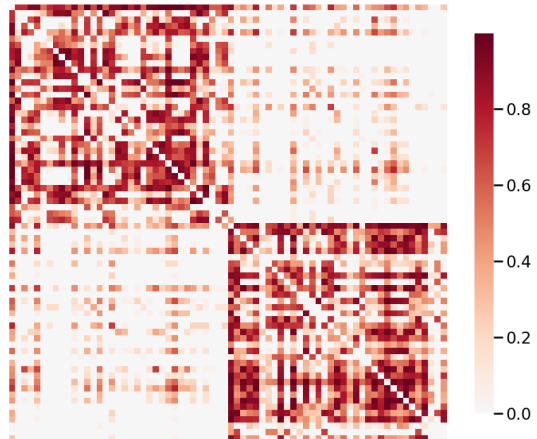


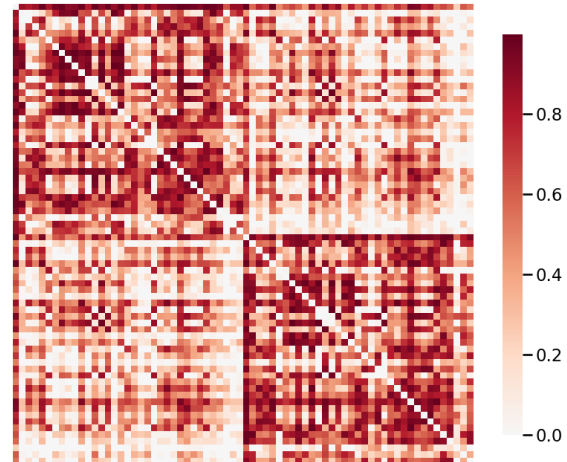
Compare different results with different pipeline version

# Data: BNU1

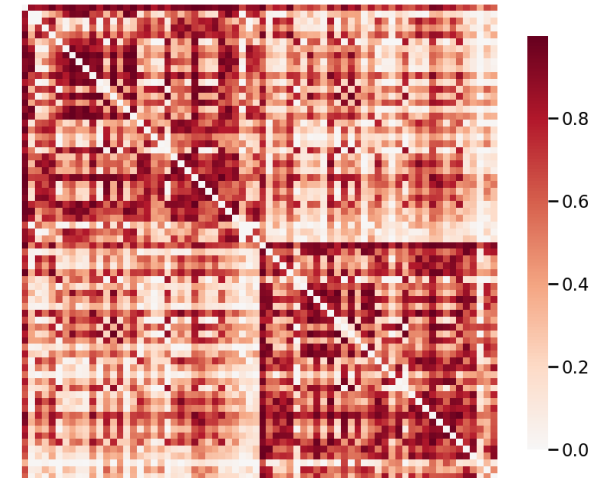
FAST



DiPy's TissueClassifierHMRF

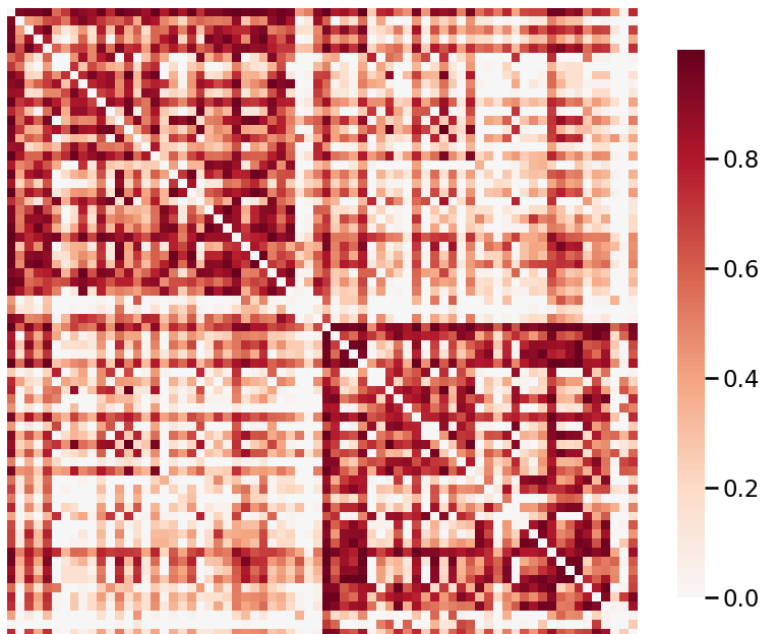


Seeds = '20'

