
PathFlowAI Documentation

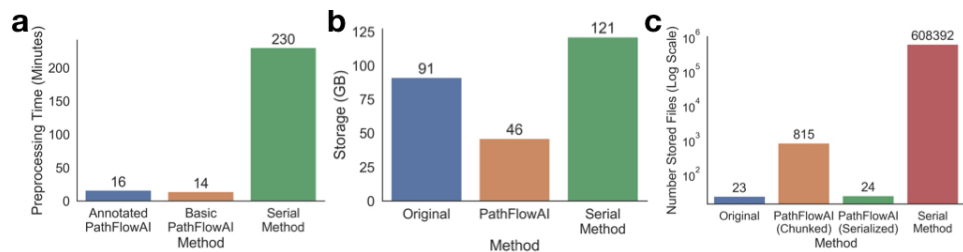
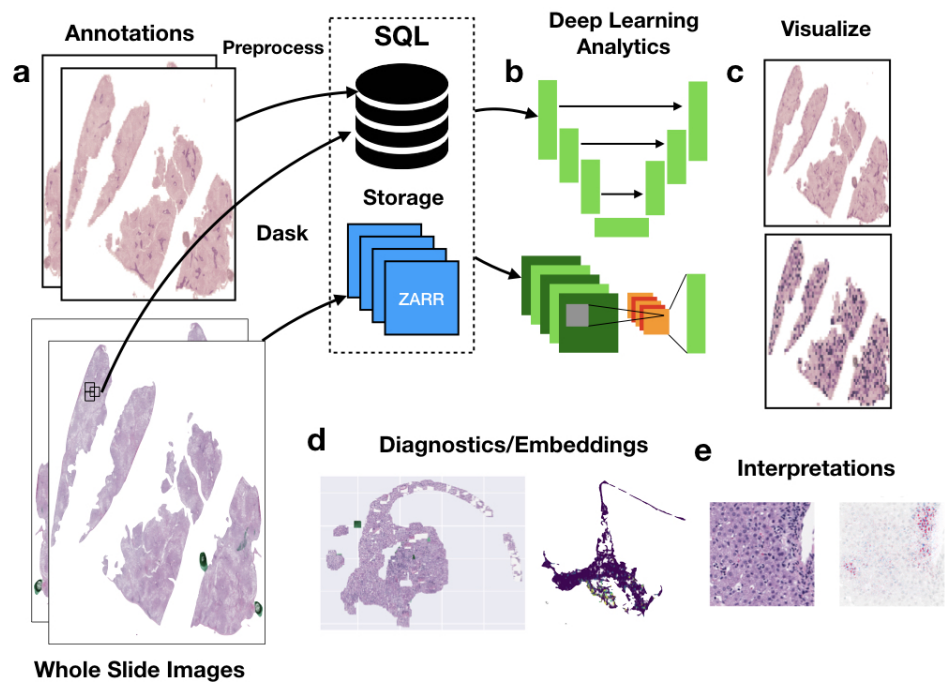
Release 0.1

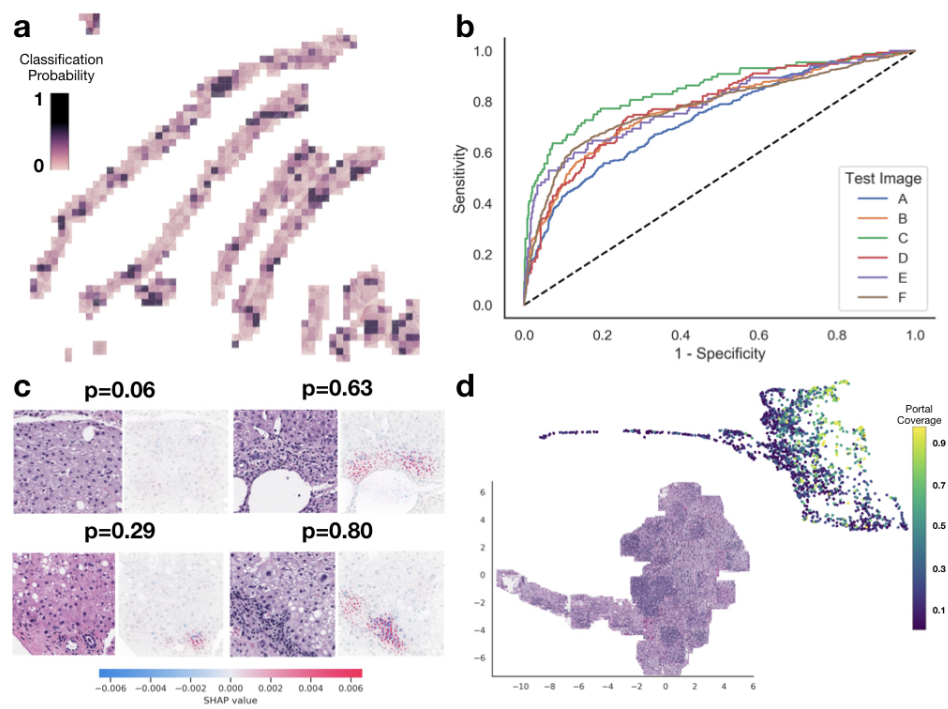
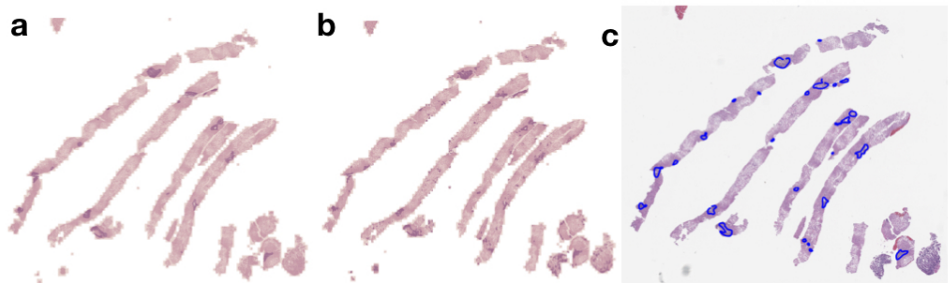
Joshua Levy

Jul 31, 2019

CONTENTS:

1	pathflowai-preprocess	3
1.1	alter_masks	3
1.2	collapse_annotations	3
1.3	preprocess_pipeline	4
1.4	remove_basename_from_db	5
2	pathflowai-visualize	7
2.1	extract_patch	7
2.2	overlay_new_annotations	8
2.3	plot_embeddings	8
2.4	plot_image	9
2.5	plot_image_umap_embeddings	9
2.6	plot_predictions	10
2.7	shapley_plot	11
3	pathflowai-monitor	13
3.1	monitor_usage	13
4	datasets.py	15
5	losses.py	19
6	sampler.py	25
7	schedulers.py	27
8	visualize.py	29
9	utils.py	35
10	Indices and tables	43
	Python Module Index	45
	Index	47





PATHFLOWAI-PREPROCESS

```
pathflowai-preprocess [OPTIONS] COMMAND [ARGS]...
```

Options

--version
Show the version and exit.

1.1 alter_masks

Map list of values to other values in mask.

```
pathflowai-preprocess alter_masks [OPTIONS]
```

Options

-i, --mask_dir <mask_dir>
Input directory for masks. [default: ./inputs/]

-o, --output_dir <output_dir>
Output directory for new masks. [default: ./outputs/]

-fr, --from_annotations <from_annotations>
Annotations to switch from. [default:]

-to, --to_annotations <to_annotations>
Annotations to switch to. [default:]

1.2 collapse_annotations

Adds annotation classes areas to other annotation classes in SQL DB when getting rid of some annotation classes.

```
pathflowai-preprocess collapse_annotations [OPTIONS]
```

Options

- i, --input_patch_db** <input_patch_db>
Input db. [default: patch_info_input.db]
- o, --output_patch_db** <output_patch_db>
Output db. [default: patch_info_output.db]
- fr, --from_annotations** <from_annotations>
Annotations to switch from. [default:]
- to, --to_annotations** <to_annotations>
Annotations to switch to. [default:]
- ps, --patch_size** <patch_size>
Patch size. [default: 224]
- rb, --remove_background_annotation** <remove_background_annotation>
If selected, removes 100% background patches based on this annotation. [default:]
- ma, --max_background_area** <max_background_area>
Max background area before exclusion. [default: 0.05]

1.3 preprocess_pipeline

Preprocessing pipeline that accomplishes 3 things. 1: storage into ZARR format, 2: optional mask adjustment, 3: storage of patch-level information into SQL DB

`pathflowai-preprocess preprocess_pipeline [OPTIONS]`

Options

- np, --img2numpy**
Image to numpy for faster read. [default: False]
- b, --basename** <basename>
Basename of patches. [default: A01]
- i, --input_dir** <input_dir>
Input directory for patches. [default: ./inputs/]
- a, --annotations** <annotations>
Annotations in image in order. [default:]
- pr, --preprocess**
Run preprocessing pipeline. [default: False]
- pa, --patches**
Add patches to SQL. [default: False]
- t, --threshold** <threshold>
Threshold to remove non-purple slides. [default: 0.05]
- ps, --patch_size** <patch_size>
Patch size. [default: 224]
- it, --intensity_threshold** <intensity_threshold>
Intensity threshold to rate a pixel as non-white. [default: 100.0]

