

# Model Card — version 1.0 — Model EPTN2021\_T1CT

Task: Segmentation

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## 0. Card Metadata

Creation date \* : 2026/02/20

### Versioning

- Version number \* : 1.0
  - Version changes \* : NA
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## 1. Model Basic Information

Name \* : EPTN2021\_T1CT

Creation date \* : 2025/07/05

### Versioning

- Version number \* : 01.00.0000
- Version changes \* : NA

DOI: <https://doi.org/10.17195/candat.2025.10.1>

### Model scope

- Summary \* : Delineation of 25 organs-at-risk defined in the EPTN atlas for neuro-oncological radiotherapy, input to the model are rigidly registered T1-weighted MR (gadolinium-enhanced) and CT
- Anatomical site \* : Brain

### Clearance

- Type \* : None

### Approved by

- Name(s): —
- Institution(s) \* : NA
- Contact email(s): —

### Additional Information

While the model and associated code can be directly used for research, deployment as clinical software is possible but requires compliance with applicable medical device and AI regulations. Each clinical team is responsible for undertaking the actions necessary to meet relevant regulatory requirements. In the EU, this includes compliance with

the Medical Device Regulation, covering quality management, risk assessment, and documentation, alongside AI Act requirements for transparency and post-market monitoring

**Intended users:** Medical Physicists, Radiation Oncologists, Radiologists, Neuro-Oncologists

**Observed limitations \*** : Only tested in adults (might not work well for pediatric cases) and single-institution data. Structures with multiple counterparts (e.g. Left / right, or anterior / posterior) are merged into a single label. Brain has holes due to extraction of the rest of the organs (no overlapping masks)

**Type of learning architecture \*** : nnU-Net

## Developed by

- **Name:** Ana M. Barragán-Montero<sup>1\*</sup>, Margerie Huet-Dastarac<sup>1</sup>, Dario Di Perri<sup>1,2</sup>, David Hofstede<sup>4</sup>, Nikolina E Birimac<sup>4</sup>, Matijs Geerts<sup>1</sup>, Benjamin Roberfroid<sup>1</sup>, Emilien Quéré<sup>1,3</sup>, John A. Lee<sup>1</sup>, Erik Roelofs<sup>4</sup>, Wouter van Elmpt<sup>4</sup>, Daniëlle BP Eekers<sup>4</sup>, Catharina M.L. Zegers<sup>4</sup>
- **Institution(s) \*** : 1 UCLouvain – Institut de Recherche Expérimentale et Clinique - Molecular Imaging Radiotherapy and Oncology (MIRO), Brussels, Belgium 2 Department of Radiation Oncology, Cliniques Universitaires Saint-Luc, Brussels, Belgium 3 École nationale supérieure de techniques avancées Bretagne (ENSTA), Brest, France 4 Department of Radiation Oncology (Maastr), GROW Research Institute for Oncology and Reproduction, Maastricht University Medical Centre+, Maastricht, The Netherlands
- **Contact email(s):** ana.barragan@uclouvain.be

**Conflict of interest \*** : NA

**Software licence \*** : Apache 2.0

**Code source:** [https://gitlab.com/ai4miro/nnunet\\_workflow\\_eptn](https://gitlab.com/ai4miro/nnunet_workflow_eptn)

**Model source:** <https://doi.org/10.17195/candat.2025.10.1>

**Citation details:** Ana M. Barragán-Montero<sup>1</sup>, Margerie Huet-Dastarac<sup>1</sup>, Dario di Perri<sup>1,2</sup>, David Hofstede<sup>3</sup>, Nikolina E Birimac<sup>3</sup>, Benjamin Roberfroid<sup>1</sup>, Emilien Quéré<sup>1</sup>, John Lee<sup>1</sup>, Wouter Van Elmpt<sup>3</sup>, Danielle BP Eekers<sup>3</sup>, Catharina M.L.Zegers<sup>3</sup> Deep learning (nnUNet) model for the EPTN contouring guidelines for OARs in neuro-oncology CancerData, 2025; doi:10.17195/candat.2025.10.1

**URL info:** <https://doi.org/10.17195/candat.2025.10.1>

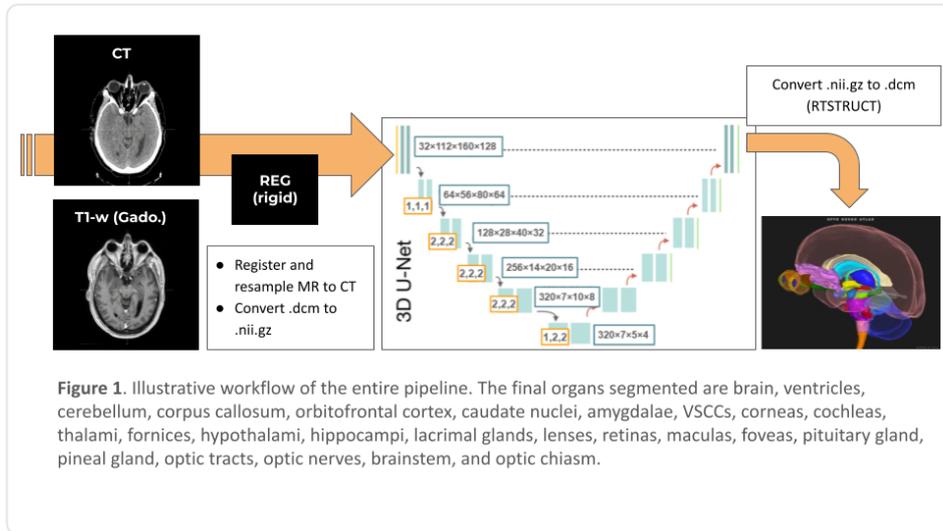
## 2. Technical specifications

### 2.1 Model overview

#### Model pipeline

- **Summary \*** : The available code supports end-to-end workflow generation of AI-predicted RTSTRUCT from DICOM inputs (T1w Gado. MR, CT, and corresponding REG file). The DICOM MR and CT registered with the REG and converted into nifti nnU-Net compatible format (i.e. images ending in 0000.nii.gz or 00001.nii.gz for the two input channels). The prediction is a nifti file with the 25 organs from the EPTN atlas, subsequently converted into DICOM RTSTRUCT

