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Computational Medicine, Dept. of Medical Sciences
Signals & Systems, Dept. of Electrical Engineering
Uppsala University, March 2020
----- COMBO-M Initiated
Select mode for COMBO-M:
1. Intra-Plate Analysis
2. Inter-Plate Analysis
---- Inter-Plate Analysis ---
Choose feature extraction method:
1. Multi Resolution Histograms
2. Local Binary Patterns
3. Multi Resolution Local Binary Patterns
4. Local Eigenfilters
1
Global Experiment Path: F:\CUSP9A\Mendeley\1-4
Enter hours after drug addition for the 1st recorded time point/frame:
0
BridgeAnnot mat path: F:\CUSP9A\Mendeley\1-✓
4\9093\Morphology\PHHC\BridgeAnnot Vis 9093 PHHC Run03 r05 b0125.mat
BridgeAnnot mat path: F:\CUSP9A\Mendeley\1-✓
4\9095\Morphology\PHHC\BridgeAnnot Vis 9095 PHHC Run03 r05 b0125.mat
BridgeAnnot mat path: F:\CUSP9A\Mendeley\1-\
4\9097\Morphology\PHHC\BridgeAnnot Vis 9097 PHHC Run03 r05 b0125.mat
BridgeAnnot mat path: F:\CUSP9A\Mendeley\1-\(\vec{\cutech}\)
4\9099\Morphology\PHHC\BridgeAnnot Vis 9099 PHHC Run03 r05 b0125.mat
Inter-Plate results successfully parsed...
Enter number of simulations for the resampling-based NHST:
1000000
Enter probability of false alarm (%) for the NHST:
5
Inter-Plate Analysis started...
Inter-Plate Analysis completed...
```

Generation of CSV file with time evolving changes in cell culture morphology started
Generation of CSV file with time evolving changes in cell culture morphology ✓
completed
Generation of time evolving cell culture morphology curves started
Generation of time evolving cell culture morphology curves completed
Time elapsed for COMBO-M: 0.00 (hrs) 2.00 (min) 34.23 (sec)
COMBO-M Completed ✓