- g, --generate_finetune_segmentation**
Generate patches for one segmentation mask class for targeted finetuning. [default: False]
- tc, --target_segmentation_class** <target_segmentation_class>
Segmentation Class to finetune on, output patches to another db. [default: 0]
- tt, --target_threshold** <target_threshold>
Threshold to include target for segmentation if saving one class. [default: 0.0]
- odb, --out_db** <out_db>
Output patch database. [default: ./patch_info.db]
- am, --adjust_mask**
Remove additional background regions from annotation mask. [default: False]
- nn, --n_neighbors** <n_neighbors>
If adjusting mask, number of neighbors connectivity to remove. [default: 5]
- bp, --basic_preprocess**
Basic preprocessing pipeline, annotation areas are not saved. Used for benchmarking tool against comparable pipelines [default: False]

1.4 remove_basename_from_db

Removes basename/ID from SQL DB.

```
pathflowai-preprocess remove_basename_from_db [OPTIONS]
```

Options

- i, --input_patch_db** <input_patch_db>
Input db. [default: patch_info_input.db]
- o, --output_patch_db** <output_patch_db>
Output db. [default: patch_info_output.db]
- b, --basename** <basename>
Basename. [default: A01]
- ps, --patch_size** <patch_size>
Patch size. [default: 224]

PATHFLOWAI-VISUALIZE

```
pathflowai-visualize [OPTIONS] COMMAND [ARGS]...
```

Options

--version
Show the version and exit.

2.1 extract_patch

Extract image of patch of any size/location and output to image file

```
pathflowai-visualize extract_patch [OPTIONS]
```

Options

-i, --input_dir <input_dir>
Input directory for patches. [default: ./inputs/]

-b, --basename <basename>
Basename of patches. [default: A01]

-p, --patch_info_file <patch_info_file>
Database containing all patches [default: patch_info.db]

-ps, --patch_size <patch_size>
Patch size. [default: 224]

-x, --x <x>
X Coordinate of patch. [default: 0]

-y, --y <y>
Y coordinate of patch. [default: 0]

-o, --output_fname <output_fname>
Output extracted image. [default: ./output_image.png]

-s, --segmentation
Plot segmentations. [default: False]

-sc, --n_segmentation_classes <n_segmentation_classes>
Number segmentation classes [default: 4]

-c, --custom_segmentation <custom_segmentation>
Add custom segmentation map from prediction, in npy [default:]

2.2 overlay_new_annotations

Custom annotations, in format [Point: x, y, Point: x, y ...] one line like this per polygon, overlap these polygons on top of WSI.

```
pathflowai-visualize overlay_new_annotations [OPTIONS]
```

Options

-i, --img_file <img_file>
Input image. [default: image.txt]

-a, --annotation_txt <annotation_txt>
Column of annotations [default: annotation.txt]

-ocf, --original_compression_factor <original_compression_factor>
How much compress image. [default: 1.0]

-cf, --compression_factor <compression_factor>
How much compress image. [default: 3.0]

-o, --outputfilename <outputfilename>
Output extracted image. [default: ./output_image.png]

2.3 plot_embeddings

Perform UMAP embeddings of patches and plot using plotly.

```
pathflowai-visualize plot_embeddings [OPTIONS]
```

Options

-i, --embeddings_file <embeddings_file>
Embeddings. [default: predictions/embeddings.pkl]

-o, --plotly_output_file <plotly_output_file>
Plotly output file. [default: predictions/embeddings.html]

-a, --annotations <annotations>
Multiple annotations to color image. [default:]

-rb, --remove_background_annotation <remove_background_annotation>
If selected, removes 100% background patches based on this annotation. [default:]

-ma, --max_background_area <max_background_area>
Max background area before exclusion. [default: 0.05]

-b, --basename <basename>
Basename of patches. [default:]

-nn, --n_neighbors <n_neighbors>
Number nearest neighbors. [default: 8]

2.4 plot_image

Plots the whole slide image supplied.

```
pathflowai-visualize plot_image [OPTIONS]
```

Options

-i, --image_file <image_file>
Input image file. [default: ./inputs/a.svs]

-cf, --compression_factor <compression_factor>
How much compress image. [default: 3.0]

-o, --outputfname <outputfname>
Output extracted image. [default: ./output_image.png]

2.5 plot_image_umap_embeddings

Plots a UMAP embedding with each point as its corresponding patch image.

```
pathflowai-visualize plot_image_umap_embeddings [OPTIONS]
```

Options

-i, --input_dir <input_dir>
Input directory for patches. [default: ./inputs/]

-e, --embeddings_file <embeddings_file>
Embeddings. [default: predictions/embeddings.pkl]

-b, --basename <basename>
Basename of patches. [default:]

-o, --outputfilename <outputfilename>
Embedding visualization. [default: predictions/shap_plots.png]

-mpl, --mpl_scatter
Plot segmentations. [default: False]

-rb, --remove_background_annotation <remove_background_annotation>
If selected, removes 100% background patches based on this annotation. [default:]

-ma, --max_background_area <max_background_area>
Max background area before exclusion. [default: 0.05]

-z, --zoom <zoom>
Size of images. [default: 0.05]

-nn, --n_neighbors <n_neighbors>
Number nearest neighbors. [default: 8]

-sc, --sort_col <sort_col>
Sort samples on this column. [default:]

-sm, --sort_mode <sort_mode>
Sort ascending or descending. [default: asc]

Options ascldesc

2.6 plot_predictions

Overlays classification, regression and segmentation patch level predictions on top of whole slide image.

```
pathflowai-visualize plot_predictions [OPTIONS]
```

Options

-i, --input_dir <input_dir>
Input directory for patches. [default: ./inputs/]

-b, --basename <basename>
Basename of patches. [default: A01]

-p, --patch_info_file <patch_info_file>
Database containing all patches [default: patch_info.db]

-ps, --patch_size <patch_size>
Patch size. [default: 224]

-o, --outputfname <outputfname>
Output extracted image. [default: ./output_image.png]

-an, --annotations
Plot annotations instead of predictions. [default: False]

-cf, --compression_factor <compression_factor>
How much compress image. [default: 3.0]

-al, --alpha <alpha>
How much to give annotations/predictions versus original image. [default: 0.8]

-s, --segmentation
Plot segmentations. [default: False]

-sc, --n_segmentation_classes <n_segmentation_classes>
Number segmentation classes [default: 4]

-c, --custom_segmentation <custom_segmentation>
Add custom segmentation map from prediction, npy format. [default:]

-ac, --annotation_col <annotation_col>
Column of annotations [default: annotation]

-sf, --scaling_factor <scaling_factor>
Multiply all prediction scores by this amount. [default: 1.0]

-tif, --tif_file
Write to tiff file. [default: False]

2.7 shapley_plot

Run SHAPley attribution method on patches after classification task to see where model made prediction based on.

```
pathflowai-visualize shapley_plot [OPTIONS]
```

Options

```
-m, --model_pkl <model_pkl>
    Plotly output file. [default: ]

-bs, --batch_size <batch_size>
    Batch size. [default: 32]

-o, --outputfilename <outputfilename>
    SHAPley visualization. [default: predictions/shap_plots.png]

-mth, --method <method>
    Method of explaining. [default: deep]
        Options deep|gradient

-l, --local_smoothing <local_smoothing>
    Local smoothing of SHAP scores. [default: 0.0]

-ns, --n_samples <n_samples>
    Number shapley samples for shapley regression (gradient explainer). [default: 32]

-p, --pred_out <pred_out>
    If not none, output prediction as shap label. [default: none]
        Options none|sigmoid|softmax
```


PATHFLOWAI-MONITOR

```
pathflowai-monitor [OPTIONS] COMMAND [ARGS]...
```

Options

--version
Show the version and exit.

3.1 monitor_usage

Monitor Usage over Time Interval.

```
pathflowai-monitor monitor_usage [OPTIONS]
```

Options

-csv, --records_output_csv <records_output_csv>
Where to store records. [default: records.csv]

-tt, --total_time <total_time>
Total time to monitor for in minutes. [default: 1.0]

-dt, --delay_time <delay_time>
Time between samples, in seconds. [default: 1.0]

DATASETS.PY

Houses the DynamicImageDataset class, also functions to help with image color channel normalization, transformers, etc..

```
class pathflowai.datasets.DynamicImageDataset (dataset_df,      set,      patch_info_file,
                                              transformers,      input_dir,      tar-
                                              get_names,      pos_annotation_class,
                                              other_annotations=[],
                                              segmentation=False,
                                              patch_size=224,      fix_names=True,
                                              target_segmentation_class=-
                                              1,      target_threshold=0.0,
                                              oversampling_factor=1.0,
                                              n_segmentation_classes=4,
                                              gdl=False,      mt_bce=False,      clas-
                                              sify_annotations=False)
```

Generate image dataset that accesses images and annotations via dask.

