Data Management Plan (DMP)

FRENCH NATIONAL RESEARCH AGENCY (ANR):

ANR DMP

GENERAL INFORMATION

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1. DATA DESCRIPTION AND COLLECTION OR RE-USE OF EXISTING DATA

1a. How will new data be collected or produced and/or how will existing data be re-used?

- New data will be collected by acquisition using a spinning disk microscope (PLBS-BiCel, Cité Scientifique, SN3, room 322). After, they are transferred using FileSender, to be then processed. Existing data will be reused for future processing tools, and for internship report redaction.

- The data are .nd2 images of a bone sample, recent or archaelogical. First, a stichted image (8x8) using 4X objective in BrightField is taken. After, a hyperstack of 6 fluorescence channels (DAPI, CFP, BrightField, Cy3, YFP, GFP) and 7 z plans is taken with a 20X objective, for 4 chosen positions on the 4X stitched image of the sample.

- A stitched image takes 167448 Ko, and a hyperstack takes 344 668 Ko of the storage. The created application takes 33 103 Ko.

2. DOCUMENTATION AND DATA QUALITY

- The architecture of data is as following

```
Maria
 |_ data
     |_ 19/12/2025
             |_ anat-1
                    |_ anat-1-stich-bf.nd2
                    |_ anat-1-fluo-spinning-blanc.nd2
                    |_ anat-1- fluo-spinning-bord.nd2
                    |_ anat-1- fluo-spinning-bernique.nd2
                    |_ anat-1- fluo-spinning-alteration.nd2
 |_ sam2
     |_ checkpoints
             |_ finetuned_checkpoints
                    |_ checkpoint_objet_DAPI.pt
                    |_ checkpoint_blanc_BrightField.pt
                    |_ checkpoint_blanc_DAPI.pt
             |_ sam2.1_hiera_base_plus.pt
```

```
|_ BoneSeg.py
|_ requirements.txt
|_ setup_me.bat
|_ build_app.bat
|_ icon.ico
|_ logo.png
|_ pca.py
|_ results.txt
|_ run_pca.bat
|_ README.md
```

- In the 'data' folder, it is adviced to have the same architecture for next acquisitions, but not mandatory. However, the 'data' folder must be at the same level than the others as shown before. The images used in BoneSeg application have to be .nd2 hyperstacks, with fluorescence channels in this order: DAPI, CFP, BrightField, Cy3, YFP, GFP. Also, the user must take 7 'z' plans.

- The 'sam2' folder has to be downloaded in the SAM2 Github repository: facebookresearch/sam2. A subfolder 'finetuned_checkpoints' must be created in "sam2/checkpoints" folder, and finetuned checkpoints are available here to download: https://doi.org/10.5281/zenodo.18241548. Then, put them all in the folder, except the checkpoint "sam2.1_hiera_base_plus.pt" that must be put in "sam2/checkpoints" folder.

- A "README.md" file is available in the Github repository created for the "BoneSeg" application: mariaramdane/BoneSeg, explaining the steps to download the app.

- A detailed procedure is given in the BoneSeg Github repository for a standardized data capture.

DMP template

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