**Figure:** Figure1\_pipeline.png



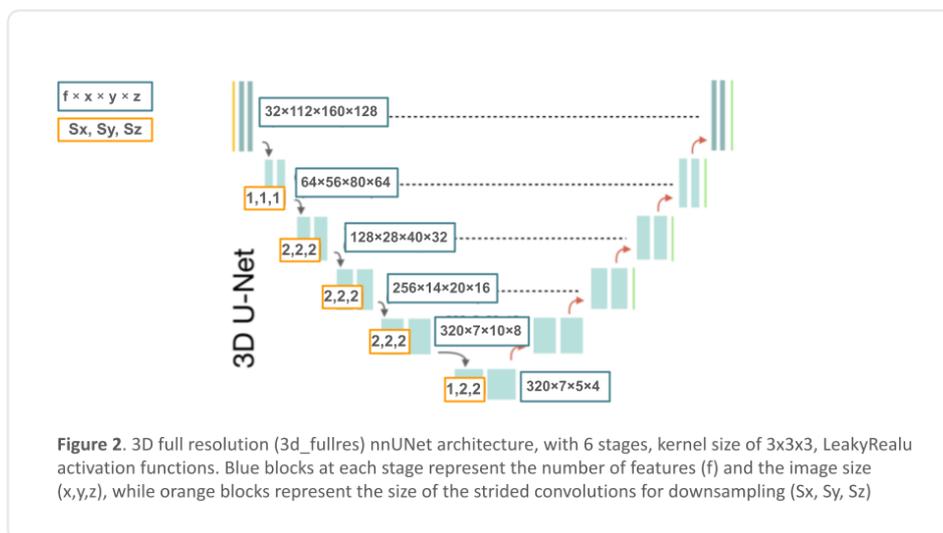
- **Model inputs \*** : ['CT', 'MR T1', 'REG']
- **Additional information:** —
- **Model outputs \*** : ['RTSTRUCT: Brain, Ventricle, Cerebellum, Corpus Callosum, Orbitofrontal Cortex, Caudate Nuclei, Amygdalae, VSCCs, Corneas, Cochleas, Thalami, Fornices, Hypothalami, Hippocampi, Lacrimal Glands, Lenses, Retinas, Maculas, Foveas, Pituitary Gland, Pineal Gland, Optic Tracts, Optic Nerves, Brainstem, Optic Chiasm']
- **Additional information:** —
- **Pre-processing \*** : Rigid registration with available REG DICOM file, conversion to nifti nnUNet compatible format. Organs with left/right (e.g. cochleas) and anterior/posterior parts (e.g. cerebellum) were merged into a single label. The nnU-Net requires non-overlapping labels, since it assigns a unique integer value to each voxel and each structure: 0 for background and 1 to N for the N structures. Thus, a structure-priority scheme was defined by the clinical experts to minimize information loss in regions where contours may overlap. The following order (increasing priority) was used during label encoding: brain, ventricles, cerebellum, corpus callosum, orbitofrontal cortex, caudate nuclei, amygdalae, VSCCs, corneas, cochleas, thalami, fornices, hypothalami, hippocampi, lacrimal glands, lenses, retinas, maculas, foveas, pituitary gland, pineal gland, optic tracts, optic nerves, brainstem, and optic chiasm. Then, standard preprocessing from nnUNet pipeline is applied:  $\text{oversampling\_foreground} = 0.33$ , MR is applied ZScoreNormalization, CT is applied CTNormalizationZ.
- **Post-processing \*** : Conversion to DICOM RTSTRUCT

## 2.2 Learning architecture(s)

### Learning architecture 1

Field	Value
<b>Total number of trainable parameters *</b>	88233570
<b>Number of inputs</b>	2
<b>Input content</b>	—
<b>Additional information regarding input content</b>	The images need to be registered and resampled to same resolution (that of the CT). The MR should end

Field	Value
	in _0000.nii.gz (first channel) and CT in _0001.nii.gz (second channel)
Input format	nifti
Input size	[112, 160, 128]
Number of outputs	1
Output content	—
Output format	nifti
Output size	[112, 160, 128]
Loss function *	DC_and_CE_loss
Batch size	2
Regularisation	Dropout=None, Weight decay: 3e-05, Instance Normalisation
Architecture figure *	Figure2_architecture.png



|| **Uncertainty quantification techniques \*** | NA | | **Explainability techniques \*** | NA | | **Citation(s)** | Ana M. Barragán-Montero<sup>1</sup>, Margerie Huet-Dastarac<sup>1</sup>, Dario di Perri<sup>1,2</sup>, David Hofstede<sup>3</sup>, Nikolina E Birimac<sup>3</sup>, Benjamin Roberfroid<sup>1</sup>, Emilien Quéré<sup>1</sup>, John Lee<sup>1</sup>, Wouter Van Elmpt<sup>3</sup>, Danielle BP Eekers<sup>3</sup>, Catharina M.L.Zegers<sup>3</sup> Deep learning (nnUNet) model for the EPTN contouring guidelines for OARs in neuro-oncology CancerData, 2025; doi: 10.17195/candat.2025.10.1 |