Parameters

dataset_df: dataframe Dataframe with WSI, which set it is in (train/test/val) and corresponding WSI labels if applicable.

set: str Whether train, test, val or pass (normalization) set.

patch_info_file: str SQL db with positional and annotation information on each slide.

transformers: dict Contains transformers to apply on images.

input_dir: str Directory where images comes from.

target_names: list/str Names of initial targets, which may be modified.

pos_annotation_class: str If selected and predicting on WSI, this class is labeled as a positive from the WSI, while the other classes are not.

other_annotations: list Other annotations to consider from patch info db.

segmentation: bool Conducting segmentation task?

patch_size: int Patch size.

fix_names: bool Whether to change the names of dataset_df.

target_segmentation_class: list Now can be used for classification as well, matched with two below options, samples images only from this class. Can specify this and below two options multiple times.

target_threshold: list Sampled only if above this threshold of occurrence in the patches.

oversampling_factor:list Over sample them at this amount.

n_segmentation_classes:int Number classes to segment.

gdl:bool Using generalized dice loss?

mt_bce:bool For multi-target prediction tasks.

classify_annotations:bool For classifying annotations.

Methods

<code>binarize_annotations(self[, binarizer, ...])</code>	Label binarize some annotations or threshold them if classifying slide annotations.
<code>concat(self, other_dataset)</code>	Concatenate this dataset with others.
<code>get_class_weights(self[, i])</code>	Weight loss function with weights inversely proportional to the class appearance.
<code>retain_ID(self, ID)</code>	Reduce the sample set to just images from one ID.
<code>split_by_ID(self)</code>	Generator similar to groupby, but splits up by ID, generates (ID,data) using retain_ID.
<code>subsample(self, p)</code>	Sample subset of dataset.

binarize_annotations (*self*, *binarizer=None*, *num_targets=1*, *binary_threshold=0.0*)

Label binarize some annotations or threshold them if classifying slide annotations.

Parameters

binarizer:LabelBinarizer Binarizes the labels of a column(s)

num_targets:int Number of desired targets to predict on.

binary_threshold:float Amount of annotation in patch before positive annotation.

Returns

binarizer

concat (*self*, *other_dataset*)

Concatenate this dataset with others. Updates its own internal attributes.

Parameters

other_dataset:DynamicImageDataset Other image dataset.

get_class_weights (*self*, *i=0*)

Weight loss function with weights inversely proportional to the class appearance.

Parameters

i:int If multi-target, class used for weighting.

Returns

self Dataset.

retain_ID (*self*, *ID*)

Reduce the sample set to just images from one ID.

Parameters

ID:str Basename/ID to predict on.

Returns

self

split_by_ID (*self*)

Generator similar to groupby, but splits up by ID, generates (ID,data) using retain_ID.

Returns

generator ID, DynamicDataset

subsample (*self*, *p*)

Sample subset of dataset.

Parameters

p:float Fraction to subsample.

`pathflowai.datasets.RandomRotate90()`

Transformer for random 90 degree rotation image.

Returns

function Transformer function for operation.

`pathflowai.datasets.create_transforms(mean, std)`

Create transformers.

Parameters

mean:list See get_data_transforms.

std:list See get_data_transforms.

Returns

dict Transformers.

`pathflowai.datasets.get_data_transforms(patch_size=None, mean=[], std=[], resize=False, transform_platform='torch', elastic=True)`

Get data transformers for training test and validation sets.

Parameters

patch_size:int Original patch size being transformed.

mean:list of float Mean RGB

std:list of float Std RGB

resize:int Which patch size to resize to.

transform_platform:str Use pytorch or albumentation transforms.

elastic:bool Whether to add elastic deformations from albumentations.

Returns

dict Transformers.

`pathflowai.datasets.get_normalizer(normalization_file, dataset_opts)`

Find mean and standard deviation of images in batches.

Parameters

normalization_file:str File to store normalization information.

dataset_opts:type Dictionary storing information to create DynamicDataset class.

Returns

dict Stores RGB mean, stdev.

`pathflowai.datasets.segmentation_transform(img, mask, transformer)`

Run augmentations and return an image and its segmentation mask.

Parameters

img:array Image as array

mask:array Categorical pixel by pixel.

transformer : Transformation object.

Returns

tuple arrays Image and mask array.

LOSSES.PY

Some additional loss functions that can be called using the pipeline, some of which still to be implemented.

```
class pathflowai.losses.FocalLoss (num_class, alpha=None, gamma=2, balance_index=-1,
                                   smooth=None, size_average=True)
# https://raw.githubusercontent.com/Hsuxu/Loss\_ToolBox-PyTorch/master/FocalLoss/FocalLoss.py This is a
implementation of Focal Loss with smooth label cross entropy supported which is proposed in 'Focal Loss
for Dense Object Detection. (https://arxiv.org/abs/1708.02002)'
```

```
Focal_Loss= -1*alpha*(1-pt)*log(pt)
```

Parameters

- **num_class** –
- **alpha** – (tensor) 3D or 4D the scalar factor for this criterion
- **gamma** – (float,double) gamma > 0 reduces the relative loss for well-classified examples (p>0.5) putting more focus on hard misclassified example
- **smooth** – (float,double) smooth value when cross entropy
- **balance_index** – (int) balance class index, should be specific when alpha is float
- **size_average** – (bool, optional) By default, the losses are averaged over each loss element in the batch.

Methods

<code>__call__(self, *input, **kwargs)</code>	Call self as a function.
<code>add_module(self, name, module)</code>	Adds a child module to the current module.
<code>apply(self, fn)</code>	Applies fn recursively to every submodule (as returned by <code>.children()</code>) as well as self.
<code>buffers(self[, recurse])</code>	Returns an iterator over module buffers.
<code>children(self)</code>	Returns an iterator over immediate children modules.
<code>cpu(self)</code>	Moves all model parameters and buffers to the CPU.
<code>cuda(self[, device])</code>	Moves all model parameters and buffers to the GPU.
<code>double(self)</code>	Casts all floating point parameters and buffers to double datatype.
<code>eval(self)</code>	Sets the module in evaluation mode.
<code>extra_repr(self)</code>	Set the extra representation of the module
<code>float(self)</code>	Casts all floating point parameters and buffers to float datatype.

Continued on next page

Table 1 – continued from previous page

<code>forward(self, logit, target)</code>	Defines the computation performed at every call.
<code>half(self)</code>	Casts all floating point parameters and buffers to <code>half</code> datatype.
<code>load_state_dict(self, state_dict[, strict])</code>	Copies parameters and buffers from <code>state_dict</code> into this module and its descendants.
<code>modules(self)</code>	Returns an iterator over all modules in the network.
<code>named_buffers(self[, prefix, recurse])</code>	Returns an iterator over module buffers, yielding both the name of the buffer as well as the buffer itself.
<code>named_children(self)</code>	Returns an iterator over immediate children modules, yielding both the name of the module as well as the module itself.
<code>named_modules(self[, memo, prefix])</code>	Returns an iterator over all modules in the network, yielding both the name of the module as well as the module itself.
<code>named_parameters(self[, prefix, recurse])</code>	Returns an iterator over module parameters, yielding both the name of the parameter as well as the parameter itself.
<code>parameters(self[, recurse])</code>	Returns an iterator over module parameters.
<code>register_backward_hook(self, hook)</code>	Registers a backward hook on the module.
<code>register_buffer(self, name, tensor)</code>	Adds a persistent buffer to the module.
<code>register_forward_hook(self, hook)</code>	Registers a forward hook on the module.
<code>register_forward_pre_hook(self, hook)</code>	Registers a forward pre-hook on the module.
<code>register_parameter(self, name, param)</code>	Adds a parameter to the module.
<code>state_dict(self[, destination, prefix, ...])</code>	Returns a dictionary containing a whole state of the module.
<code>to(self, *args, **kwargs)</code>	Moves and/or casts the parameters and buffers.
<code>train(self[, mode])</code>	Sets the module in training mode.
<code>type(self, dst_type)</code>	Casts all parameters and buffers to <code>dst_type</code> .
<code>zero_grad(self)</code>	Sets gradients of all model parameters to zero.

share_memory

forward (*self, logit, target*)

Defines the computation performed at every call.

Should be overridden by all subclasses.

Note: Although the recipe for forward pass needs to be defined within this function, one should call the `Module` instance afterwards instead of this since the former takes care of running the registered hooks while the latter silently ignores them.

class `pathflowai.losses.GeneralizedDice` (***kwargs*)
<https://raw.githubusercontent.com/LIVIAETS/surface-loss/master/losses.py>

Methods

<code>__call__(self, probs, target, _)</code>	Call self as a function.
---	--------------------------

class pathflowai.losses.**GeneralizedDiceLoss** (*weight=None, channelwise=False, eps=1e-06, add_softmax=False*)

https://raw.githubusercontent.com/inferno-pytorch/inferno/0561e8a95cde6bfc5e10a3609841b7b0ca5b03ca/inferno/extensions/criteria/set_similarity_measures.py Computes the scalar Generalized Dice Loss defined in <https://arxiv.org/abs/1707.03237>

This version works for multiple classes and expects predictions for every class (e.g. softmax output) and one-hot targets for every class.

