A prospectively matching model given the target values as model search params.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **target_values** (*list*) – list of target values used to evaluate if a *ModelMatchCandidate* instance is a match
- **target_values_operator** (*str*) – the operator indicating the relationship between *values* in the evaluation of *ModelMatchCandidate* instances. Should be either "AND", "OR", or "XOR".
- **is_case_sensitive** (*bool*) – flag indicating whether the matching of *values* (and) keys should be case-sensitive
- **are_keys_also_matched** (*bool*) – flag indicating whether, apart from *values*, keys should also be matched
- **is_match** (*bool*) – flag indicating whether the *ModelMatchCandidate* instance is a match

**model_id**

The generative model's unique id

**Type** str

**target_values**

list of target values used to evaluate if a *ModelMatchCandidate* instance is a match

**Type** list

**target_values_operator**

the operator indicating the relationship between *values* in the evaluation of *ModelMatchCandidate* instances. Should be either "AND", "OR", or "XOR".

**Type** str

**is_case_sensitive**

flag indicating whether the matching of *values* (and) keys should be case-sensitive

**Type** bool

**are_keys_also_matched**

flag indicating whether, apart from values, keys should also be matched

**Type** bool

**matched_entries**

contains iteratively added *MatchedEntry* class instances. Each of the *MatchedEntry* instances indicates a match between one of the user specified values in *self.target_values* and the selection config keys or *values* of the model of this *ModelMatchCandidate*.

**Type** list

**is_match**

flag indicating whether the *ModelMatchCandidate* instance is a match

**Type** bool

**add_matched_entry**(*matched_entry:* medigan.select_model.matched_entry.MatchedEntry) → None

Add a *MatchedEntry* instance to the *matched_entries* list.

**check_if_is_match**() → bool

Evaluates whether the model represented by this instance is a match given search values and operator.

The matching element from each *MatchEntry* of this instance ('self.matched_entries') are retrieved. To be a match, this instance ('self') needs to fulfill the requirement of the operator, which can be of value 'AND', or 'OR', or 'XOR'. For example, the default 'AND' requires that each search value ('self.target_values') has at least one corresponding *MatchEntry*, while in 'OR' only one of the search values needs to have been matched by a corresponding *MatchedEntry*.

**Returns** flag that, only if True, indicates that this instance is a match given the search values and operator.

**Return type** bool

**get_all_matching_elements**() → list

Get the matching element from each of the *MatchedEntry* instances in the *matched_entries* list.

**Returns** list of all matching elements (i.e. string that matched a search value) from each *MatchedEntry* in *matched_entries*

**Return type** list

### medigan.select_model.model_selector module

Model selection class that describes, finds, compares, and ranks generative models.

**class** medigan.select_model.model_selector.**ModelSelector**(*config_manager: Optional[*medigan.config_manager.ConfigManager*] = None*)

Bases: object

*ModelSelector* class: Given a config dict, gets, searches, and ranks matching models.

**Parameters** **config_manager** (ConfigManager) – Provides the config dictionary, based on which models are selected and compared.

`config_manager`

Provides the config dictionary, based on which models are selected and compared.

**Type** *ConfigManager*

`model_selection_dicts`

Contains a dictionary for each model id that consists of the *model_id* and the selection config of that model

**Type** list

`find_matching_models_by_values`(*values: list*, *target_values_operator: str = 'AND'*, *are_keys_also_matched: bool = False*, *is_case_sensitive: bool = False*) → list

Search for values (and keys) in model configs and return a list of each matching *ModelMatchCandidate*.

Uses *self.recursive_search_for_values* to recursively populate each *ModelMatchCandidate* with *MatchedEntry* instances. After populating, each *ModelMatchCandidate* is evaluated based on the provided *target_values_operator* and *values* list using *ModelMatchCandidate.check_if_is_match*.

**Parameters**

- **values** (*list*) – list of values used to search and find models corresponding to these values
- **target_values_operator** (*str*) – the operator indicating the relationship between *values* in the evaluation of model search results. Should be either "AND", "OR", or "XOR".
- **are_keys_also_matched** (*bool*) – flag indicating whether, apart from values, the keys in the model config should also be searchable
- **is_case_sensitive** (*bool*) – flag indicating whether the search for values (and) keys in the model config should be case-sensitive.

**Returns** a list of *ModelMatchCandidate* class instances each of which was successfully matched against the search values.

**Return type** list

`find_models_and_rank`(*values: list*, *target_values_operator: str = 'AND'*, *are_keys_also_matched: bool = False*, *is_case_sensitive: bool = False*, *metric: str = 'SSIM'*, *order: str = 'asc'*) → list

Search for values (and keys) in model configs, rank results and return sorted list of model dicts.

**Parameters**

- **values** (*list*) – list of values used to search and find models corresponding to these *values*
- **target_values_operator** (*str*) – the operator indicating the relationship between *values* in the evaluation of model search results. Should be either "AND", "OR", or "XOR".
- **are_keys_also_matched** (*bool*) – flag indicating whether, apart from *values*, the keys in the model config should also be searchable
- **is_case_sensitive** (*bool*) – flag indicating whether the search for values (and) keys in the model config should be case-sensitive.
- **metric** (*str*) – The key in the selection dict that corresponds to the *metric* of interest
- **order** (*str*) – the sorting order of the ranked results. Should be either "asc" (ascending) or "desc" (descending)

**Returns** a list of the searched and matched model dictionaries containing *metric* and *model_id*, sorted by *metric*.

**Return type** list

**get_models_by_key_value_pair**(*key1: str*, *value1: str*, *is_case_sensitive: bool = False*) → list

Get and return a list of *model_id* dicts that contain the specified key value pair in their selection config.

The key param can contain '.' (dot) separations to allow for retrieval of nested config keys such as 'execution.generator.name'. If *key1* points to a list, any value in the list that matches value1` is accepted.

**Parameters**

- **key1** (*str`*) – The key in the selection dict
- **value1** (*str*) – The value in the selection dict that corresponds to key1
- **is_case_sensitive** (*bool*) – flag to evaluate keys and values with case sensitivity if set to True

**Returns** a list of the dictionaries each containing a model's *model_id* and the found key-value pair in the models config

**Return type** list

**get_selection_criteria_by_id**(*model_id: str*, *is_model_id_removed: bool = True*) → dict

Get and return the selection config dict for a specific *model_id*.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **is_model_id_removed** (*bool*) – flag to to remove the *model_id* from first level of each dictionary.

**Returns** a dictionary corresponding to the selection config of a model

**Return type** dict

**get_selection_criteria_by_ids**(*model_ids: Optional[list] = None*, *are_model_ids_removed: bool = True*) → list

Get and return a list of selection config dicts for each of the specified *model_ids*.

**Parameters**

- **model_ids** (*list*) – A list of generative models' unique ids
- **are_model_ids_removed** (*bool*) – flag to remove the *model_ids* from first level of dictionary.

**Returns** a list of dictionaries each corresponding to the selection config of a model

**Return type** list

**get_selection_keys**(*model_id: Optional[str] = None*) → list

Get and return all first level keys from the selection config dict for a specific *model_id*.

**Parameters** **model_id** (*str*) – The generative model's unique id

**Returns** a list containing the keys as strings of the selection config of the *model_id*.

**Return type** list

**get_selection_values_for_key**(*key: str*, *model_id: Optional[str] = None*) → list

Get and return the value of a specified key of the selection dict in the config for a specific *model_id*.

The key param can contain '.' (dot) separations to allow for retrieval of nested config keys such as 'execution.generator.name'

**Parameters**

- **key** (*str*) – The key in the selection dict
- **model_id** (*str*) – The generative model's unique id

**Returns** a list of the values that correspond to the key in the selection config of the *model_id*.

**Return type** list

**rank_models_by_performance**(*model_ids: Optional[list] = None*, *metric: str = 'SSIM'*, *order: str = 'asc'*) → list

Rank model based on a provided metric and return sorted list of model dicts.

The metric param can contain '.' (dot) separations to allow for retrieval via nested metric config keys such as 'downstream_task.CLF.accuracy'. If the value found for the metric key is of type list, then the largest value in the list is used for ranking if *order* is descending, while the smallest value is used if *order* is ascending.

**Parameters**

- **model_ids** (*list*) – only evaluate the model_ids in this list. If none, evaluate all available *model_ids*
- **metric** (*str*) – The key in the selection dict that corresponds to the metric of interest
- **order** (*str*) – the sorting order of the ranked results. Should be either "asc" (ascending) or "desc" (descending)

**Returns** a list of model dictionaries containing metric and *model_id*, sorted by *metric*.

**Return type** list

**recursive_search_for_values**(*search_dict: dict*, *model_match_candidate: medigan.select_model.model_match_candidate.ModelMatchCandidate*)

Do a recursive search to match values in the *search_dict* with values (and keys) in a model's config.

