

1. Provide your team background and organization description (if applicable).

Dr. Emmanuelle Salin and Arijana Bohr are both researchers at the Department of Artificial Intelligence in Biomedical Engineering's machine learning and data analytics lab at the Friedrich-Alexander University of Erlangen-Nuremberg.

Emmanuelle Salin is a PostDoc and Group Leader and Arijana Bohr is a PhD Candidate.

Background (CVs are attached in the mail):

- **Emmanuelle Salin:** PhD in Computer Science from Aix-Marseille Université. During her PhD she worked on NLP, Computer Vision and Multimodality in the context of Vision-Language Transformers.
- **Arijana Bohr:** Master's in mathematics from Friedrich Alexander University Erlangen-Nuremberg. In her master's thesis she worked on the topic of distributional robustness with application to Parkinson's Disease.
- **Organization Description:**
 - University: Friedrich Alexander University Erlangen-Nuremberg (FAU)
 - Department: Artificial Intelligence in Biomedical Engineering
 - Lab: Machine Learning and Data Analytics (MaD):
<https://www.mad.tf.fau.de/>
 - Supervisor: Prof. Dr. Bjoern Eskofier
 - Further affiliation: Center for AI in medicine (collaboration between FAU and University Hospital Erlangen)
The Center aims to foster interdisciplinary research to leverage AI capabilities in the medical domain.
We aim to work with medical partners to develop AI tools that will support their medical research.

2. Explain why you participated in the DigiLut challenge:

The DigiLut challenge aligns with the core mission of the Center for AI in medicine FAU to which we belong to, which is to leverage AI to address exciting research questions in the medical field, with the potential for translational impact (research that leads to concrete use of machine learning in the medical context). Detecting graft rejection following lung transplantation is particularly compelling, as it represents an area where an AI-based algorithm could support a pathologist in identifying crucial regions.

Furthermore, the challenge of working with pathology images and managing their substantial data size intrigued us as we had little experience with this kind of data. This project provided an opportunity for us to explore and develop efficient methods for handling large-scale medical imaging data. By participating, we sought to deepen our expertise in this context.

3. Describe how you built your winning model and elaborate on the technical and modeling choices you made:

For the model we used a patch-based approach.

1. We select appropriate patches using color thresholds and artifact removal. We used the zoom levels 2 and 3 of the python open-source library Openslide. We consider them to be the most appropriate given the size of the lesions.
2. We classify those patches into positive and negative, where positive labels required at least an intersection with a ground-truth bounding box with a giou of 0.01. This threshold was chosen because of the high imbalance between positive and negative patches but may not be the most medical relevant threshold.
3. For this part we built two classification models, each classifying patches for one zoom level (level 2 or 3). These models are computer vision transformers. We used open-source checkpoints available on hugging-face (facebook/dinov2-small-imagenet1k-1-layer) and trained the models using a soft-focal loss.
4. For prediction we use overlapping patches for more robustness. We first estimate the potential level 3 bounding boxes and then predict the potential level 2 bounding boxes by grouping positive patches that intersect. We first predict level 3 bounding boxes to be more time-efficient, and then use level 2 to be more precise.

For more information, please see our attached pdf.

4. What GPU/CPU/RAM resources you used to build your model:

We used the resources of the Erlangen National High Performance Computing Center (NHR@FAU).

For training we used one A100 GPU (40 GB).

There are 512 GB Ram/128 cores (2 x AMD EPYC 7662) shared between four GPUs (a node).