Methods

<code>__call__(self, *input, **kwargs)</code>	Call self as a function.
<code>add_module(self, name, module)</code>	Adds a child module to the current module.
<code>apply(self, fn)</code>	Applies <code>fn</code> recursively to every submodule (as returned by <code>.children()</code>) as well as self.
<code>buffers(self[, recurse])</code>	Returns an iterator over module buffers.
<code>children(self)</code>	Returns an iterator over immediate children modules.
<code>cpu(self)</code>	Moves all model parameters and buffers to the CPU.
<code>cuda(self[, device])</code>	Moves all model parameters and buffers to the GPU.
<code>double(self)</code>	Casts all floating point parameters and buffers to double datatype.
<code>eval(self)</code>	Sets the module in evaluation mode.
<code>extra_repr(self)</code>	Set the extra representation of the module
<code>float(self)</code>	Casts all floating point parameters and buffers to float datatype.
<code>forward(self, input, target)</code>	input: torch.FloatTensor or torch.cuda.FloatTensor target: torch.FloatTensor or torch.cuda.FloatTensor
<code>half(self)</code>	Casts all floating point parameters and buffers to half datatype.
<code>load_state_dict(self, state_dict[, strict])</code>	Copies parameters and buffers from <code>state_dict</code> into this module and its descendants.
<code>modules(self)</code>	Returns an iterator over all modules in the network.
<code>named_buffers(self[, prefix, recurse])</code>	Returns an iterator over module buffers, yielding both the name of the buffer as well as the buffer itself.
<code>named_children(self)</code>	Returns an iterator over immediate children modules, yielding both the name of the module as well as the module itself.
<code>named_modules(self[, memo, prefix])</code>	Returns an iterator over all modules in the network, yielding both the name of the module as well as the module itself.
<code>named_parameters(self[, prefix, recurse])</code>	Returns an iterator over module parameters, yielding both the name of the parameter as well as the parameter itself.
<code>parameters(self[, recurse])</code>	Returns an iterator over module parameters.
<code>register_backward_hook(self, hook)</code>	Registers a backward hook on the module.
<code>register_buffer(self, name, tensor)</code>	Adds a persistent buffer to the module.
<code>register_forward_hook(self, hook)</code>	Registers a forward hook on the module.
<code>register_forward_pre_hook(self, hook)</code>	Registers a forward pre-hook on the module.
<code>register_parameter(self, name, param)</code>	Adds a parameter to the module.

Continued on next page

Table 3 – continued from previous page

<code>state_dict(self[, destination, prefix, ...])</code>	Returns a dictionary containing a whole state of the module.
<code>to(self, *args, **kwargs)</code>	Moves and/or casts the parameters and buffers.
<code>train(self[, mode])</code>	Sets the module in training mode.
<code>type(self, dst_type)</code>	Casts all parameters and buffers to <code>dst_type</code> .
<code>zero_grad(self)</code>	Sets gradients of all model parameters to zero.

share_memory	
--------------	--

forward (*self*, *input*, *target*)

input: torch.FloatTensor or torch.cuda.FloatTensor target: torch.FloatTensor or torch.cuda.FloatTensor

Expected shape of the inputs:

- if not channelwise: (batch_size, nb_classes, ...)
- if channelwise: (batch_size, nb_channels, nb_classes, ...)

exception pathflowai.losses.ShapeError**class** pathflowai.losses.SurfaceLoss (***kwargs*)<https://raw.githubusercontent.com/LIVIAETS/surface-loss/master/losses.py>

Methods

<code>__call__(self, probs, dist_maps, _)</code>	Call self as a function.
--	--------------------------

pathflowai.losses.assert_ (*condition*, *message*=", *exception_type*=<class 'AssertionError'>)<https://raw.githubusercontent.com/inferno-pytorch/inferno/0561e8a95cde6bfc5e10a3609841b7b0ca5b03ca/inferno/utils/exceptions.py> Like assert, but with arbitrary exception types.pathflowai.losses.class2one_hot (*seg:torch.Tensor*, *C:int*) → torch.Tensor<https://raw.githubusercontent.com/LIVIAETS/surface-loss/master/utils.py>pathflowai.losses.eq (*a:torch.Tensor*, *b*) → bool<https://raw.githubusercontent.com/LIVIAETS/surface-loss/master/utils.py>pathflowai.losses.flatten_samples (*input_*)https://raw.githubusercontent.com/inferno-pytorch/inferno/0561e8a95cde6bfc5e10a3609841b7b0ca5b03ca/inferno/utils/torch_utils.py Flattens a tensor or a variable such that the channel axis is first and the sample axis is second. The shapes are transformed as follows:

(N, C, H, W) → (C, N * H * W) (N, C, D, H, W) → (C, N * D * H * W) (N, C) → (C, N)

The input must be atleast 2d.

pathflowai.losses.one_hot (*t:torch.Tensor*, *axis=1*) → bool<https://raw.githubusercontent.com/LIVIAETS/surface-loss/master/utils.py>pathflowai.losses.one_hot2dist (*seg:numpy.ndarray*) → numpy.ndarray<https://raw.githubusercontent.com/LIVIAETS/surface-loss/master/utils.py>pathflowai.losses.simplex (*t:torch.Tensor*, *axis=1*) → bool<https://raw.githubusercontent.com/LIVIAETS/surface-loss/master/utils.py>pathflowai.losses.sset (*a:torch.Tensor*, *sub:Iterable*) → bool<https://raw.githubusercontent.com/LIVIAETS/surface-loss/master/utils.py>

`pathflowai.losses.uniq` (*a:torch.Tensor*) → Set
<https://raw.githubusercontent.com/LIVIAETS/surface-loss/master/utils.py>

SAMPLER.PY

Balanced sampling based on one of the columns of the patch information.

```
class pathflowai.sampler.ImbalancedDatasetSampler (dataset, indices=None,  
 num_samples=None)
```

Samples elements randomly from a given list of indices for imbalanced dataset <https://raw.githubusercontent.com/ufoym/imbalanced-dataset-sampler/master/sampler.py> Arguments:

indices (list, optional): a list of indices num_samples (int, optional): number of samples to draw

SCHEDULERS.PY

Modulates the learning rate during the training process.

```
class pathflowai.schedulers.CosineAnnealingWithRestartsLR(optimizer,      T_max,
                                                         eta_min=0,
                                                         last_epoch=-1,
                                                         T_mult=1.0,          al-
                                                         pha_decay=1.0)
```

Set the learning rate of each parameter group using a cosine annealing schedule, where η_{max} is set to the initial lr and T_{cur} is the number of epochs since the last restart in SGDR:

$$\eta_t = \eta_{min} + \frac{1}{2}(\eta_{max} - \eta_{min})(1 + \cos(\frac{T_{cur}}{T_{max}}\pi))$$

When last_epoch=-1, sets initial lr as lr. It has been proposed in

SGDR: Stochastic Gradient Descent with Warm Restarts. This implements the cosine annealing part of SGDR, the restarts and number of iterations multiplier.

Args: optimizer (Optimizer): Wrapped optimizer. T_max (int): Maximum number of iterations.
T_mult (float): Multiply T_max by this number after each restart. Default: 1. eta_min (float):
Minimum learning rate. Default: 0. last_epoch (int): The index of last epoch. Default: -1.

Attributes

step_n

Methods

load_state_dict(self, state_dict)	Loads the schedulers state.
state_dict(self)	Returns the state of the scheduler as a dict.

cosine	
get_lr	
restart	
step	

```
class pathflowai.schedulers.Scheduler(optimizer=None, opts={'T_max': 10, 'T_mult': 2,
                                                         'eta_min': 5e-08, 'lr_scheduler_decay': 0.5, 'scheduler': 'null'})
```

Scheduler class that modulates learning rate of torch optimizers over epochs.

Parameters

- optimizer** [type] torch.Optimizer object
- opts** [type] Options of setting the learning rate scheduler, see default.

Attributes

- schedulers** [type] Different types of schedulers to choose from.
- scheduler_step_fn** [type] How scheduler updates learning rate.
- initial_lr** [type] Initial set learning rate.
- scheduler_choice** [type] What scheduler type was chosen.
- scheduler** [type] Scheduler object chosen that will more directly update optimizer LR.

Methods

<code>get_lr(self)</code>	Return current learning rate.
<code>step(self)</code>	Update optimizer learning rate

`get_lr(self)`

Return current learning rate.

Returns

float Current learning rate.

`step(self)`

Update optimizer learning rate

VISUALIZE.PY

Plots SHAP outputs, UMAP embeddings, and overlays predictions on top of WSI.

```
class pathflowai.visualize.PlotlyPlot  
    Creates plotly html plots.
```

Methods

<code><i>add_plot</i>(self, t_data_df[, G, color_col, ...])</code>	Adds plotting data to be plotted.
<code><i>plot</i>(self, output_fname[, axes_off])</code>	Plot embedding of patches to html file.

```
add_plot (self, t_data_df, G=None, color_col='color', name_col='name', xyz_cols=['x', 'y', 'z'],  
          size=2, opacity=1.0, custom_colors=[])  
    Adds plotting data to be plotted.
```

Parameters

t_data_df: dataframe 3-D transformed dataframe.

G:nx.Graph Networkx graph.

color_col:str Column to use to color points.

name_col:str Column to use to name points.

xyz_cols:list 3 columns that denote x,y,z coords.

size:int Marker size.

opacity:float Marker opacity.

custom_colors:list Custom colors to supply.

```
plot (self, output_fname, axes_off=False)  
    Plot embedding of patches to html file.
```

Parameters

output_fname:str Output html file.

axes_off:bool Remove axes.

```
class pathflowai.visualize.PredictionPlotter (dask_arr_dict, patch_info_db, compression_factor=3, alpha=0.5, patch_size=224, no_db=False, plot_annotation=False, segmentation=False, n_segmentation_classes=4, input_dir="", annotation_col='annotation', scaling_factor=1.0)
```

Plots predictions over entire image.