## 2.3 Hardware & software

- **Libraries and dependencies:** nnunet\_v2, pytorch - see requirements at [https://gitlab.com/ai4miro/nnunet\\_workflow\\_eptn](https://gitlab.com/ai4miro/nnunet_workflow_eptn)
- **Hardware (recommended):** we recommend a GPU to make predictions as this will be substantially faster than the other options. However, inference times are typically still manageable on CPU and MPS (Apple M1/M2). If

using a GPU, it should have at least 4 GB of available (unused) VRAM - See more at [https://github.com/MIC-DKFZ/nUNet/blob/master/documentation/installation\\_instructions.md#hardware-requirements](https://github.com/MIC-DKFZ/nUNet/blob/master/documentation/installation_instructions.md#hardware-requirements)

### 3. Training Data Methodology and Information

#### Fine tuned form

- **Model name \*** : NA
- **URL/DOI to model card \*** : NA
- **Tuning technique \*** : NA

#### Training Dataset

##### General information

- **Total size \*** : [59,59,59,59,59]
- **Number of patients \*** : 74
- **Source \*** : Private dataset from Department of Radiotherapy at Maastrro (Maastricht, The Netherlands)
- **Acquisition period \*** : Between 2019 and 2021
- **Inclusion / exclusion criteria \*** : Adults, brain lesions
- **Type of data augmentation**: Default data augmentation in nnUNetv2: rotation, scaling, Gaussian noise, Gaussian blur, brightness, contrast, simulation of low resolution, gamma correction and mirroring
- **Strategy for data augmentation**: Default strategy in data augmentation in nnUNetv2 (on the fly)

##### Technical specifications

**RTSTRUCT: Brain, Ventricle, Cerebellum, Corpus Callosum, Orbitofrontal Cortex, Caudate Nuclei, Amygdalae, VSCCs, Corneas, Cochleas, Thalami, Fornices, Hypothalami, Hippocampi, Lacrimal Glands, Lenses, Retinas, Maculas, Foveas, Pituitary Gland, Pineal Gland, Optic Tracts, Optic Nerves, Brainstem, Optic Chiasm**

(model\_outputs)

Field	Value
Image resolution *	NA
Patient positioning *	NA
Scan(s) manufacturer and model *	NA
Scan acquisition parameters *	NA
Scan reconstruction parameters *	NA
FOV *	NA

CT (model\_inputs)

Field	Value
Image resolution *	[0.684, 0.684, 1]
Patient positioning *	HFS
Scan(s) manufacturer and model *	SIEMENS SOMATOM Confidence/Drive
Scan acquisition parameters *	KVP = 120, DataCollectionDiameter = 500, DistanceSourceToDetector = 1085.6, DistanceSourceToPatient = 595, GantryDetectorTilt = 0, RotationDirection = CW, ExposureTime = 1000
Scan reconstruction parameters *	SoftwareVersion = syngo CT VB10A, ConvolutionKernel = Qr40 or Br38s
FOV *	350x350

#### MR T1 (model\_inputs)

Field	Value
Image resolution *	median = [1,1,1], min = [0.36,0.36,1], max = [1,1,1]
Patient positioning *	HFS
Scan(s) manufacturer and model *	PHILIPS INGENIA (CX)
Scan acquisition parameters *	ScanningSequence = GR, SequenceVariant = MR, AcquisitionType = 3D
Scan reconstruction parameters *	NA
FOV *	NA

#### REG (model\_inputs)

Field	Value
Image resolution *	NA
Patient positioning *	NA
Scan(s) manufacturer and model *	NA
Scan acquisition parameters *	NA
Scan reconstruction parameters *	NA
FOV *	NA

- Reference standard \* : EPTN consensus atlas 2021 - <https://doi.org/10.1016/j.radonc.2021.05.013>
- Reference standard QA \* : Peer review

## Patient demographics and clinical characteristics

- **Age \*** : median 50.5 years (range [19, 91])
- **Sex \*** : 51% female and 49% male

**Validation strategy \*** : 5 folds cross-validation

**Validation data partition \*** : [15,15,15,15,14]

**Weights initialization:** Kaiming (He) **Epochs:** [1000,1000,1000,1000,1000] **Optimiser:** self.initial\_lr = 1e-2; self.weight\_decay = 3e-5; optimizer = torch.optim.SGD(self.network.parameters(), self.initial\_lr, weight\_decay=self.weight\_decay, momentum=0.99, nesterov=True) **Learning rate:** self.initial\_lr = 1e-2; self.num\_epochs = 1000; lr\_scheduler = PolyLRScheduler(optimizer, self.initial\_lr, self.num\_epochs)

**Model choice criteria \*** : The weights for the last epoch were chosen as final weights.

**Inference method \*** : Five folds are available, one can choose between using a single fold, or the average of all folds.

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## 4. Evaluation Data Methodology, Results and Commissioning

### 1 Internal eval. on validation data

**Evaluation date \*** : 2025/12/04

#### Evaluated by

- **Name(s) \*** : Ana M. Barragán Montero
- **Institution(s) \*** : MIRO - UCLouvain
- **Contact email(s) \*** : ana.barragan@uclouvain.be
- **Same as 'Approved by':** No

**Evaluation frame \*** : Retrospective evaluation, only using geometric metrics (e.g. Dice, surface Dice, Added Path Length). No separate test set was held out. Instead, the model weights from the last epoch were used for inference, rather than selecting the epoch with the best validation performance, to avoid bias toward the validation data. Model performance was evaluated using the aggregated validation predictions across all folds, resulting in 74 unique patient-level predictions.

