

Workflow

1. Running on bw-unicluster:

1. ./jobrun_all.sh

submits one job for each set $(D(\tau), |e|, acc)$

2. msub -q singlenode jobrun_Merge.sh

3. ./jobrun_Ana1_all.sh

runs with DataAna1_New.m

submits one job for each set $(entM, anaM, cm, acc)$

Attention: “entM=Mit” is hard-coded in Ana1_template.sh

2. Running locally:

1. Download of

1. Merged data

2. Output of analysis step 1

2. ./sort_Ana1.sh locDataAna1

sorts output of analysis step 1 in a way that it can be further analyzed

3. ./jobrunAna2.sh locDataAna1 locDataAna2

outputs histograms and two different text-files

and moves them into folders ‘Histos’, ‘Texts’ and ‘Ratios’

4. ./jobrunAna3.sh locDataAna2Texts locDataAna3

outputs density plots

5. ./jobrunAna4.sh locDataAna2Ratios locDataAna4

outputs ratio plots

Important commands on bw-unicluster

1. Show queue: `showq -u $USER`

2. Checking jobs: `checkjob JOBID | grep ^State`

3. Cancelling: `mjobctl -c JOBID`

Completed runs in 09/2017

Run I			
$D(\tau)$	0.15	0.3	0.45
$ e $	2	5	10
acc	0.6	0.8	1.0

Run II					
$D(\tau)$	0.15	0.2	0.3	0.4	0.45
$ e $	3	7	9		
acc	0.6	0.8	1.0		

Run III			
$D(\tau)$	0.2	0.4	
$ e $	2	5	10
acc	0.6	0.8	1.0

Run I-III						
$D(\tau)$	0.15	0.2	0.3	0.4	0.45	
$ e $	2	3	5	7	9	10
acc	0.6	0.8	1.0			