Parameters

dask_arr_dict:dict Stores all dask arrays corresponding to all of the images.

patch_info_db:str Patch level information, eg. prediction.

compression_factor:float How much to compress image by.

alpha:float Low value assigns higher weight to prediction over original image.

patch_size:int Patch size.

no_db:bool Don't use patch information.

plot_annotation:bool Plot annotations from patch information.

segmentation:bool Plot segmentation mask.

n_segmentation_classes:int Number segmentation classes.

input_dir:str Input directory.

annotation_col:str Annotation column to plot.

scaling_factor:float Multiplies the prediction scores to make them appear darker on the images when predicting.

Methods

<code>add_custom_segmentation(self, basename, npy)</code>	Replace segmentation mask with new custom segmentation.
<code>generate_image(self, ID)</code>	Generate the image array for the whole slide image with predictions overlaid.
<code>output_image(self, img, filename[, tif])</code>	Output calculated image to file.
<code>return_patch(self, ID, x, y, patch_size)</code>	Return one single patch instead of entire image.

add_custom_segmentation (*self, basename, npy*)

Replace segmentation mask with new custom segmentation.

Parameters

basename:str Patient ID

npy:str Numpy mask.

generate_image (*self, ID*)

Generate the image array for the whole slide image with predictions overlaid.

Parameters

ID:str patient ID.

Returns

array Resulting overlaid whole slide image.

output_image (*self, img, filename, tif=False*)
Output calculated image to file.

Parameters

img:array Image.

filename:str Output file name.

tif:bool Store in TIF format?

return_patch (*self, ID, x, y, patch_size*)
Return one single patch instead of entire image.

Parameters

ID:str Patient ID

x:int X coordinate.

y:int Y coordinate.

patch_size:int Patch size.

Returns

array Image.

`pathflowai.visualize. annotation2rgb (i, palette, arr)`
Go from annotation of patch to color.

Parameters

i:int Annotation index.

palette:palette Index to color mapping.

arr:array Image array.

Returns

array Resulting image.

`pathflowai.visualize. blend (arr1, arr2, alpha=0.5)`
Blend 2 arrays together, mixing with alpha.

Parameters

arr1:array Image 1.

arr2:array Image 2.

alpha:float Higher alpha makes image more like image 1.

Returns

array Resulting image.

`pathflowai.visualize. plot_image_ (image_file, test_image_name='test.png')`
compression_factor=2.0,

Plots entire SVS/other image.

Parameters

image_file:str Image file.

compression_factor:float Amount to shrink each dimension of image.

test_image_name:str Output image file.

```
pathflowai.visualize.plot_shap(model, dataset_opts, transform_opts, batch_size, outputfile-  
                               name, n_outputs=1, method='deep', local_smoothing=0.0,  
                               n_samples=20, pred_out=False)
```

Plot shapley attributions overlaid on images for classification tasks.

Parameters

model:nn.Module Pytorch model.

dataset_opts:dict Options used to configure dataset

transform_opts:dict Options used to configure transformers.

batch_size:int Batch size for training.

outputfilename:str Output filename.

n_outputs:int Number of top outputs.

method:str Gradient or deep explainer.

local_smoothing:float How much to smooth shapley map.

n_samples:int Number shapley samples to draw.

pred_out:bool Label images with binary prediction score?

```
pathflowai.visualize.plot_umap_images(dask_arr_dict, embeddings_file, ID=None,  
                                       cval=1.0, image_res=300.0, outputf-  
                                       name='output_embedding.png', mpl_scatter=True,  
                                       remove_background_annotation="",  
                                       max_background_area=0.01, zoom=0.05,  
                                       n_neighbors=10, sort_col="", sort_mode='asc')
```

Make UMAP embedding plot, overlaid with images.

Parameters

dask_arr_dict:dict Stored dask arrays for each WSI.

embeddings_file:str Embeddings pickle file stored from running using after trainign the model.

ID:str Patient ID.

cval:float Deprecated

image_res:float Image resolution.

outputfname:str Output image file.

mpl_scatter:bool Recommended: Use matplotlib for scatter plot.

remove_background_annotation:str Remove the background annotations. Enter for annota-
tion to remove.

max_background_area:float Maximum background area in each tile for inclusion.

zoom:float How much to zoom in on each patch, less than 1 is zoom out.

n_neighbors:int Number of neighbors for UMAP embedding.

sort_col:str Patch info column to sort on.

sort_mode:str Sort ascending or descending.

Returns

type Description of returned object.

Inspired by: <https://gist.github.com/lukemetz/be6123c7ee3b366e333a>

WIP!! Needs testing.

`pathflowai.visualize.prob2rbg` (*prob*, *palette*, *arr*)

Convert probability score to rgb image.

Parameters

prob:float Between 0 and 1 score.

palette:palette Pallet converts between prob and color.

arr:array Original array.

Returns

array New image colored by prediction score.

`pathflowai.visualize.seg2rgb` (*seg*, *palette*, *n_segmentation_classes*)

Color each pixel by segmentation class.

Parameters

seg:array Segmentation mask.

palette:palette Color to RGB map.

n_segmentation_classes:int Total number segmentation classes.

Returns

array Returned segmentation image.

`pathflowai.visualize.to_pil` (*arr*)

Numpy array to pil.

Parameters

arr:array Numpy array.

Returns

Image PIL Image.

UTILS.PY

General utilities that still need to be broken up into preprocessing, machine learning input preparation, and output submodules.

`pathflowai.utils.add_purple_mask(arr)`

Optional add intensity mask to the dask array.

Parameters

arr:dask.array Image data.

Returns

array Image data with intensity added as forth channel.

`pathflowai.utils.adjust_mask(mask_file, dask_img_array_file, out_npy, n_neighbors)`

Fixes segmentation masks to reduce coarse annotations over empty regions.

Parameters

mask_file:str NPY segmentation mask.

dask_img_array_file:str Dask image file.

out_npy:str Output numpy file.

n_neighbors:int Number nearest neighbors for dilation and erosion of mask from background to not background.

Returns

str Output numpy file.

`pathflowai.utils.bboxes2interior(img_size, polygons)`

Deprecated.

`pathflowai.utils.create_purple_mask(arr, img_size=None, sparse=True)`

Create a gray scale intensity mask. This will be changed soon to support other thresholding QC methods.

Parameters

arr:dask.array Dask array containing image information.

img_size:int Deprecated.

sparse:bool Deprecated

Returns

dask.array Intensity, grayscale array over image.

`pathflowai.utils.create_sparse_annotation_arrays(xml_file, img_size, annotations=[])`

Convert annotation xml to shapely objects and store in dictionary.

Parameters

xml_file:str XML file containing annotations.
img_size:int Deprecated.
annotations:list Annotations to look for in xml export.

Returns

dict Dictionary with annotation-shapely object pairs.

`pathflowai.utils.create_train_val_test(train_val_test_pkl, input_info_db, patch_size)`
Create dataframe that splits slides into training validation and test.

Parameters

train_val_test_pkl:str Pickle for training validation and test slides.
input_info_db:str Patch information SQL database.
patch_size:int Patch size looking to access.

Returns

dataframe Train test validation splits.

`pathflowai.utils.df2sql(df, sql_file, patch_size, mode='replace')`
Write dataframe containing patch level information to SQL db.

Parameters

df:dataframe Dataframe containing patch information.
sql_file:str SQL database.
patch_size:int Size of patches.
mode:str Replace or append.

`pathflowai.utils.dir2images(image_dir)`
Deprecated

`pathflowai.utils.extract_patch_information(basename, input_dir='.', annotations=[],
threshold=0.5, patch_size=224, generate_finetune_segmentation=False, target_class=0,
intensity_threshold=100.0, target_threshold=0.0, adj_mask="", basic_preprocess=False, tries=0)`

Final step of preprocessing pipeline. Break up image into patches, include if not background and of a certain intensity, find area of each annotation type in patch, spatial information, image ID and dump data to SQL table.

Parameters

basename:str Patient ID.
input_dir:str Input directory.
annotations:list List of annotations to record, these can be different tissue types, must correspond with XML labels.
threshold:float Value between 0 and 1 that indicates the minimum amount of patch that musn't be background for inclusion.
patch_size:int Patch size of patches; this will become one of the tables.
generate_finetune_segmentation:bool Deprecated.

target_class:int Number of segmentation classes desired, from 0th class to target_class-1 will be annotated in SQL.

intensity_threshold:float Value between 0 and 255 that represents minimum intensity to not include as background. Will be modified with new transforms.

target_threshold:float Deprecated.

adj_mask:str Adjusted mask if performed binary opening operations in previous preprocessing step.

basic_preprocess:bool Do not store patch level information.

tries:int Number of tries in case there is a Dask timeout, run again.

Returns

dataframe Patch information.

`pathflowai.utils.fix_name(basename)`

Fixes illegitimate basename, deprecated.

`pathflowai.utils.fix_names(file_dir)`

Fixes basenames, deprecated.