#### Evaluation dataset

##### General information

- **Total size \*** : [15,15,15,15,14]
- **Number of patients \*** : 74
- **Source \*** : Private dataset from Department of Radiotherapy at Maastricht (Maastricht, The Netherlands)
- **Acquisition period \*** : Between 2019 and 2021
- **Inclusion / Exclusion criteria \*** : Adults, brain lesions
- **URL info:** —

## Technical specifications

**RTSTRUCT: Brain, Ventricle, Cerebellum, Corpus Callosum, Orbitofrontal Cortex, Caudate Nuclei, Amygdalae, VSCCs, Corneas, Cochleas, Thalami, Fornices, Hypothalami, Hippocampi, Lacrimal Glands, Lenses, Retinas, Maculas, Foveas, Pituitary Gland, Pineal Gland, Optic Tracts, Optic Nerves, Brainstem, Optic Chiasm**  
(model\_outputs)

Field	Value
Image resolution *	NA
Patient positioning *	NA
Scan(s) manufacturer and model *	NA
Scan acquisition parameters *	NA
Scan reconstruction parameters *	NA
FOV *	NA

CT (model\_inputs)

Field	Value
Image resolution *	[0.684, 0.684, 1]
Patient positioning *	HFS
Scan(s) manufacturer and model *	SIEMENS SOMATOM Confidence/Drive
Scan acquisition parameters *	KVP = 120, DataCollectionDiameter = 500, DistanceSourceToDetecto = 1085.6, DistanceSourceToPatient = 595, GantryDetectorTilt = 0, RotationDirection = CW, ExposureTime = 1000
Scan reconstruction parameters *	SoftwareVersion = syngo CT VB10A, ConvolutionKernel = Qr40 or Br38s
FOV *	350x350

MR T1 (model\_inputs)

Field	Value
Image resolution *	median = [1,1,1], min = [0.36,0.36.1], max = [1,1,1]
Patient positioning *	HFS
Scan(s) manufacturer and model *	PHILIPS INGENIA (CX)
Scan acquisition parameters *	ScanningSequence = GR, SequenceVariant = MR, AcquisitionType = 3D
Scan reconstruction parameters *	NA

Field	Value
FOV *	NA

#### REG (model\_inputs)

Field	Value
Image resolution *	NA
Patient positioning *	NA
Scan(s) manufacturer and model *	NA
Scan acquisition parameters *	NA
Scan reconstruction parameters *	NA
FOV *	NA

- Reference standard \* : EPTN consensus atlas 2021 - <https://doi.org/10.1016/j.radonc.2021.05.013>
- Reference standard QA \* : Peer review

#### Patient demographics and clinical characteristics

- Age \* : median 50.5 years (range [19, 91])
- Sex \* : 51% female and 49% male

#### Quantitative evaluation

##### Geometric Metrics

##### surface DSC (Dice Similarity Coefficient)

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	Monai implementation: from monai.metrics import SurfaceDiceMetric; SurfaceDiceMetric(include_background=True, class_thresholds=[1.0])
On Volume *	Brain
Sample Data	—
Mean Data *	0.843 [0.789-0.866]
Figure Appendix Label	Figure 8

##### surface DSC (Dice Similarity Coefficient)

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	Ventricles
Sample Data	—
Mean Data *	0.924 [0.872-0.944]
Figure Appendix Label	Figure 8

**surface DSC (Dice Similarity Coefficient)**

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	Cerebellum
Sample Data	—
Mean Data *	0.735 [0.666-0.778]
Figure Appendix Label	Figure 8

**surface DSC (Dice Similarity Coefficient)**

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	Corpus callosum
Sample Data	—
Mean Data *	0.875 [0.838-0.919]
Figure Appendix Label	Figure 8

**surface DSC (Dice Similarity Coefficient)**

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	Orbitofrontal cortex
Sample Data	—

Field	Value
Mean Data *	0.799 [0.764-0.831]
Figure Appendix Label	Figure 8

surface DSC (Dice Similarity Coefficient)

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	Caudate nuclei
Sample Data	—
Mean Data *	0.906 [0.847-0.94]
Figure Appendix Label	Figure 8

surface DSC (Dice Similarity Coefficient)

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	Amygdalae
Sample Data	—
Mean Data *	0.747 [0.65-0.817]
Figure Appendix Label	Figure 8

surface DSC (Dice Similarity Coefficient)

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	VSCCs
Sample Data	—
Mean Data *	0.784 [0.685-0.84]
Figure Appendix Label	Figure 8

surface DSC (Dice Similarity Coefficient)

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	Corneas
Sample Data	—
Mean Data *	0.769 [0.675-0.841]
Figure Appendix Label	Figure 8

**surface DSC (Dice Similarity Coefficient)**

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	Cochleas
Sample Data	—
Mean Data *	0.897 [0.826-0.942]
Figure Appendix Label	Figure 8

**surface DSC (Dice Similarity Coefficient)**

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	Thalami
Sample Data	—
Mean Data *	0.767 [0.697-0.821]
Figure Appendix Label	Figure 8

**surface DSC (Dice Similarity Coefficient)**

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	Fornices
Sample Data	—

Field	Value
Mean Data *	0.881 [0.822-0.91]
Figure Appendix Label	Figure 8

surface DSC (Dice Similarity Coefficient)

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	Hypothalami
Sample Data	—
Mean Data *	0.707 [0.616-0.799]
Figure Appendix Label	Figure 8

surface DSC (Dice Similarity Coefficient)

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	Hippocampi
Sample Data	—
Mean Data *	0.848 [0.796-0.891]
Figure Appendix Label	Figure 8

surface DSC (Dice Similarity Coefficient)

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	Lacrimal glands
Sample Data	—
Mean Data *	0.749 [0.644-0.82]
Figure Appendix Label	Figure 8

surface DSC (Dice Similarity Coefficient)