The provided *ModelMatchCandidate* instance is recursively populated with *MatchedEntry* instances. A *MatchedEntry* instance contains a key-value pair found in the model's config that matches with one search term of interest.

The search terms of interest are stored in *ModelMatchCandidate.target_values*. The model's selection config is provided in the 'search_dict'.

To traverse the *search_dict*, the value for each key in the *search_dict* is retrieved.

- If that value is of type dictionary, the function calls itself with that nested dictionary as new *search_dict*.
- If that value is of type list, each value in the list is compared with each search term of interest in *ModelMatchCandidate.target_values*.
- If the value of the *search_dict* is of another type (i.e. str), it is compared with each search term of interest in *ModelMatchCandidate.target_values*.

**Parameters**

- **search_dict** (*dict*) – contains keys and values from a model's config that are matched against a set of search values.
- **model_match_candidate** (ModelMatchCandidate) – a class instance representing a model to be prepared for evaluation (populated with *MatchedEntry* objects), as to whether it is a match given its search values (*self.target_values*).

**Returns** a *ModelMatchCandidate* class instance that has been populated with *MatchedEntry* class instances.

**Return type** list

### Module contents

### Submodules

### medigan.config_manager module

Config manager class that downloads, ingests, parses, and prepares the config information for all models.

**class** medigan.config_manager.**ConfigManager**(*config_dict: Optional[dict] = None*, *is_new_download_forced: bool = False*)

Bases: `object`

*ConfigManager* class: Downloads, loads and parses medigan's config json as dictionary.

**Parameters**

- **config_dict** (*dict*) – Optionally provides the config dictionary if already loaded and parsed in a previous process.
- **is_new_download_forced** (*bool*) – Flags, if True, that a new config file should be downloaded from the config link instead of parsing an existing file.

**config_dict**

Optionally provides the config dictionary if already loaded and parsed in a previous process.

**Type** dict

**is_new_download_forced**

Flags, if True, that a new config file should be downloaded from the config link instead of parsing an existing file.

**Type** bool

**model_ids**

Lists the unique id's of the generative models specified in the *config_dict*

**Type** list

**is_config_loaded**

Flags if the loading and parsing of the config file was successful (True) or not (False).

**Type** bool

**add_model_to_config**(*model_id: str*, *metadata: dict*, *is_local_model: bool = True*, *overwrite_existing_metadata: bool = False*, *store_new_config: bool = True*) → bool

Adding or updating a model entry in the global metadata.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **metadata** (*dict*) – The model's corresponding metadata
- **is_local_model** (*bool*) – flag indicating whether the tested model is a new local user model i.e not yet part of medigan's official models
- **overwrite_existing_metadata** (*bool*) – in case of *is_local_model*, flag indicating whether existing metadata for this model in medigan's *config/global.json* should be overwritten.

- **store_new_config** (*bool*) – flag indicating whether the current model metadata should be stored on disk i.e. in config/

**Returns** Flag indicating whether model metadata update was successfully concluded

**Return type** bool

**get_config_by_id**(*model_id: str*, *config_key: Optional[str] = None*) → dict

From *config_manager*, get and return the part of the config below a config_key for a specific *model_id*.

The key param can contain '.' (dot) separations to allow for retrieval of nested config keys such as 'execution.generator.name'

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **config_key** (*str*) – A key of interest present in the config dict

**Returns** a dictionary from the part of the config file corresponding to *model_id* and *config_key*.

**Return type** dict

**is_model_in_config**(*model_id: str*) → bool

Checking if a *model_id* is present in the global model metadata file

**Parameters** **model_id** (*str*) – The generative model's unique id

**Returns** Flag indicating whether a *model_id* is present in global model metadata

**Return type** bool

**is_model_metadata_valid**(*model_id: str*, *metadata: dict*, *is_local_model: bool = True*) → bool

Checking if a model's corresponding metadata is valid.

Specific fields in the model's metadata are mandatory. It is asserted if these key value pairs are present.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **metadata** (*dict*) – The model's corresponding metadata
- **is_local_model** (*bool*) – flag indicating whether the tested model is a new local user model i.e not yet part of medigan's official models

**Returns** Flag indicating whether the specific model's metadata format and fields are valid

**Return type** bool

**load_config_file**(*is_new_download_forced: bool = False*) → bool

Load a config file and return boolean flag indicating success of loading process.

If the config file is not present in *medigan.CONSTANTS.CONFIG_FILE_FOLDER*, it is per default downloaded from the web resource specified in *medigan.CONSTANTS.CONFIG_FILE_URL*.

**Parameters** **is_new_download_forced** (*bool*) – Forces new download of config file even if the file has been downloaded before.

**Returns** a boolean flag indicating true only if the config file was loaded successfully.

**Return type** bool

**match_model_id**(*provided_model_id: str*) → bool

Replacing a model_id acronym (e.g. 00005 or 5) with the unique *model_id* present in the model metadata

**Parameters** **provided_model_id** (*str*) – The user-provided model_id that might be shorter (e.g. "00005" or "5") than the real unique model id

**Returns** If matched, returning the unique *model_id* present in global model metadata.

**Return type** str

### medigan.constants module

Global constants of the medigan library

medigan.constants.**CONFIG_FILE_FOLDER = 'config'**

Name and extensions of config file.

medigan.constants.**CONFIG_FILE_KEY_DEPENDENCIES = 'dependencies'**

Below the execution dict, the key under which the package link of a model is present in the config file. Note: The model packages are per convention stored on Zenodo where they retrieve a static DOI avoiding security issues due to static non-modifiable content on Zenodo. Zenodo also helps to maintain clarity of who the owners and contributors of each generative model (and its IP) in medigan are.

medigan.constants.**CONFIG_FILE_KEY_DESCRIPTION = 'description'**

Below the selection dict, the key under which the performance dictionary of a model is nested in the config file.

medigan.constants.**CONFIG_FILE_KEY_EXECUTION = 'execution'**

The key under which the selection dictionary of a model is nested in the config file.

medigan.constants.**CONFIG_FILE_KEY_GENERATE = 'generate_method'**

Below the execution dict, the key under which the exact name of a model's generate() function is present.

medigan.constants.**CONFIG_FILE_KEY_GENERATE_ARGS = 'args'**

Below the execution dict, the key under which an array of mandatory base arguments of any model's generate() function is present.

medigan.constants.**CONFIG_FILE_KEY_GENERATE_ARGS_BASE = 'base'**

Below the execution dict, the key under which a nested dict of key-value pairs of model specific custom arguments of a model's generate() function are present.

medigan.constants.**CONFIG_FILE_KEY_GENERATE_ARGS_CUSTOM = 'custom'**

Below the execution dict, the key under which the model_file argument value of any model's generate() function is present.

medigan.constants.**CONFIG_FILE_KEY_GENERATE_ARGS_INPUT_LATENT_VECTOR_SIZE = 'input_latent_vector_size'**

Below the selectoin dict, the key under which the tags (list of strings) is present.

medigan.constants.**CONFIG_FILE_KEY_GENERATE_ARGS_MODEL_FILE = 'model_file'**

Below the execution dict, the key under which the num_samples argument value of any model's generate() function is present.

medigan.constants.**CONFIG_FILE_KEY_GENERATE_ARGS_NUM_SAMPLES = 'num_samples'**

Below the execution dict, the key under which the output_path argument value of any model's generate() function is present.

medigan.constants.**CONFIG_FILE_KEY_GENERATE_ARGS_OUTPUT_PATH = 'output_path'**

Below the execution dict, the key under which the save images boolean flag argument value of any model's generate() function is present.

medigan.constants.**CONFIG_FILE_KEY_GENERATE_ARGS_SAVE_IMAGES = 'save_images'**

Below the execution dict, the key under which the random input_latent_vector_size argument value of model's generate() function is present.

medigan.constants.**CONFIG_FILE_KEY_GENERATE_NAME = 'name'**

Below the execution dict, the key under which a nested dict with info on the arguments of a model's generate() function is present.

medigan.constants.**CONFIG_FILE_KEY_GENERATOR = 'generator'**

Below the execution dict, the key under which a model's generator's is present in the config file.

medigan.constants.**CONFIG_FILE_KEY_GENERATOR_NAME = 'name'**

Below the execution dict, the key under which a model's image_size is present in the config file.

medigan.constants.**CONFIG_FILE_KEY_IMAGE_SIZE = 'image_size'**

Below the execution dict, the key under which a model's name is present in the config file. This is the name of the weights file!

medigan.constants.**CONFIG_FILE_KEY_MODEL_EXTENSION = 'extension'**

Below the execution dict, the key under which the package_name of a model is present in the config file.

