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Relion-5 is now installed on the Unistra HPC (hpc-login.u-strasbg.fr). To use it simply load the module: module load relion/relion-5.0 The new version of Relion comes with: 1) Blush regularisation: a machine-learning based prior that improves 3D refinement and classification of low SNR data sets https://www.biorxiv.org/content/10.1101/2023.10.23.563586v1

2) DynaMight: a variational auto-encoder for modelling continuous structural heterogeneity and a deformed backprojection algorithm for reconstruction of improved consensus maps https://www.biorxiv.org/content/10.1101/2023.10.18.562877v1

3) ModelAngelo: a machine-learning approach for automated atomic model building and identification of unknown proteins in cryo-EM maps https://www.biorxiv.org/content/10.1101/2023.05.16.541002v2

4) Select subsets of filaments using dendrograms make from 2D class averaging assignments https://www.biorxiv.org/content/10.1101/2023.07.24.550295v1

5) Support for AMD and Intel GPUs (CUDA and intel CPU-acceleration continue to work too) → your feedback on these new accelerators, especially when also using the cheaper gaming cards, are welcomed. For the moment, Topaz, Blush, class_ranker, DynaMight and ModelAngelo only work on NVIDIA cards.

6) A sub-tomogram averaging pipeline from raw movies until atomic modelling → please note that this part of RELION-5.0 is not yet finished. We are still writing a tutorial & documentation, and we are still running tests. You are welcome to already try the new code (relion –tomo), but until we are ready with the documentation and testing, we cannot yet provide feedback on this part of the code. Please be patient. If you use this part of the code and would like to cite us, in the mean time you can cite this paper: https://elifesciences.org/articles/83724

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