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	Lenses
Sample Data	—
Mean Data *	0.98 [0.948-0.989]
Figure Appendix Label	Figure 8

**surface DSC (Dice Similarity Coefficient)**

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	Retinas
Sample Data	—
Mean Data *	0.931 [0.897-0.946]
Figure Appendix Label	Figure 8

**surface DSC (Dice Similarity Coefficient)**

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	Maculas
Sample Data	—
Mean Data *	0.91 [0.853-0.955]
Figure Appendix Label	Figure 8

**surface DSC (Dice Similarity Coefficient)**

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	Foveas
Sample Data	—

Field	Value
Mean Data *	0.667 [0.533-0.815]
Figure Appendix Label	Figure 8

surface DSC (Dice Similarity Coefficient)

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	Pituitary
Sample Data	—
Mean Data *	0.803 [0.624-0.889]
Figure Appendix Label	Figure 8

surface DSC (Dice Similarity Coefficient)

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	Pineal gland
Sample Data	—
Mean Data *	0.868 [0.779-0.93]
Figure Appendix Label	Figure 8

surface DSC (Dice Similarity Coefficient)

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	Optic tracts
Sample Data	—
Mean Data *	0.763 [0.658-0.832]
Figure Appendix Label	Figure 8

surface DSC (Dice Similarity Coefficient)

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	Optic nerves
Sample Data	—
Mean Data *	0.944 [0.923-0.959]
Figure Appendix Label	Figure 8

#### surface DSC (Dice Similarity Coefficient)

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	Brainstem
Sample Data	—
Mean Data *	0.781 [0.67-0.83]
Figure Appendix Label	Figure 8

#### surface DSC (Dice Similarity Coefficient)

Field	Value
Type *	surface DSC (Dice Similarity Coefficient)
Metric Specifications *	NA
On Volume *	Optic chiasm
Sample Data	—
Mean Data *	0.904 [0.849-0.941]
Figure Appendix Label	Figure 8

### Qualitative evaluation

Evaluators information \* : NA

#### Likert scoring

- Method \* : NA
- Results \* : —

#### Turing test

- Method \* : NA

– Results \* : —

#### Time saving

– Method \* : NA

– Results \* : —

#### Other

– Method \* : —

– Results \* : —

Explainability \* : NA

Citation details: —

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## 5. Other considerations

- **Responsible Use and Ethical Considerations:** We release the model publicly to the international community, while explicitly acknowledging that clinical use remains the responsibility of each institution within its regulatory context.
  - **Risk Analysis:** None performed for this specific model. But we refer to common failure modes of typical automation pipelines in <https://doi.org/10.1016/j.phro.2025.100765>
  - **Post-Market Surveillance / Live Monitoring:** It is recommended to use a monitoring based at least on geometric metrics to track automation bias and potential drop of performance due to data domain shifts/changes. Suggested techniques are Statistical Process Control (e.g. <https://doi.org/10.1016/j.ppro.2023.09.004>, <https://doi.org/10.1016/j.phro.2025.100886>))
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## Appendix