medigan.constants.**CONFIG_FILE_KEY_MODEL_NAME = 'model_name'**

Below the execution dict, the key under which a nested dict with info on the model's generate() function is present.

medigan.constants.**CONFIG_FILE_KEY_PACKAGE_LINK = 'package_link'**

Below the execution dict, the key under which the extension of a model is present in the config file.

medigan.constants.**CONFIG_FILE_KEY_PACKAGE_NAME = 'package_name'**

Below the execution dict, the key under which the package_name of a model is present in the config file.

medigan.constants.**CONFIG_FILE_KEY_PERFORMANCE = 'performance'**

Below the execution dict, the key under which the dependencies dictionary of a model is nested in the config file.

medigan.constants.**CONFIG_FILE_KEY_SELECTION = 'selection'**

The key under which the description dictionary of a model is nested in the config file.

medigan.constants.**CONFIG_FILE_KEY_TAGS = 'tags'**

The filetype of any of the generative model's python packages after download and before unpacking.

medigan.constants.**CONFIG_FILE_NAME_AND_EXTENSION = 'global.json'**

The key under which the execution dictionary of a model is nested in the config file.

medigan.constants.**CONFIG_FILE_URL =**
**'https://raw.githubusercontent.com/RichardObi/medigan/main/config/global.json'**

Folder path that will be created to locally store the config file.

medigan.constants.**CONFIG_TEMPLATE_FILE_NAME_AND_EXTENSION = 'template.json'**

Download link to template.json file.

medigan.constants.**CONFIG_TEMPLATE_FILE_URL =**
**'https://raw.githubusercontent.com/RichardObi/medigan/main/templates/template.json'**

Name and extensions of template of config file.

medigan.constants.**DEFAULT_OUTPUT_FOLDER = 'output'**

The folder containing an __init__.py file is a python module.

medigan.constants.**GITHUB_REPO = 'RichardObi/medigan'**

The assignee of the Github Issue when adding a model to medigan

medigan.constants.**GITHUB_TITLE = 'Model Integration Request for medigan'**

The repository of the Github Issue when adding a model to medigan

medigan.constants.**INIT_PY_FILE = '__init__.py'**

Name and extensions of template of config file.

medigan.constants.**MODEL_FOLDER = 'models'**

To add a model, please create pull request in this github repo.

**Type** Static link to the config of medigan. Note

medigan.constants.**MODEL_ID = 'model_id'**

The default path to a folder under which the outputs of the medigan package (i.e. generated samples) are stored.

medigan.constants.**PACKAGE_EXTENSION = '.zip'**

The string describing a model's unique id in medigan's data structures.

medigan.constants.**TEMPLATE_FOLDER = 'templates'**

The line break in the Zenodo description that appears together with the pushed model on Zenodo

medigan.constants.**ZENODO_API_URL = 'https://zenodo.org/api/deposit/depositions'**

The HEADER for Zenodo REST API requests

medigan.constants.**ZENODO_GENERIC_MODEL_DESCRIPTION = " Usage:
This GAN is used as part of the medigan library. This
GANs metadata is therefore stored in and retrieved from medigan's <a
href='https://raw.githubusercontent.com/RichardObi/medigan/main/config/global.
json'>config file</a>. medigan is an open-source
Python library on <a href='https://github.com/RichardObi/medigan'>Github</a>
that allows developers and researchers to easily add synthetic imaging data into
their model training pipelines. medigan is documented <a
href='https://readthedocs.org/projects/medigan/'>here</a> and can be used via pip
install: <pre><code class='language-python'>pip install medigan</code></pre> To
run this model in medigan, use the following commands. <pre> <code
class='language-python'> from medigan import Generators </code></pre><pre> <code
class='language-python'> generators = Generators() </code></pre><pre> <code
class='language-python'>
generators.generate(model_id='YOUR_MODEL_ID',num_samples=10)</code></pre>   "**

The REST API to interact with Zenodo

medigan.constants.**ZENODO_HEADERS = {'Content-Type': 'application/json'}**

The title of the Github Issue when adding a model to medigan

medigan.constants.**ZENODO_LINE_BREAK = '   '**

A generic description appended to model uploads that are automatically uploaded to zenodo via Zenodo API call in medigan

### medigan.exceptions module

Custom exceptions to handle module specific error and facilitate bug fixes and debugging.

### medigan.generators module

Base class providing user-library interaction methods for config management, and model selection and execution.

**class** medigan.generators.**Generators**(*config_manager: Optional[*medigan.config_manager.ConfigManager*] = None*, *model_selector: Optional[*medigan.select_model.model_selector.ModelSelector*] = None*, *model_executors: Optional[list] = None*, *model_contributors: Optional[list] = None*, *initialize_all_models: bool = False*)

Bases: `object`

*Generators* class: Contains medigan's public methods to facilitate users' automated sample generation workflows.

**Parameters**

- **config_manager** (ConfigManager) – Provides the config dictionary, based on which *model_ids* are retrieved and models are selected and executed
- **model_selector** (ModelSelector) – Provides model comparison, search, and selection based on keys/values in the selection part of the config dict
- **model_executors** (*list*) – List of initialized *ModelExecutor* instances that handle model package download, init, and sample generation
- **initialize_all_models** (*bool*) – Flag indicating, if True, that one *ModelExecutor* for each *model_id* in the config dict should be initialized triggered by creation of *Generators* class instance. Note that, if False, the *Generators* class will only initialize a *ModelExecutor* on the fly when need be i.e. when the generate method for the respective model is called.

**config_manager**

Provides the config dictionary, based on which model_ids are retrieved and models are selected and executed

**Type** *ConfigManager*

**model_selector**

Provides model comparison, search, and selection based on keys/values in the selection part of the config dict

**Type** *ModelSelector*

**model_executors**

List of initialized *ModelExecutor* instances that handle model package download, init, and sample generation

**Type** list

**add_all_model_executors**()

Add *ModelExecutor* class instances for all models available in the config.

**Return type** None

**add_metadata_from_file**(*model_id: str*, *metadata_file_path: str*) → dict

Read and parse the metadata of a local model, identified by *model_id*, from a metadata file in json format.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **metadata_file_path** (*str*) – the path pointing to the metadata file

**Returns** Returns a dict containing the contents of parsed metadata json file.

**Return type** dict

**add_metadata_from_input**(*model_id: str*, *model_weights_name: str*, *model_weights_extension: str*, *generate_method_name: str*, *dependencies: list*, *fill_more_fields_interactively: bool = True*, *output_path: str = 'config'*) → dict

Create a metadata dict for a local model, identified by *model_id*, given the necessary minimum metadata contents.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **model_weights_name** (*str*) – the name of the checkpoint file containing the model's weights
- **model_weights_extension** (*str*) – the extension (e.g. .pt) of the checkpoint file containing the model's weights
- **generate_method_name** (*str*) – the name of the sample generation method inside the models __init__.py file
- **dependencies** (*list*) – the list of dependencies that need to be installed via pip to run the model
- **fill_more_fields_interactively** (*bool*) – flag indicating whether a user will be interactively asked via command line for further input to fill out missing metadata content
- **output_path** (*str*) – the path where the created metadata json file will be stored

**Returns** Returns a dict containing the contents of the metadata json file.

**Return type** dict

**add_model_contributor**(*model_id: str*, *init_py_path: Optional[str] = None*) → *medigan.contribute_model.model_contributor.ModelContributor*

Add a *ModelContributor* instance of this model_id to the *self.model_contributors* list.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **init_py_path** (*str*) – The path to the local model's __init__.py file needed for importing and running this model.

**Returns** *ModelContributor* class instance corresponding to the *model_id*

**Return type** *ModelContributor*

**add_model_executor**(*model_id: str*, *install_dependencies: bool = False*)

Add one *ModelExecutor* class instance corresponding to the specified *model_id*.

**Parameters**

- **model_id** (*str*) – The generative model's unique id

- **install_dependencies** (*bool*) – flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.