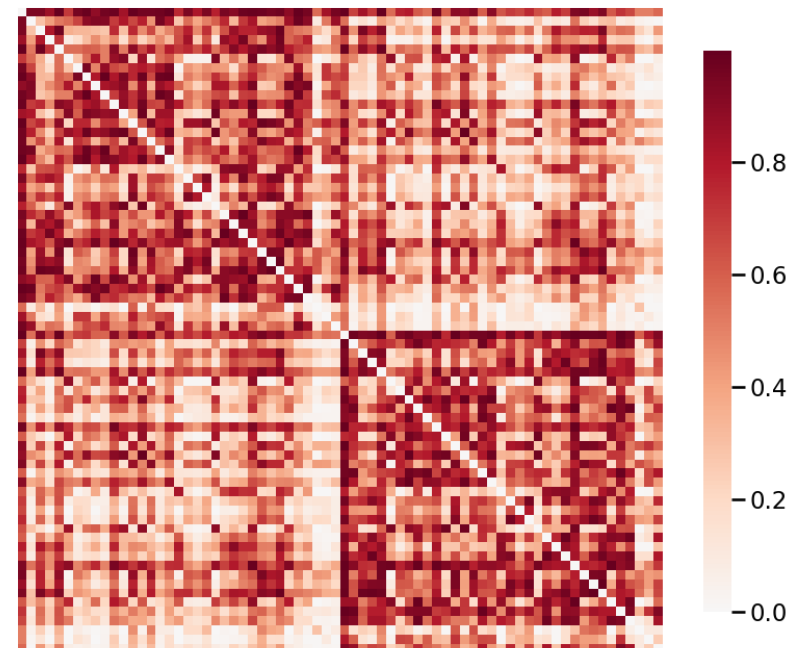


Data: SWU4\_1\_1

FAST

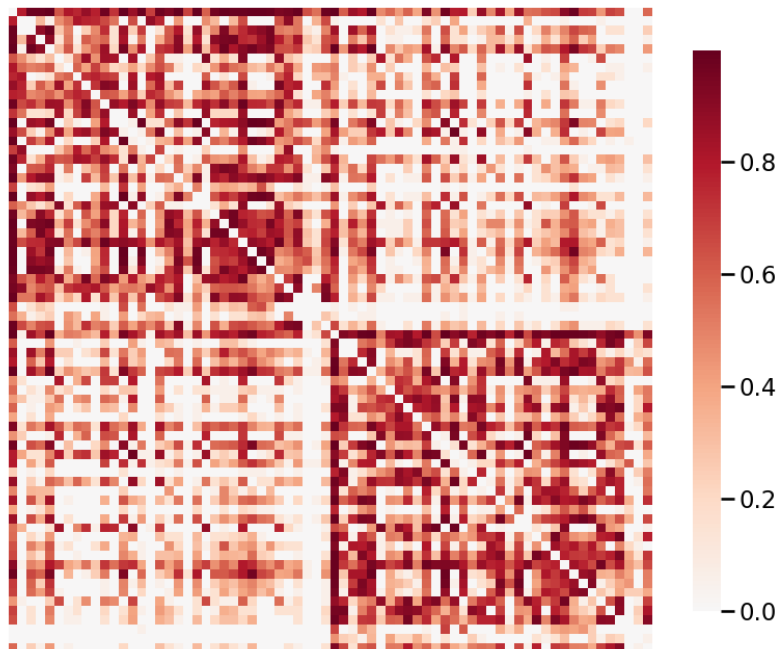


DiPy's TissueClassifierHMRF

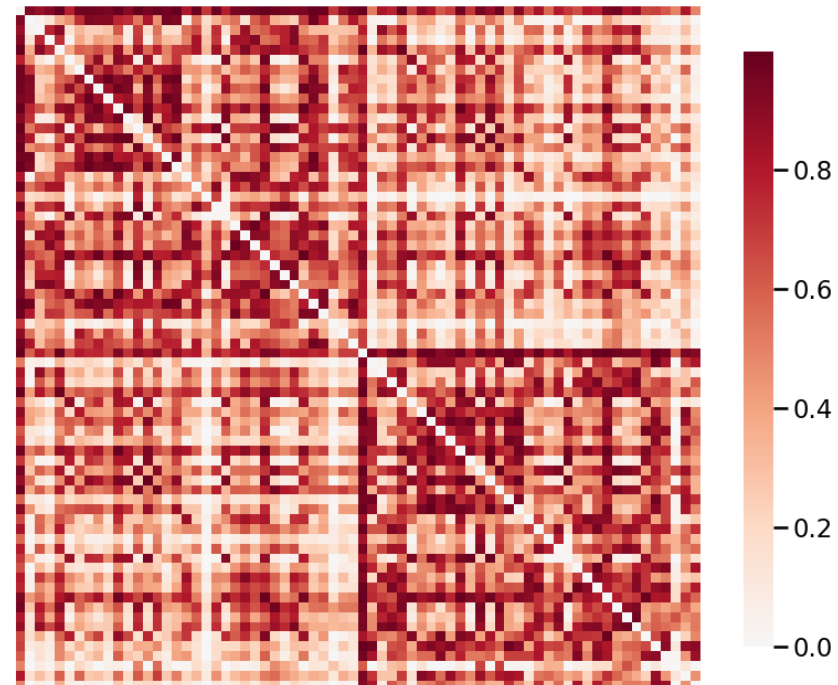


Data: SWU4\_1\_3

FAST

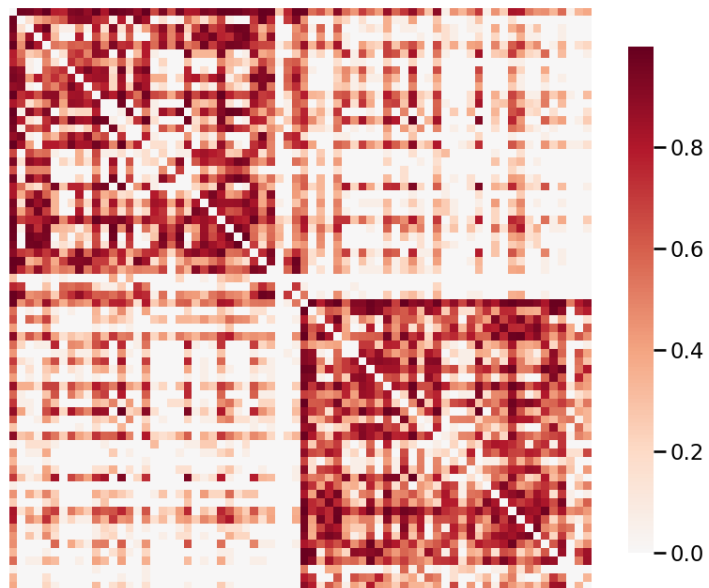


DiPy's TissueClassifierHMRF



Data: SWU4\_1\_3

FAST



DiPy's TissueClassifierHMRF