Figure3\_progress\_fold\_0.png

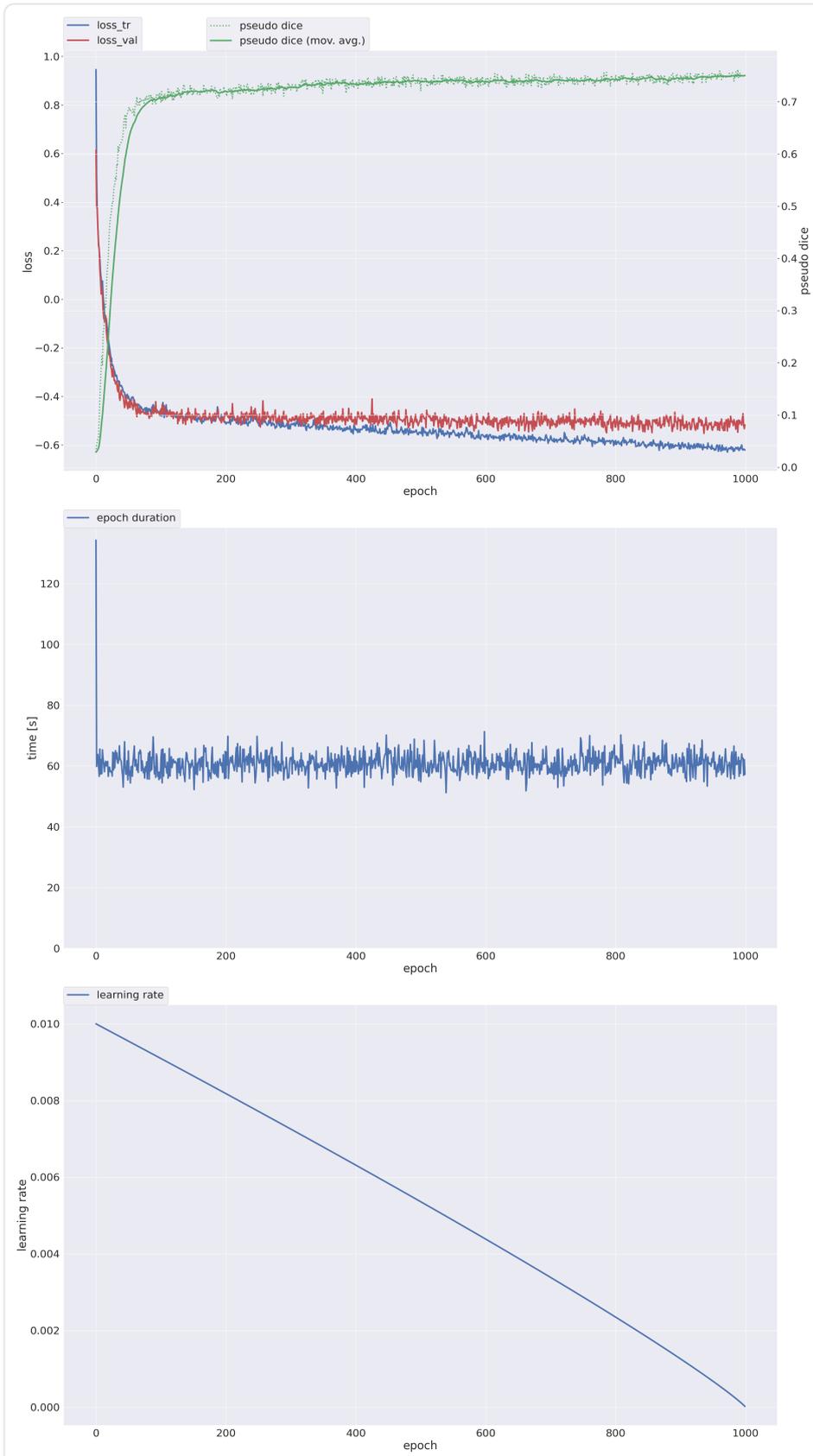


Figure4\_progress\_fold\_1.png

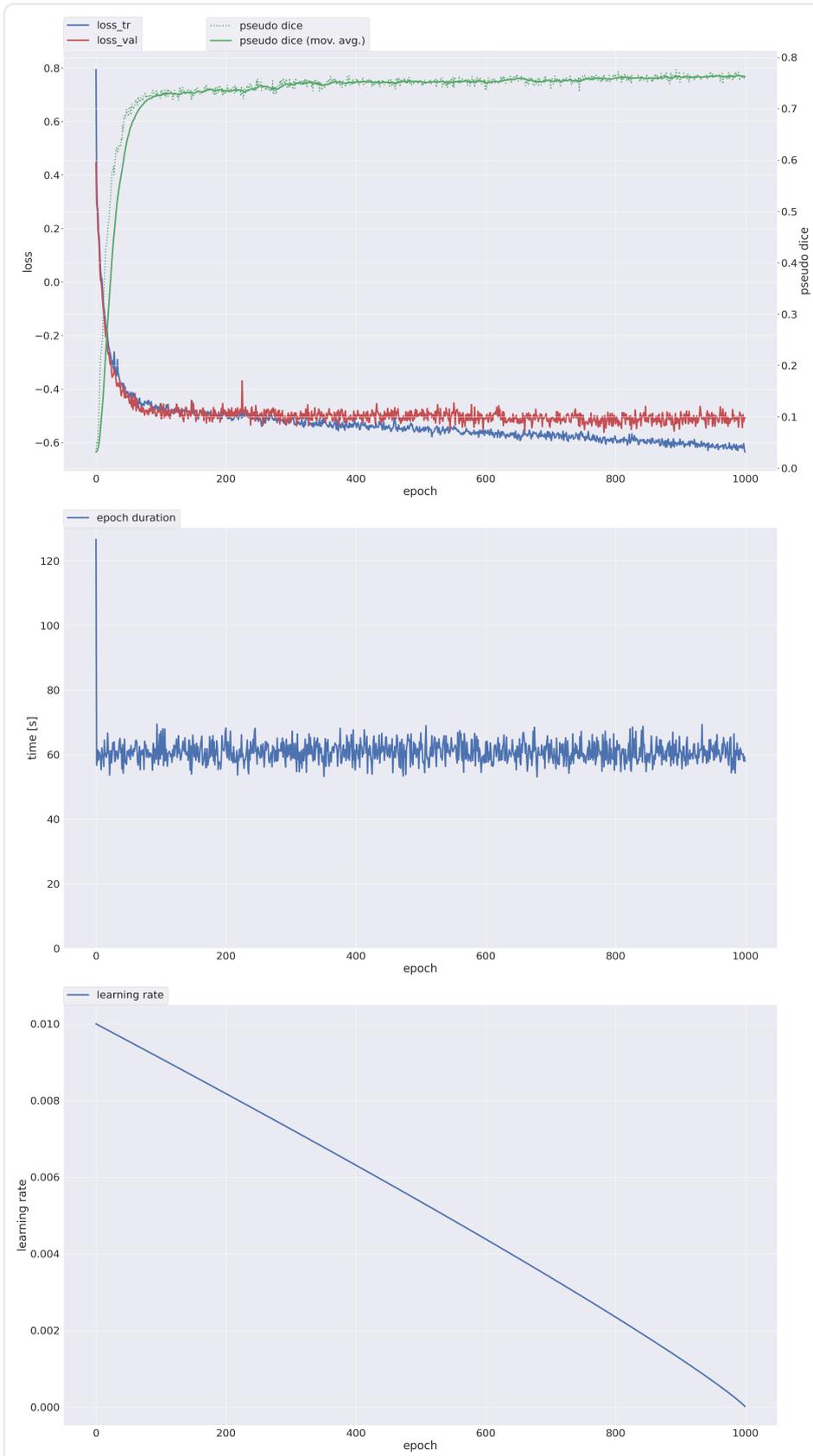