**Return type** None

**add_model_to_config**(*model_id: str*, *metadata: dict*, *is_local_model: Optional[bool] = None*, *overwrite_existing_metadata: bool = False*, *store_new_config: bool = True*) → bool

Adding or updating a model entry in the global metadata.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **metadata** (*dict*) – The model's corresponding metadata
- **is_local_model** (*bool*) – flag indicating whether the tested model is a new local user model i.e not yet part of medigan's official models
- **overwrite_existing_metadata** (*bool*) – in case of *is_local_model*, flag indicating whether existing metadata for this model in medigan's *config/global.json* should be overwritten.
- **store_new_config** (*bool*) – flag indicating whether the current model metadata should be stored on disk i.e. in config/

**Returns** Flag indicating whether model metadata update was successfully concluded

**Return type** bool

**contribute**(*model_id: str*, *init_py_path: str*, *github_access_token: str*, *zenodo_access_token: str*, *metadata_file_path: Optional[str] = None*, *model_weights_name: Optional[str] = None*, *model_weights_extension: Optional[str] = None*, *generate_method_name: Optional[str] = None*, *dependencies: Optional[list] = None*, *fill_more_fields_interactively: bool = True*, *overwrite_existing_metadata: bool = False*, *output_path: str = 'config'*, *creator_name: str = 'unknown name'*, *creator_affiliation: str = 'unknown affiliation'*, *model_description: str = ''*, *install_dependencies: bool = False*)

Implements the full model contribution workflow including model metadata generation, model test, model Zenodo upload, and medigan github issue creation.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **init_py_path** (*str*) – The path to the local model's __init__.py file needed for importing and running this model.
- **github_access_token** (*str*) – a personal access token linked to your github user account, used as means of authentication
- **zenodo_access_token** (*str*) – a personal access token in Zenodo linked to a user account for authentication
- **metadata_file_path** (*str*) – the path pointing to the metadata file
- **model_weights_name** (*str*) – the name of the checkpoint file containing the model's weights
- **model_weights_extension** (*str*) – the extension (e.g. .pt) of the checkpoint file containing the model's weights
- **generate_method_name** (*str*) – the name of the sample generation method inside the models __init__.py file

- **dependencies** (*list*) – the list of dependencies that need to be installed via pip to run the model
- **fill_more_fields_interactively** (*bool*) – flag indicating whether a user will be interactively asked via command line for further input to fill out missing metadata content
- **overwrite_existing_metadata** (*bool*) – flag indicating whether existing metadata for this model in medigan's *config/global.json* should be overwritten.
- **output_path** (*str*) – the path where the created metadata json file will be stored
- **creator_name** (*str*) – the creator name that will appear on the corresponding github issue
- **creator_affiliation** (*str*) – the creator affiliation that will appear on the corresponding github issue
- **model_description** (*list*) – the model_description that will appear on the corresponding github issue
- **install_dependencies** (*bool*) – flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.

**Returns** Returns the url pointing to the corresponding issue on github

**Return type** str

**find_matching_models_by_values**(*values: list*, *target_values_operator: str = 'AND'*, *are_keys_also_matched: bool = False*, *is_case_sensitive: bool = False*) → list

Search for values (and keys) in model configs and return a list of each matching *ModelMatchCandidate*.

This function calls an identically named function in a *ModelSelector* instance.

**Parameters**

- **values** (*list*) – list of values used to search and find models corresponding to these *values*
- **target_values_operator** (*str*) – the operator indicating the relationship between *values* in the evaluation of model search results. Should be either "AND", "OR", or "XOR".
- **are_keys_also_matched** (*bool*) – flag indicating whether, apart from values, the keys in the model config should also be searchable
- **is_case_sensitive** (*bool*) – flag indicating whether the search for values (and) keys in the model config should be case-sensitive.

**Returns** a list of *ModelMatchCandidate* class instances each of which was successfully matched against the search values.

**Return type** list

**find_model_and_generate**(*values: list*, *target_values_operator: str = 'AND'*, *are_keys_also_matched: bool = False*, *is_case_sensitive: bool = False*, *num_samples: int = 30*, *output_path: Optional[str] = None*, *is_gen_function_returned: bool = False*, *install_dependencies: bool = False*, ***kwargs*)

Search for values (and keys) in model configs to generate samples with the found model.

Note that the number of found models should be ==1. Else no samples will be generated and a error is logged to console.

**Parameters**

- **values** (*list*) – list of values used to search and find models corresponding to these *values*

- **target_values_operator** (*str*) – the operator indicating the relationship between *values* in the evaluation of model search results. Should be either "AND", "OR", or "XOR".
- **are_keys_also_matched** (*bool*) – flag indicating whether, apart from values, the keys in the model config should also be searchable
- **is_case_sensitive** (*bool*) – flag indicating whether the search for values (and) keys in the model config should be case-sensitive.
- **num_samples** (*int*) – the number of samples that will be generated
- **output_path** (*str*) – the path as str to the output folder where the generated samples will be stored
- **is_gen_function_returned** (*bool*) – flag indicating whether, instead of generating samples, the sample generation function will be returned
- **install_dependencies** (*bool*) – flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.
- ****kwargs** – arbitrary number of keyword arguments passed to the model's sample generation function

**Returns** However, if *is_gen_function_returned* is True, it returns the internal generate function of the model.

**Return type** None

**find_model_executor_by_id**(*model_id: str*) → *medigan.execute_model.model_executor.ModelExecutor*

Find and return the *ModelExecutor* instance of this model_id in the *self.model_executors* list.

**Parameters** **model_id** (*str*) – The generative model's unique id

**Returns** *ModelExecutor* class instance corresponding to the *model_id*

**Return type** *ModelExecutor*

**find_models_and_rank**(*values: list*, *target_values_operator: str = 'AND'*, *are_keys_also_matched: bool = False*, *is_case_sensitive: bool = False*, *metric: str = 'SSIM'*, *order: str = 'asc'*) → list

Search for values (and keys) in model configs, rank results and return sorted list of model dicts.

This function calls an identically named function in a *ModelSelector* instance.

**Parameters**

- **values** (*list`*) – list of values used to search and find models corresponding to these *values*
- **target_values_operator** (*str*) – the operator indicating the relationship between *values* in the evaluation of model search results. Should be either "AND", "OR", or "XOR".
- **are_keys_also_matched** (*bool*) – flag indicating whether, apart from values, the keys in the model config should also be searchable
- **is_case_sensitive** (*bool*) – flag indicating whether the search for values (and) keys in the model config should be case-sensitive.
- **metric** (*str*) – The key in the selection dict that corresponds to the metric of interest
- **order** (*str*) – the sorting order of the ranked results. Should be either "asc" (ascending) or "desc" (descending)

**Returns** a list of the searched and matched model dictionaries containing metric and model_id, sorted by metric.

**Return type** list

**find_models_rank_and_generate**(*values: list*, *target_values_operator: str = 'AND'*, *are_keys_also_matched: bool = False*, *is_case_sensitive: bool = False*, *metric: str = 'SSIM'*, *order: str = 'asc'*, *num_samples: int = 30*, *output_path: Optional[str] = None*, *is_gen_function_returned: bool = False*, *install_dependencies: bool = False*, ***kwargs*)

Search for values (and keys) in model configs, rank results to generate samples with highest ranked model.

**Parameters**

- **values** (*list*) – list of values used to search and find models corresponding to these *values*
- **target_values_operator** (*str*) – the operator indicating the relationship between *values* in the evaluation of model search results. Should be either "AND", "OR", or "XOR".
- **are_keys_also_matched** (*bool*) – flag indicating whether, apart from values, the keys in the model config should also be searchable
- **is_case_sensitive** (*bool*) – flag indicating whether the search for values (and) keys in the model config should be case-sensitive.
- **metric** (*str*) – The key in the selection dict that corresponds to the metric of interest
- **order** (*str*) – the sorting order of the ranked results. Should be either "asc" (ascending) or "desc" (descending)
- **num_samples** (*int*) – the number of samples that will be generated
- **output_path** (*str*) – the path as str to the output folder where the generated samples will be stored
- **is_gen_function_returned** (*bool*) – flag indicating whether, instead of generating samples, the sample generation function will be returned
- **install_dependencies** (*bool*) – flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.
- ****kwargs** – arbitrary number of keyword arguments passed to the model's sample generation function

**Returns** However, if *is_gen_function_returned* is True, it returns the internal generate function of the model.

**Return type** None

**generate**(*model_id: str*, *num_samples: int = 30*, *output_path: Optional[str] = None*, *save_images: bool = True*, *is_gen_function_returned: bool = False*, *install_dependencies: bool = False*, ***kwargs*)

Generate samples with the model corresponding to the *model_id* or return the model's generate function.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **num_samples** (*int*) – the number of samples that will be generated
- **output_path** (*str*) – the path as str to the output folder where the generated samples will be stored

- **save_images** (*bool*) – flag indicating whether generated samples are returned (i.e. as list of numpy arrays) or rather stored in file system (i.e in *output_path*)
- **is_gen_function_returned** (*bool*) – flag indicating whether, instead of generating samples, the sample generation function will be returned
- **install_dependencies** (*bool*) – flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.
- ****kwargs** – arbitrary number of keyword arguments passed to the model's sample generation function

**Returns** Returns images as list of numpy arrays if *save_images* is False. However, if *is_gen_function_returned* is True, it returns the internal generate function of the model.