`pathflowai.utils.generate_patch_pipeline(basename, input_dir='.', annotations=[], threshold=0.5, patch_size=224, out_db='patch_info.db', generate_finetune_segmentation=False, target_class=0, intensity_threshold=100.0, target_threshold=0.0, adj_mask="", basic_preprocess=False)`

Short summary.

Parameters

basename:str Patient ID.

input_dir:str Input directory.

annotations:list List of annotations to record, these can be different tissue types, must correspond with XML labels.

threshold:float Value between 0 and 1 that indicates the minimum amount of patch that musn't be background for inclusion.

patch_size:int Patch size of patches; this will become one of the tables.

out_db:str Output SQL database.

generate_finetune_segmentation:bool Deprecated.

target_class:int Number of segmentation classes desired, from 0th class to target_class-1 will be annotated in SQL.

intensity_threshold:float Value between 0 and 255 that represents minimum intensity to not include as background. Will be modified with new transforms.

target_threshold:float Deprecated.

adj_mask:str Adjusted mask if performed binary opening operations in previous preprocessing step.

basic_preprocess:bool Do not store patch level information.

`pathflowai.utils.grab_interior_points(xml_file, img_size, annotations=[])`

Deprecated.

`pathflowai.utils.image2coords(image_file, output_point=False)`

Deprecated.

`pathflowai.utils.images2coord_dict(images, output_point=False)`

Deprecated

`pathflowai.utils.img2numpy_(input_dir, basename, svs_file)`

Convert SVS, TIF, TIFF to NPY.

Parameters

input_dir:str Output file dir.

basename:str Basename of output file

svs_file:str SVS, TIF, TIFF file input.

Returns

str NPY output file.

`pathflowai.utils.is_coords_in_box(coords, patch_size, boxes)`

Get area of annotation in patch.

Parameters

coords:array X,Y coordinates of patch.

patch_size:int Patch size.

boxes:list Shapely objects for annotations.

Returns

float Area of annotation type.

`pathflowai.utils.is_image_in_boxes(image_coord_dict, boxes)`

Find if image intersects with annotations.

Parameters

image_coord_dict:dict Dictionary of patches.

boxes:list Shapely annotation shapes.

Returns

dict Dictionary of whether image intersects with any of the annotations.

`pathflowai.utils.is_valid_patch(xs, ys, patch_size, purple_mask, intensity_threshold, threshold=0.5)`

Deprecated, computes whether patch is valid.

`pathflowai.utils.load_dataset(in_zarr, in_pkl)`

Load ZARR image and annotations pickle.

Parameters

in_zarr:str Input image.

in_pkl:str Input annotations.

Returns

dask.array Image array.

dict Annotations dictionary.

`pathflowai.utils.load_image(svs_file)`
Load SVS, TIF, TIFF

Parameters

svs_file: type Description of parameter *svs_file*.

Returns

type Description of returned object.

`pathflowai.utils.load_process_image(svs_file, xml_file=None, npy_mask=None, annotations=[])`

Load SVS-like image (including NPY), segmentation/classification annotations, generate dask array and dictionary of annotations.

Parameters

svs_file: str Image file

xml_file: str Annotation file.

npy_mask: array Numpy segmentation mask.

annotations: list List of annotations in xml.

Returns

array Dask array of image.

dict Annotation masks.

`pathflowai.utils.load_sql_df(sql_file, patch_size)`

Load pandas dataframe from SQL, accessing particular patch size within SQL.

Parameters

sql_file: str SQL db.

patch_size: int Patch size.

Returns

dataframe Patch level information.

`modify_patch_info(input_info_db='patch_info.db', slide_labels=Empty DataFrame
Columns: [])`

`Index: [], pos_annotation_class='', patch_size=224, segmentation=False, other_annotations=`

Modify the patch information to get ready for deep learning, incorporate whole slide labels if needed.

Parameters

input_info_db: str SQL DB file.

slide_labels: dataframe Dataframe with whole slide labels.

pos_annotation_class: str Tissue/annotation label to label with whole slide image label, if not supplied, any slide's patches receive the whole slide label.

patch_size: int Patch size.

segmentation: bool Segmentation?

other_annotations: list Other annotations to access from patch information.

target_segmentation_class: int Segmentation class to threshold.

target_threshold:float Include patch if patch has target area greater than this.

classify_annotations:bool Classifying annotations for pretraining, or final model?

Returns

dataframe Modified patch information.

`pathflowai.utils.npy2da(npy_file)`

Numpy to dask array.

Parameters

npv_file:str Input npv file.

Returns

dask.array Converted numpy array to dask.

`pathflowai.utils.parse_coord_return_boxes(xml_file, annotation_name="", return_coords=False)`

Get list of shapely objects for each annotation in the XML object.

Parameters

xml_file:str Annotation file.

annotation_name:str Name of xml annotation.

return_coords:bool Just return list of coords over shapes.

Returns

list List of shapely objects.

`pathflowai.utils.process_svs(svs_file, xml_file, annotations=[], output_dir='.')`

Store images into npv format and store annotations into pickle dictionary.

Parameters

svs_file:str Image file.

xml_file:str Annotations file.

annotations:list List of annotations in image.

output_dir:str Output directory.

`pathflowai.utils.retain_images(image_dir, xml_file, annotation="")`

Deprecated

`pathflowai.utils.return_image_coord(nx=0, ny=0, xl=3333, yl=3333, xi=0, yi=0, xc=3, yc=3, dimx=224, dimy=224, output_point=False)`

Deprecated

`pathflowai.utils.return_image_in_boxes_dict(image_dir, xml_file, annotation="")`

Deprecated

`pathflowai.utils.run_preprocessing_pipeline(svs_file, xml_file=None, npv_mask=None, annotations=[], out_zarr='output_zarr.zarr', out_pkl='output.pkl')`

Run preprocessing pipeline. Store image into zarr format, segmentations maintain as npv, and xml annotations as pickle.

Parameters

svs_file:str Input image file.

xml_file:str Input annotation file.

numpy_mask:str NPY segmentation mask.

annotations:list List of annotations.

out_zarr:str Output zarr for image.

out_pkl:str Output pickle for annotations.

```
pathflowai.utils.save_all_patch_info(basenames, input_dir='./', annotations=[],
                                     threshold=0.5, patch_size=224, out-
                                     put_pkl='patch_info.pkl')
```

Deprecated.

```
pathflowai.utils.save_dataset(arr, masks, out_zarr, out_pkl)
Saves dask array image, dictionary of annotations to zarr and pickle respectively.
```

Parameters

arr:array Image.

masks:dict Dictionary of annotation shapes.

out_zarr:str Zarr output file for image.

out_pkl:str Pickle output file.

```
pathflowai.utils.segmentation_predictions2numpy(y_pred, patch_info, segmentation_map,
                                                  numpy_output)
```

Convert segmentation predictions from model to numpy masks.

Parameters

y_pred:list List of patch segmentation masks

patch_info:dataframe Patch information from DB.

segmentation_map:array Existing segmentation mask.

numpy_output:str Output npy file.

```
pathflowai.utils.svs2dask_array(svs_file, tile_size=1000, overlap=0, remove_last=True, al-
                                low_unknown_chunksizes=False)
```

Convert SVS, TIF or TIFF to dask array.

Parameters

svs_file:str Image file.

tile_size:int Size of chunk to be read in.

overlap:int Do not modify, overlap between neighboring tiles.

remove_last:bool Remove last tile because it has a custom size.

allow_unknown_chunksizes: bool Allow different chunk sizes, more flexible, but slowdown.

Returns

dask.array Dask Array.

```
>>> arr=svs2dask_array(svs_file, tile_size=1000, overlap=0, remove_
↪last=True, allow_unknown_chunksizes=False)
..
```

```
>>> arr2=arr.compute()  
..
```

```
>>> arr3=to_pil(cv2.resize(arr2, dsize=(1440,700), interpolation=cv2.  
↪INTER_CUBIC))  
..
```

```
>>> arr3.save(test_image_name)  
..
```

INDICES AND TABLES

- `genindex`
- `modindex`
- `search`

PYTHON MODULE INDEX

p

- `pathflowai.datasets`, [13](#)
- `pathflowai.losses`, [18](#)
- `pathflowai.sampler`, [23](#)
- `pathflowai.schedulers`, [25](#)
- `pathflowai.utils`, [33](#)
- `pathflowai.visualize`, [28](#)

