HybPhyloMaker ‘rapid instructions’

1. Log in to skirit (skirit. ics.muni.cz aka brno2) MetaCentrum frontend

```
ssh metausername@skirit.ics.muni.cz
```

2. Clone HybPhyloMaker from GitHub and move HybSeqSource folder to home folder, download reference

```
git clone https://github.com/tomas-fer/HybPhyloMaker
```

```
mv HybPhyloMaker/HybSeqSource/ .
```

```
cd HybSeqSource
```

```
wget https://raw.githubusercontent.com/tomas-fer/HybSeqCourse/master/curcuma_HybSeqProbes_first958.fa
```

```
cd ../HybPhyloMaker
```

3. Copy test dataset

```
cp -r /storage/projects/botany-uk/HybSeqCourse2024 .
```

4. Edit file settings.cfg (Ctrl+W to search, Ctrl+O to save changes, Ctrl+X to exit editor)

```
nano settings.cfg
```

```
location=1
server=brno2
data=HybPhyloMaker/HybSeqCourse2024
OUTGROUP="Zingiber-officinale_S242"
MISSINGPERCENT=75
SPECIESPRESENCE=40
probes=curcuma_HybSeqProbes_first958.fa
raxmlperjob=1
phypartsbs=50
```

5. Prepare pseudoreference

```
qsub HybPhyloMaker0b_preparereference.sh
```

6. Install appropriate R packages (and wait until this and previous jobs are finished)

```
qsub HybPhyloMaker0c_Rsetup_MetaCentrum.sh
```

7. Filter the raw data

```
qsub HybPhyloMaker1a_rawprocessParallel.sh
```

8. Run this submitter created by the previous job (this script submits 35 jobs)

```
cd HybSeqCourse2024/20filtered/ && ./submitRawProcessJobs.sh && cd ../..
```

9. Run the summary script (after all jobs are finished)

```
qsub HybPhyloMaker1a2_rawprocessParallel_summary.sh
```

10. Map reads to pseudoreference

```
qsub HybPhyloMaker2a_readmappingParallel.sh
```

11. Run this submitter created by the previous job (this script submits 35 jobs)

```
cd HybSeqCourse2024/exons/21mapped_bwa/ && ./submitMappingJobs.sh && cd ../../..
```

12. Run the summary script (after all jobs are finished)

```
qsub HybPhyloMaker2a2_readmappingParallel_summary.sh
```

13. Generate PSLX files

```
qsub HybPhyloMaker3_generatepslx.sh
```

14. Copy PSLX files

```
mkdir pslx_HybSeqCourse2024
```

```
cp HybSeqCourse2024/exons/50pslx/*.pslx pslx_HybSeqCourse2024
```

15. Edit file settings.cfg

```
nano settings.cfg
```

```
otherpslx=HybPhyloMaker/pslx_HybSeqCourse2024
```

16. Generate exon assemblies

```
qsub HybPhyloMaker4a_processpslx.sh
```

17. Filter missing data

```
qsub HybPhyloMaker5_missingdataremoval.sh
```

18. Generate RAxML trees

```
qsub HybPhyloMaker6a_RAxML_for_selected.sh
```

19. Run this submitter created by the previous job (this script submits 246 jobs)

```
cd HybSeqCourse2024/exons/72trees75_40/RAxML/ && ./submitRAxMLjobs.sh && cd ../../../..
```

20. Run the summary script (after all jobs are finished)

```
qsub HybPhyloMaker6a2_RAxML_trees_summary.sh
```

21. Create tree files

```
qsub HybPhyloMaker7_roottrees.sh
```

22. Create diverse species trees (run all four, no need to wait...)

```
qsub HybPhyloMaker8a_astral.sh
```

```
qsub HybPhyloMaker8b_astrid.sh
```

```
qsub HybPhyloMaker8c_mrl.sh
```

```
qsub HybPhyloMaker8e_concatenatedFastTree.sh
```

23. After all jobs are finished run these additional scripts

```
qsub HybPhyloMaker8h_neighbourNetwork.sh
```

```
qsub HybPhyloMaker8k_quartetsampling.sh
```

```
qsub HybPhyloMaker11_phyparts.sh
```