**Return type** list

**get_as_torch_dataloader**(*dataset=None*, *model_id: Optional[str] = None*, *num_samples: int = 1000*, *install_dependencies: bool = False*, *transform=None*, *batch_size=1*, *shuffle=False*, *sampler=None*, *batch_sampler=None*, *num_workers=0*, *collate_fn=None*, *pin_memory=False*, *drop_last=False*, *timeout=0*, *worker_init_fn=None*, *prefetch_factor=2*, *persistent_workers=False*, ***kwargs*) → torch.utils.data.dataloader.DataLoader

Get torch Dataloader sampling synthetic data from medigan model.

Dataloader combines a dataset and a sampler, and provides an iterable over the given torch dataset. Dataloader is created for synthetic data for the specified medigan model.

**Parameters**

- **dataset** (*Dataset*) – dataset from which to load the data.
- **model_id** – str The generative model's unique id
- **num_samples** – int the number of samples that will be generated
- **install_dependencies** – bool flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.
- ****kwargs** – arbitrary number of keyword arguments passed to the model's sample generation function (e.g. the input path for image-to-image translation models in medigan).
- **transform** – the torch data transformation functions to be applied to the data in the dataset.
- **batch_size** (*int, optional*) – how many samples per batch to load (default: 1).
- **shuffle** (*bool, optional*) – set to `True` to have the data reshuffled at every epoch (default: `False`).
- **sampler** (*Sampler or Iterable, optional*) – defines the strategy to draw samples from the dataset. Can be any `Iterable` with `__len__` implemented. If specified, `shuffle` must not be specified.
- **batch_sampler** (*Sampler or Iterable, optional*) – like `sampler`, but returns a batch of indices at a time. Mutually exclusive with `batch_size`, `shuffle`, `sampler`, and `drop_last`.
- **num_workers** (*int, optional*) – how many subprocesses to use for data loading. `0` means that the data will be loaded in the main process. (default: `0`)
- **collate_fn** (*callable, optional*) – merges a list of samples to form a mini-batch of Tensor(s). Used when using batched loading from a map-style dataset.

- **pin_memory** (*bool, optional*) – If `True`, the data loader will copy Tensors into CUDA pinned memory before returning them. If your data elements are a custom type, or your `collate_fn` returns a batch that is a custom type, see the example below.
- **drop_last** (*bool, optional*) – set to `True` to drop the last incomplete batch, if the dataset size is not divisible by the batch size. If `False` and the size of dataset is not divisible by the batch size, then the last batch will be smaller. (default: `False`)
- **timeout** (*numeric, optional*) – if positive, the timeout value for collecting a batch from workers. Should always be non-negative. (default: `0`)
- **worker_init_fn** (*callable, optional*) – If not `None`, this will be called on each worker subprocess with the worker id (an int in `[0, num_workers - 1]`) as input, after seeding and before data loading. (default: `None`)
- **prefetch_factor** (*int, optional, keyword-only arg*) – Number of samples loaded in advance by each worker. `2` means there will be a total of 2 * num_workers samples prefetched across all workers. (default: `2`)
- **persistent_workers** (*bool, optional*) – If `True`, the data loader will not shutdown the worker processes after a dataset has been consumed once. This allows to maintain the workers *Dataset* instances alive. (default: `False`)

**Returns** a torch.utils.data.DataLoader object with data generated by model corresponding to inputted *Dataset* or *model_id*.

**Return type** DataLoader

**get_as_torch_dataset**(*model_id: str*, *num_samples: int = 100*, *install_dependencies: bool = False*, *transform=None*, ***kwargs*) → torch.utils.data.dataset.Dataset

Get synthetic data in a torch Dataset for specified medigan model.

The dataset returns a dict with keys sample (== image), labels (== condition), and mask (== segmentation mask). While key 'sample' is mandatory, the other key value pairs are only returned if applicable to generative model.

**Parameters**

- **model_id** – str The generative model's unique id
- **num_samples** – int the number of samples that will be generated
- **install_dependencies** –

  **bool** flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.

  **transform** the torch data transformation functions to be applied to the data in the dataset.
- ****kwargs** – arbitrary number of keyword arguments passed to the model's sample generation function (e.g. the input path for image-to-image translation models in medigan).

**Returns** a torch.utils.data.Dataset object with data generated by model corresponding to *model_id*.

**Return type** Dataset

**get_config_by_id**(*model_id: str*, *config_key: Optional[str] = None*) → dict

Get and return the part of the config below a *config_key* for a specific *model_id*.

The config_key parameters can be separated by a '.' (dot) to allow for retrieval of nested config keys, e.g, 'execution.generator.name'

This function calls an identically named function in a *ConfigManager* instance.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **config_key** (*str*) – A key of interest present in the config dict

**Returns** a dictionary from the part of the config file corresponding to *model_id* and *config_key*.

**Return type** dict

**get_generate_function**(*model_id: str*, *num_samples: int = 30*, *output_path: Optional[str] = None*, *install_dependencies: bool = False*, ***kwargs*)

Return the model's generate function.

Relies on the *self.generate* function.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **num_samples** (*int*) – the number of samples that will be generated
- **output_path** (*str*) – the path as str to the output folder where the generated samples will be stored
- **install_dependencies** (*bool*) – flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.
- ****kwargs** – arbitrary number of keyword arguments passed to the model's sample generation function

**Returns** The internal reusable generate function of the generative model.

**Return type** function

**get_model_contributor_by_id**(*model_id: str*) → *medigan.contribute_model.model_contributor.ModelContributor*

Find and return the *ModelContributor* instance of this model_id in the *self.model_contributors* list.

**Parameters** **model_id** (*str*) – The generative model's unique id

**Returns** *ModelContributor* class instance corresponding to the *model_id*

**Return type** *ModelContributor*

**get_model_executor**(*model_id: str*, *install_dependencies: bool = False*) → *medigan.execute_model.model_executor.ModelExecutor*

Add and return the *ModelExecutor* instance of this model_id from the *self.model_executors* list.

Relies on *self.add_model_executor* and *self.find_model_executor_by_id* functions.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **install_dependencies** (*bool*) – flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.

**Returns** *ModelExecutor* class instance corresponding to the *model_id*

**Return type** *ModelExecutor*

**get_models_by_key_value_pair**(*key1: str*, *value1: str*, *is_case_sensitive: bool = False*) → list

Get and return a list of model_id dicts that contain the specified key value pair in their selection config.

The key param can contain '.' (dot) separations to allow for retrieval of nested config keys such as 'execution.generator.name'

This function calls an identically named function in a *ModelSelector* instance.

**Parameters**

- **key1** (*str*) – The key in the selection dict
- **value1** (*str*) – The value in the selection dict that corresponds to key1
- **is_case_sensitive** (*bool*) – flag to evaluate keys and values with case sensitivity if set to True

**Returns** a list of the dictionaries each containing a models id and the found key-value pair in the models config

**Return type** list

**get_selection_criteria_by_id**(*model_id: str*, *is_model_id_removed: bool = True*) → dict

Get and return the selection config dict for a specific model_id.

This function calls an identically named function in a *ModelSelector* instance.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **is_model_id_removed** (*bool*) – flag to to remove the model_ids from first level of dictionary.

**Returns** a dictionary corresponding to the selection config of a model

**Return type** dict

**get_selection_criteria_by_ids**(*model_ids: Optional[list] = None*, *are_model_ids_removed: bool = True*) → list

Get and return a list of selection config dicts for each of the specified model_ids.

This function calls an identically named function in a *ModelSelector* instance.

**Parameters**

- **model_ids** (*list*) – A list of generative models' unique ids or ids abbreviated as integers (e.g. 1, 2, .. 21)
- **are_model_ids_removed** (*bool*) – flag to remove the model_ids from first level of dictionary.

**Returns** a list of dictionaries each corresponding to the selection config of a model

**Return type** list

**get_selection_keys**(*model_id: Optional[str] = None*) → list

Get and return all first level keys from the selection config dict for a specific model_id.

This function calls an identically named function in a *ModelSelector* instance.

**Parameters** **model_id** (*str*) – The generative model's unique id

**Returns** a list containing the keys as strings of the selection config of the *model_id*.

**Return type** list

**get_selection_values_for_key**(*key: str*, *model_id: Optional[str] = None*) → list

Get and return the value of a specified key of the selection dict in the config for a specific model_id.

The key param can contain '.' (dot) separations to allow for retrieval of nested config keys such as 'execution.generator.name'

This function calls an identically named function in a *ModelSelector* instance.

**Parameters**

- **key** (*str*) – The key in the selection dict
- **model_id** (*str*) – The generative model's unique id

**Returns** a list of the values that correspond to the key in the selection config of the *model_id*.

**Return type** list

**is_model_executor_already_added**(*model_id*) → bool

Check whether the *ModelExecutor* instance of this model_id is already in *self.model_executors* list.