INDEX

Symbols

-version
 pathflowai-monitor command line option, 13
 pathflowai-preprocess command line option, 3
 pathflowai-visualize command line option, 7
 -a, -annotation_txt <annotation_txt>
 pathflowai-visualize-overlay_new_annotations command line option, 8
 -a, -annotations <annotations>
 pathflowai-preprocess-preprocess_pipeline command line option, 4
 pathflowai-visualize-plot_embeddings command line option, 8
 -ac, -annotation_col <annotation_col>
 pathflowai-visualize-plot_predictions command line option, 10
 -al, -alpha <alpha>
 pathflowai-visualize-plot_predictions command line option, 10
 -am, -adjust_mask
 pathflowai-preprocess-preprocess_pipeline command line option, 5
 -an, -annotations
 pathflowai-visualize-plot_predictions command line option, 10
 -b, -basename <basename>
 pathflowai-preprocess-preprocess_pipeline command line option, 4
 pathflowai-preprocess-remove_basename_from_db command line option, 5
 pathflowai-visualize-extract_patch command line option, 7
 pathflowai-visualize-plot_embeddings command line option, 8
 pathflowai-visualize-plot_image_umap_embeddings command line option, 9
 pathflowai-visualize-plot_predictions command line option, 10
 -bp, -basic_preprocess
 pathflowai-preprocess-preprocess_pipeline command line option, 5
 -bs, -batch_size <batch_size>
 pathflowai-visualize-shapley_plot command line option, 11
 -c, -custom_segmentation
 <custom_segmentation>
 pathflowai-visualize-extract_patch command line option, 7
 pathflowai-visualize-plot_predictions command line option, 10
 -cf, -compression_factor
 <compression_factor>
 pathflowai-visualize-overlay_new_annotations command line option, 8
 pathflowai-visualize-plot_image command line option, 9
 pathflowai-visualize-plot_predictions command line option, 10
 -csv, -records_output_csv
 <records_output_csv>
 pathflowai-monitor-monitor_usage command line option, 13
 -dt, -delay_time <delay_time>
 pathflowai-monitor-monitor_usage command line option, 13
 -e, -embeddings_file <embeddings_file>
 pathflowai-visualize-plot_image_umap_embeddings command line option, 9
 -f, -from_annotations
 <from_annotations>
 pathflowai-preprocess-alter_masks command line option, 3
 pathflowai-preprocess-collapse_annotations command line option, 4
 -g, -generate_finetune_segmentation
 pathflowai-preprocess-preprocess_pipeline command line option, 4
 -i, -embeddings_file <embeddings_file>
 pathflowai-visualize-plot_embeddings command line option, 8
 -i, -image_file <image_file>

```

pathflowai-visualize-plot_image          pathflowai-preprocess-preprocess_pipeline
    command line option,9                command line option,4
-i, -img_file <img_file>                 -ns, -n_samples <n_samples>
pathflowai-visualize-overlay_new_annotat pathflowai-visualize-shapley_plot
    command line option,8                command line option,11
-i, -input_dir <input_dir>               -o, -output_dir <output_dir>
pathflowai-preprocess-preprocess_pipeline pathflowai-preprocess-alter_masks
    command line option,4                command line option,3
pathflowai-visualize-extract_patch        -o, -output_patch_db <output_patch_db>
    command line option,7                pathflowai-preprocess-collapse_annotations
pathflowai-visualize-plot_image_umap_embeddings command line option,4
    command line option,9                pathflowai-preprocess-remove_basename_from_db
pathflowai-visualize-plot_predictions      command line option,5
    command line option,10              -o, -outputfilename <outputfilename>
-i, -input_patch_db <input_patch_db>       pathflowai-visualize-overlay_new_annotations
pathflowai-preprocess-collapse_annotations command line option,8
    command line option,4                pathflowai-visualize-plot_image_umap_embeddings
pathflowai-preprocess-remove_basename_from_db command line option,9
    command line option,5                pathflowai-visualize-shapley_plot
-i, -mask_dir <mask_dir>                  command line option,11
pathflowai-preprocess-alter_masks          -o, -outputfname <outputfname>
    command line option,3                pathflowai-visualize-extract_patch
-i, -intensity_threshold                  command line option,7
    <intensity_threshold>                pathflowai-visualize-plot_image
pathflowai-preprocess-preprocess_pipeline command line option,9
    command line option,4                pathflowai-visualize-plot_predictions
-l, -local_smoothing <local_smoothing>     command line option,10
pathflowai-visualize-shapley_plot          -o, -plotly_output_file
    command line option,11              <plotly_output_file>
-m, -model_pkl <model_pkl>                pathflowai-visualize-plot_embeddings
pathflowai-visualize-shapley_plot          command line option,8
    command line option,11              -ocf, -original_compression_factor
-ma, -max_background_area                  <original_compression_factor>
    <max_background_area>                pathflowai-visualize-overlay_new_annotations
pathflowai-preprocess-collapse_annotations command line option,8
    command line option,4                -odb, -out_db <out_db>
pathflowai-visualize-plot_embeddings       pathflowai-preprocess-preprocess_pipeline
    command line option,8                command line option,5
pathflowai-visualize-plot_image_umap_embeddings pathflowai-visualize-plot_info_file <patch_info_file>
    command line option,9                pathflowai-visualize-extract_patch
-mpl, -mpl_scatter                        command line option,7
pathflowai-visualize-plot_image_umap_embeddings pathflowai-visualize-plot_predictions
    command line option,9                command line option,10
-mth, -method <method>                    -p, -pred_out <pred_out>
pathflowai-visualize-shapley_plot          pathflowai-visualize-shapley_plot
    command line option,11              command line option,11
-n, -n_neighbors <n_neighbors>            -pa, -patches
pathflowai-preprocess-preprocess_pipeline pathflowai-preprocess-preprocess_pipeline
    command line option,5                command line option,4
pathflowai-visualize-plot_embeddings       -pr, -preprocess
    command line option,8                pathflowai-preprocess-preprocess_pipeline
pathflowai-visualize-plot_image_umap_embeddings command line option,4
    command line option,9                -ps, -patch_size <patch_size>
-npy, -img2npz                             pathflowai-preprocess-collapse_annotations

```

command line option, 4
 pathflowai-preprocess-preprocess_pipeline command line option, 5
 command line option, 4
 pathflowai-preprocess-remove_basename_from_paths command line option, 5
 pathflowai-visualize-extract_patch -x, -x <x>
 command line option, 7
 pathflowai-visualize-plot_predictions command line option, 7
 command line option, 10
 -rb, -remove_background_annotation <remove_background_annotation>
 pathflowai-preprocess-collapse_annotations command line option, 4
 pathflowai-visualize-plot_embeddings command line option, 8
 pathflowai-visualize-plot_image_umap_embeddings command line option, 9
 -s, -segmentation
 pathflowai-visualize-extract_patch command line option, 7
 pathflowai-visualize-plot_predictions command line option, 10
 -sc, -n_segmentation_classes <n_segmentation_classes>
 pathflowai-visualize-extract_patch command line option, 7
 pathflowai-visualize-plot_predictions command line option, 10
 -sc, -sort_col <sort_col>
 pathflowai-visualize-plot_image_umap_embeddings command line option, 9
 -sf, -scaling_factor <scaling_factor>
 pathflowai-visualize-plot_predictions command line option, 10
 -sm, -sort_mode <sort_mode>
 pathflowai-visualize-plot_image_umap_embeddings command line option, 10
 -t, -threshold <threshold>
 pathflowai-preprocess-preprocess_pipeline command line option, 4
 -tc, -target_segmentation_class <target_segmentation_class>
 pathflowai-preprocess-preprocess_pipeline command line option, 5
 -tif, -tif_file
 pathflowai-visualize-plot_predictions command line option, 10
 -to, -to_annotations <to_annotations>
 pathflowai-preprocess-alter_masks command line option, 3
 pathflowai-preprocess-collapse_annotations command line option, 4
 -tt, -target_threshold <target_threshold>

pathflowai-preprocess-preprocess_pipeline
 -tt, -total_time <total_time>
 pathflowai-monitor-monitor_usage command line option, 13
 pathflowai-visualize-extract_patch
 pathflowai-visualize-extract_patch command line option, 7
 -y, -y <y>
 pathflowai-visualize-extract_patch command line option, 7
 -z, -zoom <zoom>
 pathflowai-visualize-plot_image_umap_embeddings command line option, 9

A

add_custom_segmentation() (pathflowai.visualize.PredictionPlotter method), 30
 add_plot() (pathflowai.visualize.PlotlyPlot method), 29
 add_purple_mask() (in module pathflowai.utils), 35
 adjust_mask() (in module pathflowai.utils), 35
 annotation2rgb() (in module pathflowai.visualize), 31
 assert_() (in module pathflowai.losses), 22

B

binarize_annotations() (pathflowai.datasets.DynamicImageDataset method), 16
 blend() (in module pathflowai.visualize), 31
 boxes2interior() (in module pathflowai.utils), 35

C

cosine_annealing_with_restarts_lr() (in module pathflowai.losses), 22
 concat() (pathflowai.datasets.DynamicImageDataset method), 16
 create_purple_mask() (in module pathflowai.utils), 35
 create_sparse_annotation_arrays() (in module pathflowai.utils), 35
 create_train_val_test() (in module pathflowai.utils), 36
 create_transforms() (in module pathflowai.datasets), 17

D

dir2sql() (in module pathflowai.utils), 36
 dir2images() (in module pathflowai.utils), 36
 DynamicImageDataset (class in pathflowai.datasets), 15