Figure5\_progress\_fold\_2.png

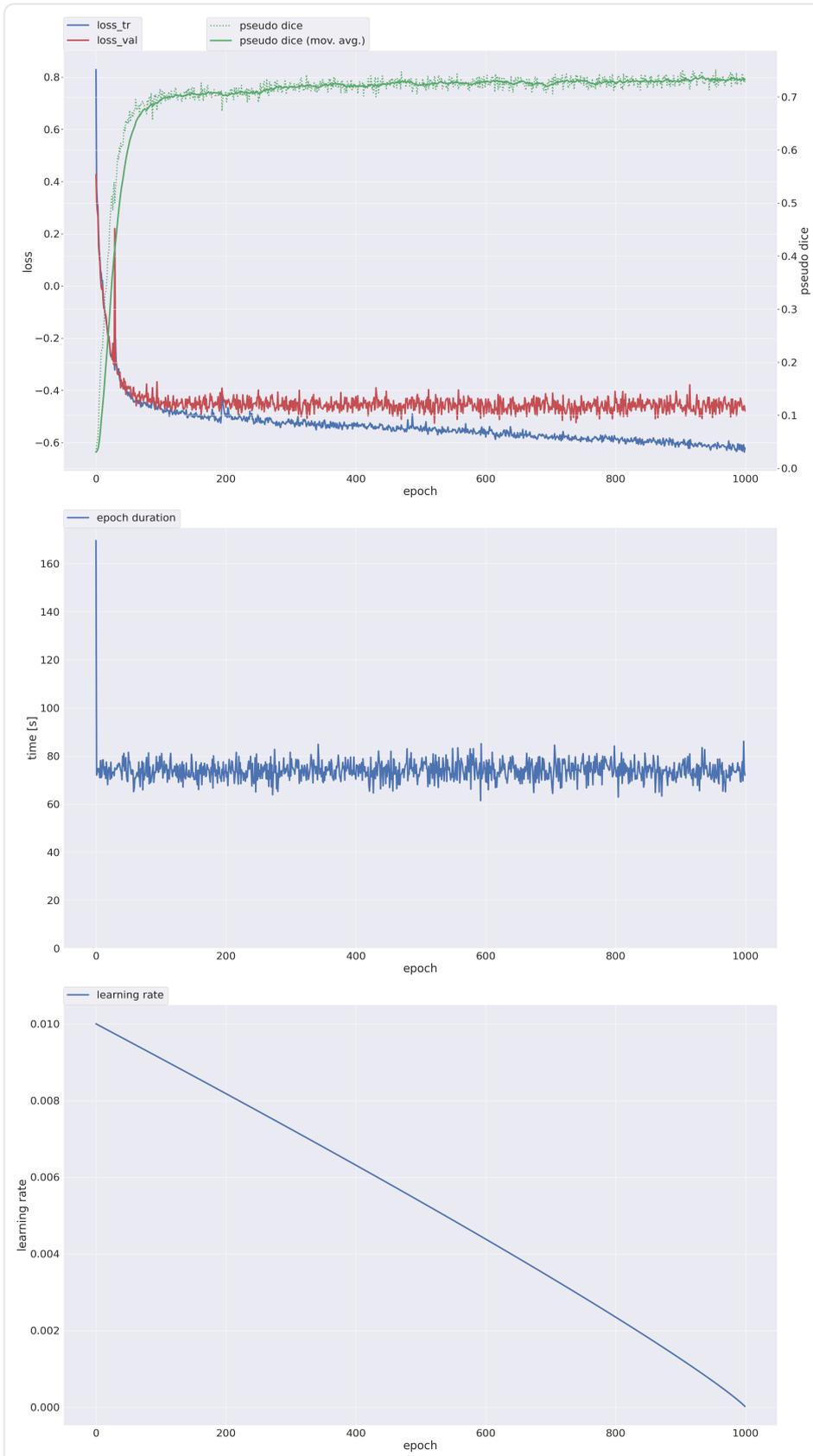


Figure6\_progress\_fold\_3.png