**Parameters** **model_id** (*str*) – The generative model's unique id

**Returns** indicating whether this *ModelExecutor* had been already previously added to *self.model_executors*

**Return type** bool

**is_model_metadata_valid**(*model_id: str*, *metadata: dict*, *is_local_model: bool = True*) → bool

Checking if a model's corresponding metadata is valid.

Specific fields in the model's metadata are mandatory. It is asserted if these key value pairs are present.

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **metadata** (*dict*) – The model's corresponding metadata
- **is_local_model** (*bool*) – flag indicating whether the tested model is a new local user model i.e not yet part of medigan's official models

**Returns** Flag indicating whether the specific model's metadata format and fields are valid

**Return type** bool

**list_models**() → list

Return the list of model_ids as strings based on config.

**Return type** list

**push_to_github**(*model_id: str*, *github_access_token: str*, *package_link: Optional[str] = None*, *creator_name: str = ''*, *creator_affiliation: str = ''*, *model_description: str = ''*)

Upload the model's metadata inside a github issue to the medigan github repository.

To add your model to medigan, your metadata will be reviewed on Github and added to medigan's official model metadata

The medigan repository issues page: https://github.com/RichardObi/medigan/issues

Get your Github access token here: https://github.com/settings/tokens

**Parameters**

- **model_id** (*str*) – The generative model's unique id

- **github_access_token** (*str*) – a personal access token linked to your github user account, used as means of authentication
- **package_link** – a package link
- **creator_name** (*str*) – the creator name that will appear on the corresponding github issue
- **creator_affiliation** (*str*) – the creator affiliation that will appear on the corresponding github issue
- **model_description** (*list*) – the model_description that will appear on the corresponding github issue

**Returns** Returns the url pointing to the corresponding issue on github

**Return type** str

**push_to_zenodo**(*model_id: str*, *zenodo_access_token: str*, *creator_name: str = 'unknown name'*, *creator_affiliation: str = 'unknown affiliation'*, *model_description: str = ''*) → str

Upload the model files as zip archive to a public Zenodo repository where the model will be persistently stored.

Get your Zenodo access token here: https://zenodo.org/account/settings/applications/tokens/new/ (Enable scopes *deposit:actions* and *deposit:write*)

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **zenodo_access_token** (*str*) – a personal access token in Zenodo linked to a user account for authentication
- **creator_name** (*str*) – the creator name that will appear on the corresponding Zenodo model upload homepage
- **creator_affiliation** (*str*) – the creator affiliation that will appear on the corresponding Zenodo model upload homepage
- **model_description** (*list*) – the model_description that will appear on the corresponding Zenodo model upload homepage

**Returns** Returns the url pointing to the corresponding Zenodo model upload homepage

**Return type** str

**rank_models_by_performance**(*model_ids: Optional[list] = None*, *metric: str = 'SSIM'*, *order: str = 'asc'*) → list

Rank model based on a provided metric and return sorted list of model dicts.

The metric param can contain '.' (dot) separations to allow for retrieval of nested metric config keys such as 'downstream_task.CLF.accuracy'

This function calls an identically named function in a *ModelSelector* instance.

**Parameters**

- **model_ids** (*list*) – only evaluate the *model_ids* in this list. If none, evaluate all available *model_ids*
- **metric** (*str*) – The key in the selection dict that corresponds to the metric of interest
- **order** (*str*) – the sorting order of the ranked results. Should be either "asc" (ascending) or "desc" (descending)

**Returns** a list of model dictionaries containing metric and *model_id*, sorted by metric.

**Return type** list

**test_model**(*model_id: str*, *is_local_model: bool = True*, *overwrite_existing_metadata: bool = False*, *store_new_config: bool = True*, *num_samples: int = 3*, *install_dependencies: bool = False*)

Test if a model generates and returns a specific number of samples in the correct format

**Parameters**

- **model_id** (*str*) – The generative model's unique id
- **is_local_model** (*bool*) – flag indicating whether the tested model is a new local user model i.e not yet part of medigan's official models
- **overwrite_existing_metadata** (*bool*) – in case of *is_local_model*, flag indicating whether existing metadata for this model in medigan's *config/global.json* should be overwritten.
- **store_new_config** (*bool*) – flag indicating whether the current model metadata should be stored on disk i.e. in config/
- **num_samples** (*int*) – the number of samples that will be generated
- **install_dependencies** (*bool*) – flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.

**visualize**(*model_id: str*, *slider_grouper: int = 10*, *auto_close: bool = False*, *install_dependencies: bool = False*) → None

Initialize and run *ModelVisualizer* of this model_id if it is available. It allows to visualize a sample from the model's output. UI window will pop up allowing the user to control the generation parameters (conditional and unconditional ones).

**Parameters**

- **model_id** (*str*) – The generative model's unique id to visualize.
- **slider_grouper** (*int*) – Number of input parameters to group together within one slider.
- **auto_close** (*bool*) – Flag for closing the user interface automatically after time. Used while testing.
- **install_dependencies** (*bool*) – flag indicating whether a generative model's dependencies are automatically installed. Else error is raised if missing dependencies are detected.

### medigan.model_visualizer module

*ModelVisualizer* class providing visualizing corresponding model input and model output changes.

**class** medigan.model_visualizer.**ModelVisualizer**(*model_executor*, *config: None*)

Bases: object

*ModelVisualizer* class: Visualises synthetic data through a user interface. Depending on a model, it is possible to control the input latent vector values and conditional input.

**Parameters**

- **model_executor** (ModelExecutor) – The generative model's executor object
- **config** (*dict*) – The config dict containing the model metadata

**model_executor**

The generative model's executor object

**Type** *ModelExecutor*

**input_latent_vector_size**

Size of the latent vector used as an input for generation

**Type** int

**conditional**

Flag for models with conditional input

**Type** bool

**condition**

Value of the conditinal input to the model

**Type** Union[int, float]

**max_input_value**

Absolute value used for setting latent values input range

**Type** float

**visualize**(*slider_grouper: int = 10*, *auto_close=False*)

Visualize the model's output. This method is called by the user. It opens up a user interface with available controls.

**Parameters**

- **slider_grouper** (*int*) – Number of input parameters to group together within one slider.
- **auto_close** (*bool*) – Flag for closing the user interface automatically after time. Used while testing.

**Return type** None

### medigan.utils module

*Utils* class providing generalized reusable functions for I/O, parsing, sorting, type conversions, etc.

**class** medigan.utils.**Utils**

Bases: object

Utils class containing reusable static methods.

**static copy**(*source_path: pathlib.Path*, *target_path: str = './'*)

copy a folder or file from *source_path* to *target_path*

**static deep_get**(*base_dict: dict*, *key: str*)

Split the key by "." to get value in nested dictionary.

**static dict_to_lowercase**(*target_dict: dict*, *string_conversion: bool = True*) → dict

transform values and keys in dict to lowercase, optionally with string conversion of the values.

Warning: Does not convert nested dicts in the *target_dict*, but rather removes them from return object.

**static download_file**(*download_link: str*, *path_as_string: str*, *file_extension: str = '.json'*)

download a file using the *requests* lib and store in *path_as_string*

**static has_more_than_n_diff_pixel_values**(*img: numpy.ndarray*, *n: int = 4*) → bool

This function checks whether an image contains more than n different pixel values.

This helps to differentiate between segmentation masks and actual images.

**static is_file_in**(*folder_path: str*, *filename: str*) → bool

Checks if a file is inside a folder

**static is_file_located_or_downloaded**(*path_as_string: str*, *download_if_not_found: bool = True*, *download_link: Optional[str] = None*, *is_new_download_forced: bool = False*, *allow_local_path_as_url: bool = True*) → bool

check if is file in *path_as_string* and optionally download the file (again).

**static is_url_valid**(*the_url: str*) → bool

Checks if a url is valid using urllib.parse.urlparse

**static list_to_lowercase**(*target_list: list*) → list

string conversion and lower-casing of values in list.

trade-off: String conversion for increased robustness > type failure detection

**static mkdirs**(*path_as_string: str*) → bool

create folder in *path_as_string* if not already created.

**static order_dict_by_value**(*dict_list*, *key: str*, *order: str = 'asc'*, *sort_algorithm='bubbleSort'*) → list

Sorting a list of dicts by the values of a specific key in the dict using a sorting algorithm.

- This function is deprecated. You may use Python List sort() with key=lambda function instead.

**static read_in_json**(*path_as_string*) → dict

read a .json file and return as dict

**static split_images_and_masks_no_ordering**(*data: list*, *num_samples: int*, *max_nested_arrays: int = 2*) → [<class 'numpy.ndarray'>, <class 'numpy.ndarray'>]

Extracts and separates the masks from the images if a model returns both in the same np.ndarray.

This extendable function assumes that, in data, a mask follows the image that it corresponds to or vice versa.

- This function is deprecated. Please use *split_images_masks_and_labels* instead.