E

`eq()` (in module `pathflowai.losses`), 22

`extract_patch_information()` (in module `pathflowai.utils`), 36

F

`fix_name()` (in module `pathflowai.utils`), 37

`fix_names()` (in module `pathflowai.utils`), 37

`flatten_samples()` (in module `pathflowai.losses`), 22

`FocalLoss` (class in `pathflowai.losses`), 19

`forward()` (`pathflowai.losses.FocalLoss` method), 20

`forward()` (`pathflowai.losses.GeneralizedDiceLoss` method), 22

G

`GeneralizedDice` (class in `pathflowai.losses`), 20

`GeneralizedDiceLoss` (class in `pathflowai.losses`), 21

`generate_image()` (`pathflowai.visualize.PredictionPlotter` method), 30

`generate_patch_pipeline()` (in module `pathflowai.utils`), 37

`get_class_weights()` (`pathflowai.datasets.DynamicImageDataset` method), 16

`get_data_transforms()` (in module `pathflowai.datasets`), 17

`get_lr()` (`pathflowai.schedulers.Scheduler` method), 28

`get_normalizer()` (in module `pathflowai.datasets`), 17

`grab_interior_points()` (in module `pathflowai.utils`), 37

I

`image2coords()` (in module `pathflowai.utils`), 38

`images2coord_dict()` (in module `pathflowai.utils`), 38

`ImbalancedDatasetSampler` (class in `pathflowai.sampler`), 25

`img2numpy_()` (in module `pathflowai.utils`), 38

`is_coords_in_box()` (in module `pathflowai.utils`), 38

`is_image_in_boxes()` (in module `pathflowai.utils`), 38

`is_valid_patch()` (in module `pathflowai.utils`), 38

L

`load_dataset()` (in module `pathflowai.utils`), 38

`load_image()` (in module `pathflowai.utils`), 39

`load_process_image()` (in module `pathflowai.utils`), 39

`load_sql_df()` (in module `pathflowai.utils`), 39

N

`numpy2da()` (in module `pathflowai.utils`), 40

O

`one_hot()` (in module `pathflowai.losses`), 22

`one_hot2dist()` (in module `pathflowai.losses`), 22

`output_image()` (`pathflowai.visualize.PredictionPlotter` method), 31

P

`parse_coord_return_boxes()` (in module `pathflowai.utils`), 40

`pathflowai-monitor` command line option `-version`, 13

`pathflowai-monitor-monitor_usage`

command line option

`-csv`, `-records_output_csv`

`<records_output_csv>`, 13

`-dt`, `-delay_time <delay_time>`, 13

`-tt`, `-total_time <total_time>`, 13

`pathflowai-preprocess` command line option

`-version`, 3

`pathflowai-preprocess-alter_masks`

command line option

`-fr`, `-from_annotations`

`<from_annotations>`, 3

`-i`, `-mask_dir <mask_dir>`, 3

`-o`, `-output_dir <output_dir>`, 3

`-to`, `-to_annotations`

`<to_annotations>`, 3

`pathflowai-preprocess-collapse_annotations`

command line option

`-fr`, `-from_annotations`

`<from_annotations>`, 4

`-i`, `-input_patch_db`

`<input_patch_db>`, 4

`-ma`, `-max_background_area`

`<max_background_area>`, 4

`-o`, `-output_patch_db`

`<output_patch_db>`, 4

`-ps`, `-patch_size <patch_size>`, 4

`-rb`, `-remove_background_annotation`

`<remove_background_annotation>`, 4

`-to`, `-to_annotations`

`<to_annotations>`, 4

`pathflowai-preprocess-preprocess_pipeline`

command line option

`-a`, `-annotations <annotations>`, 4

```

-am, -adjust_mask,5
-b, -basename <basename>,4
-bp, -basic_preprocess,5
-g, -generate_finetune_segmentation,
    4
-i, -input_dir <input_dir>,4
-it, -intensity_threshold
    <intensity_threshold>,4
-nn, -n_neighbors <n_neighbors>,5
-npy, -img2numpy,4
-odb, -out_db <out_db>,5
-pa, -patches,4
-pr, -preprocess,4
-ps, -patch_size <patch_size>,4
-t, -threshold <threshold>,4
-tc, -target_segmentation_class
    <target_segmentation_class>,5
-tt, -target_threshold
    <target_threshold>,5
pathflowai-preprocess-remove_basename_from_dir,
    command line option
-b, -basename <basename>,5
-i, -input_patch_db
    <input_patch_db>,5
-o, -output_patch_db
    <output_patch_db>,5
-ps, -patch_size <patch_size>,5
pathflowai-visualize command line
    option
-version,7
pathflowai-visualize-extract_patch
    command line option
-b, -basename <basename>,7
-c, -custom_segmentation
    <custom_segmentation>,7
-i, -input_dir <input_dir>,7
-o, -outputfname <outputfname>,7
-p, -patch_info_file
    <patch_info_file>,7
-ps, -patch_size <patch_size>,7
-s, -segmentation,7
-sc, -n_segmentation_classes
    <n_segmentation_classes>,7
-x, -x <x>,7
-y, -y <y>,7
pathflowai-visualize-overlay_new_annotations,
    command line option
-a, -annotation_txt
    <annotation_txt>,8
-cf, -compression_factor
    <compression_factor>,8
-i, -img_file <img_file>,8
-o, -outputfilename
    <outputfilename>,8
-ocf, -original_compression_factor
    <original_compression_factor>,8
pathflowai-visualize-plot_embeddings
    command line option
-a, -annotations <annotations>,8
-b, -basename <basename>,8
-i, -embeddings_file
    <embeddings_file>,8
-ma, -max_background_area
    <max_background_area>,8
-nn, -n_neighbors <n_neighbors>,8
-o, -plotly_output_file
    <plotly_output_file>,8
-rb, -remove_background_annotation
    <remove_background_annotation>,8
pathflowai-visualize-plot_image
    command line option
-cf, -compression_factor
    <compression_factor>,9
-i, -image_file <image_file>,9
-o, -outputfname <outputfname>,9
pathflowai-visualize-plot_image_umap_embeddings
    command line option
-b, -basename <basename>,9
-e, -embeddings_file
    <embeddings_file>,9
-i, -input_dir <input_dir>,9
-ma, -max_background_area
    <max_background_area>,9
-mpl, -mpl_scatter,9
-nn, -n_neighbors <n_neighbors>,9
-o, -outputfilename
    <outputfilename>,9
-rb, -remove_background_annotation
    <remove_background_annotation>,9
-sc, -sort_col <sort_col>,9
-sm, -sort_mode <sort_mode>,10
-z, -zoom <zoom>,9
pathflowai-visualize-plot_predictions
    command line option
-ac, -annotation_col
    <annotation_col>,10
-al, -alpha <alpha>,10
-an, -annotations,10
-b, -basename <basename>,10
-c, -custom_segmentation
    <custom_segmentation>,10
-cf, -compression_factor
    <compression_factor>,10
-i, -input_dir <input_dir>,10
-o, -outputfname <outputfname>,10
-p, -patch_info_file
    <patch_info_file>,10
-ps, -patch_size <patch_size>,10

```

-s, -segmentation, 10
-sc, -n_segmentation_classes
 <n_segmentation_classes>, 10
-sf, -scaling_factor
 <scaling_factor>, 10
-tif, -tif_file, 10
pathflowai-visualize-shapley_plot
 command line option
-bs, -batch_size <batch_size>, 11
-l, -local_smoothing
 <local_smoothing>, 11
-m, -model_pkl <model_pkl>, 11
-mth, -method <method>, 11
-ns, -n_samples <n_samples>, 11
-o, -outputfilename
 <outputfilename>, 11
-p, -pred_out <pred_out>, 11
pathflowai.datasets (module), 13
pathflowai.losses (module), 18
pathflowai.sampler (module), 23
pathflowai.schedulers (module), 25
pathflowai.utils (module), 33
pathflowai.visualize (module), 28
plot() (pathflowai.visualize.PlotlyPlot method), 29
plot_image_() (in module pathflowai.visualize), 31
plot_shap() (in module pathflowai.visualize), 32
plot_umap_images() (in module path-
 flowai.visualize), 32
PlotlyPlot (class in pathflowai.visualize), 29
PredictionPlotter (class in pathflowai.visualize),
 29
prob2rbg() (in module pathflowai.visualize), 33
process_svcs() (in module pathflowai.utils), 40

R

RandomRotate90() (in module pathflowai.datasets),
 17
retain_ID() (pathflowai.datasets.DynamicImageDataset
 method), 16
retain_images() (in module pathflowai.utils), 40
return_image_coord() (in module path-
 flowai.utils), 40
return_image_in_boxes_dict() (in module
 pathflowai.utils), 40
return_patch() (path-
 flowai.visualize.PredictionPlotter method),
 31
run_preprocessing_pipeline() (in module
 pathflowai.utils), 40

S

save_all_patch_info() (in module path-
 flowai.utils), 41
save_dataset() (in module pathflowai.utils), 41

Scheduler (class in pathflowai.schedulers), 27
seg2rgb() (in module pathflowai.visualize), 33
segmentation_predictions2np() (in module
 pathflowai.utils), 41
segmentation_transform() (in module path-
 flowai.datasets), 18
ShapeError, 22
simplex() (in module pathflowai.losses), 22
split_by_ID() (path-
 flowai.datasets.DynamicImageDataset
 method), 17
sset() (in module pathflowai.losses), 22
step() (pathflowai.schedulers.Scheduler method), 28
subsample() (pathflowai.datasets.DynamicImageDataset
 method), 17
SurfaceLoss (class in pathflowai.losses), 22
svcs2dask_array() (in module pathflowai.utils), 41

T

to_pil() (in module pathflowai.visualize), 33

U

uniq() (in module pathflowai.losses), 22