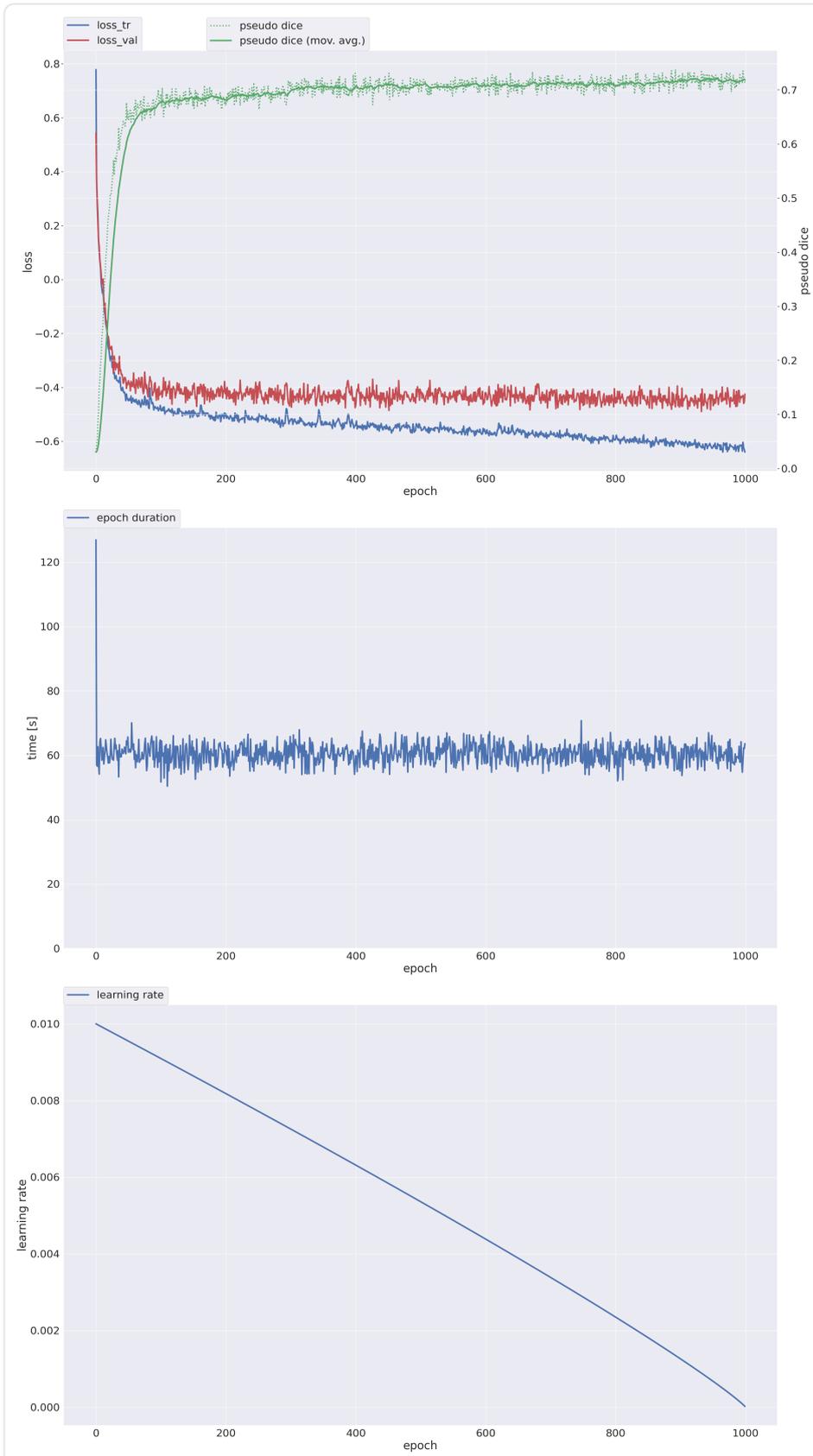


Figure7\_progress\_fold\_4.png

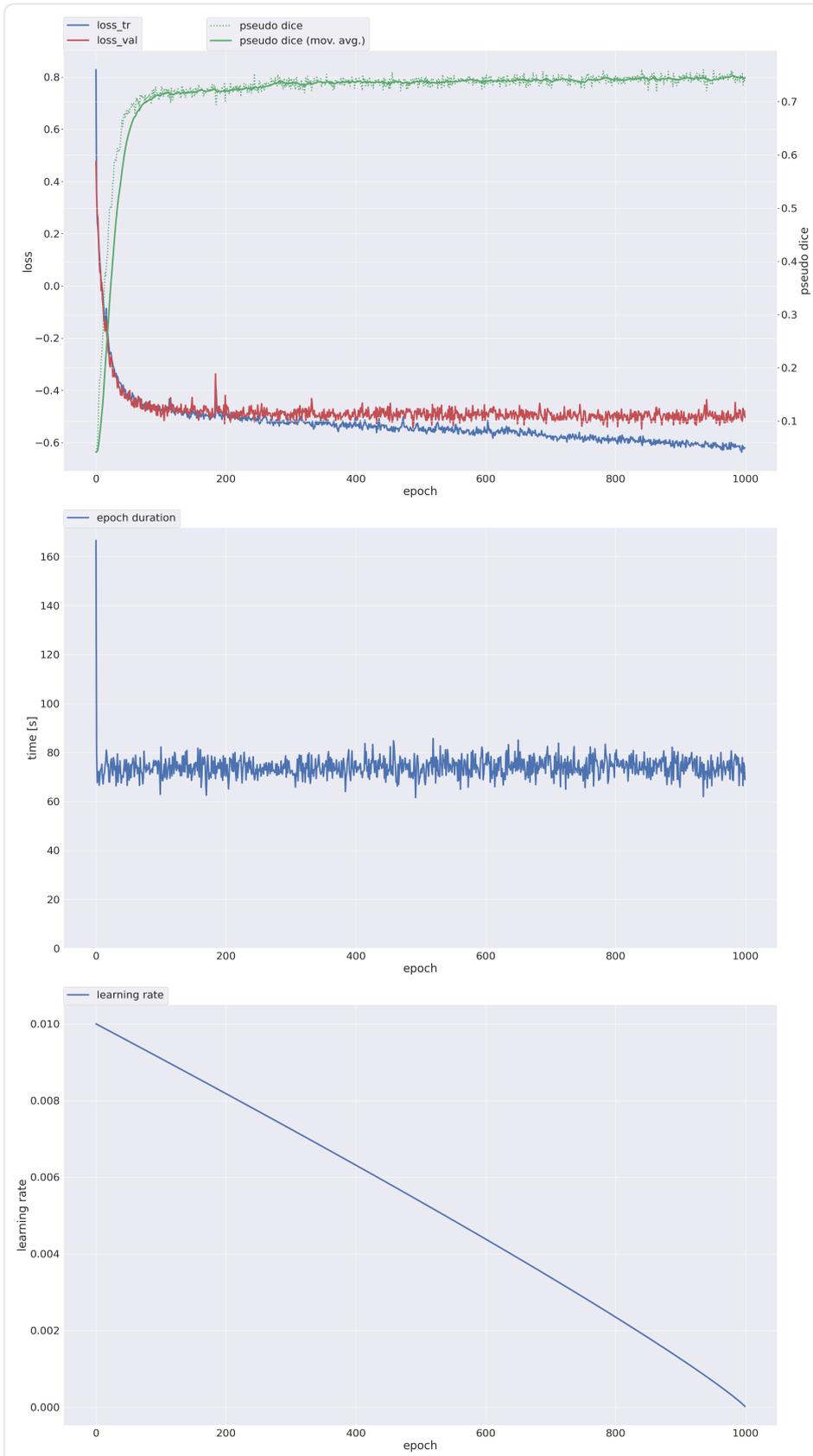


Figure8\_T1CT\_sDice\_horizontal.png