**static split_images_masks_and_labels**(*data: list*, *num_samples: int*, *max_nested_arrays: int = 2*) → [<class 'list'>, <class 'list'>, <class 'list'>, <class 'list'>]

Separates the data (sample, mask, other_imaging_data, label) returned by a generative model

This functions expects a list of tuples as input *data* and assumes that each tuple contains sample, mask, other_imaging_data, label at index positions [0], [1], [2], and [3] respectively.

samples, masks, and imaging data are expected to be of type np.ndarray and labels of type "str".

For example, this extendable function assumes that, in data, a mask follows the image that it corresponds to or vice versa.

**static store_dict_as**(*dictionary*, *extension: str = '.json'*, *output_path: str = 'config/'*, *filename: str = 'metadata.json'*)

store a Python dictionary in file system as variable filetype.

**static unzip_and_return_unzipped_path**(*package_path: str*)

if not already dir, unzip an archive with *Utils.unzip_archive*. Return path to unzipped dir/file

**static unzip_archive**(*source_path: pathlib.Path*, *target_path: str = './'*)
unzip a .zip archive in the *target_path*

### Module contents

*medigan* is a modular Python library for automating synthetic dataset generation.

## 1.6 Tests

**Table of Contents**



Automated continuous integration (CI) tests (GitHub actions) are triggered by commits to the medigan repository. These CI tests can be found here.

Apart from that, to facilitate testing if *medigan* is setup correctly and whether all of the features in *medigan* work as desired, the following set of automated test cases is provided. Below, each test function is described and a command is provided to run each test.

### 1.6.1 Setup medigan for running tests

Open your command line, and clone *medigan* from Github with:

```
git clone https://github.com/RichardObi/medigan.git
cd medigan
```

To install dependencies and to setup and activate a virtual environment, run:

```
pip install pipenv
pipenv install
pipenv shell
```

### 1.6.2 Test 1: test_medigan_imports

This test checks if *medigan* can be imported correctly.

```
python -m tests.tests TestMediganMethods.test_medigan_imports
```

### 1.6.3 Test 2: test_init_generators

This test checks if the central *generators* class can be initialised correctly.

```
python -m tests.tests TestMediganMethods.test_init_generators
```

### 1.6.4 Test 3: test_generate_methods

This test examines whether samples can be created with any of three example generative models (1, 2, 3) in *medigan*.

```
python -m tests.tests TestMediganMethods.test_generate_methods
```

### 1.6.5 Test 4: test_generate_methods_with_additional_args

Additional key-value pair arguments (kwargs) can be provided to the *generate()* method of a generative model. This test checks if these additional arguments are passed correctly to the generate method and whether the generate method's returned result corresponds to the passed arguments.

```
python -m tests.tests TestMediganMethods.test_generate_methods_with_additional_args
```

### 1.6.6 Test 5: test_get_generate_method

The *generate()* method of any of the generative models in *medigan* can be returned. This makes it easier to integrate the *generate()* function dynamically into users' data processing and training pipelines i.e. avoiding it to reload the model weights each time it is called. This test tests if the *generate()* method is successfully returned and usable thereafter.

```
python -m tests.tests TestMediganMethods.test_get_generate_method
```

### 1.6.7 Test 6: test_search_for_models_method

The tested function searches for a model by matching provided key words with the information in the model's config. This test checks whether the expected models are found accordingly.

```
python -m tests.tests TestMediganMethods.test_search_for_models_method
```

### 1.6.8 Test 7: test_find_model_and_generate_method

After searching and finding one specific model, the tested function generates samples with that model. This test checks whether the expected model is found and whether samples are generated accordingly.

```
python -m tests.tests TestMediganMethods.test_find_model_and_generate_method
```

### 1.6.9 Test 8: test_rank_models_by_performance

Provided a list of model ids, the tested function rankes these models by a performance metric. The performance metrics are stored in the models' config. This test checks whether the ranking worked and whether the expected model is ranked the highest.

```
python -m tests.tests TestMediganMethods.test_rank_models_by_performance
```

### 1.6.10 Test 9: test_find_and_rank_models_by_performance

After searching and finding various models, the tested function ranks these models by a performance metric. This test checks whether the expected model is found, and whether it is the highest ranked one and whether it generated samples accordingly.

```
python -m tests.tests TestMediganMethods.test_find_and_rank_models_by_performance
```

### 1.6.11 Test 10: test_find_and_rank_models_then_generate_method

After searching and finding various models, the tested function ranks these models by a performance metric and generates samples with the highest ranked model. This test checks whether the expected model is found, whether it is the highest ranked one and whether it generated samples accordingly.

```
python -m tests.tests TestMediganMethods.test_find_and_rank_models_then_generate_method
```

### 1.6.12 Test 11: test_get_models_by_key_value_pair

After receiving a key value pair, the tested function returns all models that have that key-value pair in their model config. This test checks whether the expected models are found and returned correctly.

```
python -m tests.tests TestMediganMethods.test_get_models_by_key_value_pair
```

## 1.7 Model Contributions

We are happy that you are considering contributing your model to *medigan*. This will make your model accessible to the community and our users can easily integrate your synthetic data into their training pipelines and experiments.

### 1.7.1 Guide: Automated Model Contribution

Create an __init__.py file in your model's root folder.

Next, run the following code to contribute your model to *medigan*.

- Your model will be stored on Zenodo.
- Also, a Github issue will be created to add your model's metadata to medigan's global.json.
- To do so, please provide a github access token (get one here) and a zenodo access token (get one here), as shown below. After creation, the zenodo access token may take a few minutes before being recognized in zenodo API calls.

```
from medigan import Generators
gen = Generators()

# Contribute your model
gen.contribute(
    model_id = "00100_YOUR_MODEL", # assign an ID
    init_py_path ="path/ending/with/__init__.py",
    model_weights_name = "10000",
    model_weights_extension = ".pt",
    generate_method_name = "generate", # in __init__.py
    dependencies = ["numpy", "torch"],
    creator_name = "YOUR_NAME",
    creator_affiliation = "YOUR_AFFILIATION",
    zenodo_access_token = 'ZENODO_ACCESS_TOKEN',
    github_access_token = 'GITHUB_ACCESS_TOKEN',
)
```

### 1.7.2 Guide: Manual Model Contribution

In the following, you find a step-by-step guide on how to contribute your generative model to *medigan*. In case you encounter problems during this process feel free to reach out by creating an issue here and we will try to help. Checkout the figure below that shows the main components of the model contribution workflow depicted in yellow (d).

If you are here, you have recently developed a generative model such as a GAN, VAE, Diffusion Model, etc and you would like to boost your model's impact, reusability, dissemination by uploading it to *medigan*. We are delighted and will assist you in adding your model.

1. **Firstly, let's create the needed files:**

   To add your model you will need the following files.

   1. A checkpoint file that contains your trained model weights (e.g., the `state_dict` in pytorch)
   2. An `__init__.py` file that contains functions that
      - load the weights file (let's call that one `weights.pt`)
      - initialize your model with these weights
      - generate samples with the initialized model.
   3. Now that you have the `weights.pt` and the `__init__.py`, let's check if we can make them work together.
      1. Run your `__init__.py`'s generate function using e.g. `python -m __init__.py generate`

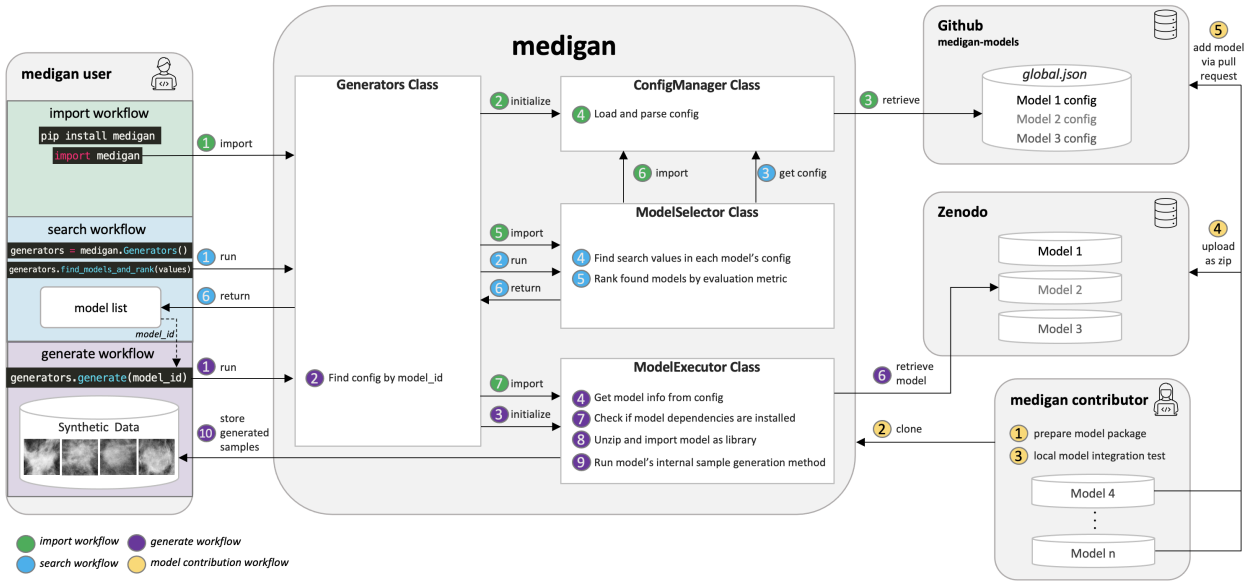



Fig. 3: Architectural overview including main workflows consisting of (a) library import and initialisation, (b) generative model search and ranking, (c) sample generation, and (d) generative model contribution.

2. Check whether your model did load the weights effectively and whether synthetic samples were generated as expected.

4. Apply some necessary adjustments to your model package, particularly to your `__init__.py`:

   1. We have some templates that you can use to guide the adjustments described below

      - If you are using a model that generates samples **without** image input (e.g., noise-to-image): Download Model 00002 from here. Unzip it and open the `__init__.py` that contains an example `generate()` method.
      - If you are using a model that generates samples **with** image input (e.g., image-to-image): Download Model 00003 from here. Unzip it and open the `__init__.py` that contains an example `generate()` method.

   2. Please note that user's of *medigan* models may add your model to their preprocessing or AI training pipelines. Please make sure that your model, hence, runs efficiently. For instance, your model should load the weights only once even though the generate() function is called multiple times.

   3. Please make sure your model is able to run both on gpu and on cpu and your code automatically detects on which one to run.

   4. Please replace all `print()` functions from your code with `logging.debug()` (for this you need to `import logging`).

   5. Please add appropriate error handling using `try, except` blocks on each possible source of error in your code. `raise` the error in your `generate()` function to allow *medigan* to handle it and pass it to the user.

   6. If your generative model needs some input images, provide a few example images in a folder called `/images`. Users may test your model with these example images before feeding their own input images to your model.

   7. There are a few parameters of the `generate()` that are mandatory in *medigan* and others that you can set optionally.

- **Mandatory:**
  - `model_file`: string, the path where your `generate()` method will find its weight file
  - `output_path`: string, the path where our `generate()` method should store the generated images
  - `save_images`: boolean, whether your `generate()` method should store generated samples in `output_path` or return them as numpy arrays.
  - `num_samples`: int, the number of samples that should be generated.
- **Optional:**
  - `input_path`: string, the path where our `generate()` method finds images that should be used as input into the generative model (i.e. in image-to-image translation).
  - `image_size`: array, that contains image height, width, and, optionally, also depth.
  - `translate_all_images`: boolean, in image-to-image translation, if `True`, this overwrites the `num_samples` and instead translates all images found in `input_path`.
  - `gpu_id`: int, if a user has various GPUs available, the user can specify which one of them to use to run your generative model.

2. **Secondly, test your model locally:** Okay, now that we know which files we need, let's test them using a local version of *medigan*.
   1. Let's start by cloning *medigan* e.g. using the command line: `git clone https://github.com/RichardObi/medigan.git`
   2. Next, cd into *medigan*, install the dependencies of *medigan*, and create a virtual environment.

      You can do so running these commands:
      - `cd medigan`
      - `pip install pipenv`
      - `pipenv install`
      - `pipenv shell`
   3. Now that you have your environment up and running, please run the following command to download the config file.
      - `python -m tests.tests TestMediganMethods.test_init_generators`
   4. In the folder `/config`, you should now see a file called global.json. In this file each model's metadata is stored.
      - Please add the metadata for your model at the bottom of the *global.json* file.
      - To add the metadata, you can use the metadata of model 00001 in global.json as example.
      - **Copy the metadata of model 00001 and add it to the bottom of `global.json`. Then adjust each entry in th**
        - The `model_id` should follow the convention `NNNNN_TTTTTT_MMMM_AAAAA_GGGG` (N = Number of model, T = Type of model, M = Modality, A = Anatomic/Ailment Information, G = Generated Sample Type information i.e. full for full image or roi for region of interest)
        - The field `package_link` (under `execution`) should point to a local zip file `NAME_OF_YOUR_MODEL_PACKAGE.zip` of your model package.

- json entries below `execution` are important and needed to run the model in *medigan*, e.g. the name and parameters of a `generate()` function in the `__init__.py`
- json entries below `selection` are important to enable users to search and rank the model compared to other models in *medigan*, e.g. the performance indicators such as SSIM, MSE, PSNR, etc.
- json entries below `description` are to allow tracing back the origin and metadata of the model and allow users to get further information about the model, e.g. license, related publications, etc.

5. You are almost done! It's Testing Time!
   - Run a local test using the following code:

```
from medigan import Generators
gen = Generators()
gen.generate(model_id="YOUR_MODEL_ID")

# Test a few variations.
test_dict = {"translate_all_images": True, "SOME_OTHER_OPTIONAL_
↪PARAMS": True}
gen.generate(model_id="YOUR_MODEL_ID", num_samples=100, output_path=
↪"here", save_images=True, **test_dict)
```

   - If you are code runs well with different settings/params, congratulations, you have made it! You integrated your model as a package into *medigan* and are now ready for the final steps.

3. **Thirdly, upload your model:**
   1. Package and upload your model to Zenodo - home to your model's code and documentation.
      1. First, check if your model package folder contains an `__init__.py`, a `weights` file, a `license` file, and optionally other files.
      2. The next step is to zip this folder. To do so (e.g., on MACOS) you may `cd` into the folder and use the following commands (while removing hidden OS system files):

```
find . -name ".DS_Store" -delete
zip -r NAME_OF_YOUR_MODEL_PACKAGE.zip . -x ".*" -x "__MACOSX"
```

**Now that you have your model package zipped and ready, note that *medigan* model's are commonly stored in Z**

- they get a DOI
- the content of their package is non editable i.e. no file modifications/updates without new DOI.
- This helps to avoid security issues as package content remains static after the model is tested, verified, and added to *medigan*.
- Zenodo has a close to unlimited storage capacity for research data/software.
- Also, the authorship/ownership of the model are clear
- There is transparent licensing.
- Each model is versioned in Zenodo with different DOIs.
- A model documentation and contact information can be added.

1. Checkout this example of our model 00001 on Zenodo. You can use the Zenodo documentation of this model as template for your own model upload.
2. Now, let's go to the Zenodo website.
3. Click on `New Upload` (if you don't have an account, you can quickly create one e.g., using your ORCID)
4. Fill in the metadata fields for your model and upload the model package zip file (i.e. drag and drop).
5. Click on `Save` and `Submit`. Congratulations your model is now on Zenodo! Good job!

4. **Finally, add your model to `medigan's` model metadata:**

   Last step!!! Your model is on Zenodo and tested locally. Now we can officially add it to *medigan*. Remember the `global.json` that you created locally to test your model? It is time for glory for this file.

   1. Now, clone the *medigan-models* repository (the home of medigan's global.json) e.g. by using `git clone https://github.com/RichardObi/medigan-models.git`
   2. Create and checkout a new local branch `git checkout -b mynewbranch`
   3. Open the `global.json` in your cloned local *medigan-models*
   4. Edit the `global.json` file and add your model's entry at the bottom, and save.
   5. Note that this is the time to replace the value of `package_link` from your local model file path to your new Zenodo model URL. To get this URL, go to the Zenodo page of your model, and scroll down to `Files`, where you see a download button. Copy the url link that this button points to, which is your `package_link`.
   6. Commit the new file (`git add .`, `git commit -m "added model YOUR_MODEL_ID."`) and push your branch (`git push`).
   7. Lastly, go to the repository medigan-models and create a pull request that merges your recently pushed branch into `main`.
   8. That's it!!! Your pull request will be evaluated asap. Once approved your model is officially part of *medigan*!

If you have suggestions on improvements for our model contribution process, please take a minute and let us know here.

### 1.7.3 Conventions that your model should follow

- Your model should have a `generate` method with the params model_file:str, num_samples:int, save_images:bool, and output_path:str (see **`template (templates/examples/__init__.py>`_**)
- Also, the model should do simple error handling, run flexibly on either gpu or cpu, use `logging` instead of `prints`, and create some sort of synthetic data.

We hope to welcome you model soon to *medigan*! If you need support, please let us now here.

CHAPTER

TWO

# INDICES

- genindex
- modindex
- search

# PYTHON MODULE INDEX

## m

# INDEX

## D



## E



## F



## G

## H



## I

## O



## P



## R

## S



## T



## U



## V



## Z