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1 HybPhyloMaker 'rapid instructions' 2023
2
3 1. Log in to skirit (skirit.ics.muni.cz aka brno2) MetaCentrum frontend
4
5 2. Clone HybPhyloMaker and enter the directory
6 git clone https://github.com/tomas-fer/HybPhyloMaker
7 mv HybPhyloMaker/HybSeqSource/ .
8 cd HybSeqSource
9 wget
10 https://raw.githubusercontent.com/tomas-fer/HybSeqCourse/master/curcuma_HybSeqProbes_f
11 rst958.fa
12 cd ../HybPhyloMaker
13
14 3. Copy test dataset
15 cp -r /storage/projects/botany-uk/HybSeqCourse2023/ .
16
17 4. Edit file settings.cfg
18 nano settings.cfg
19 location=1
20 server=brno2
21 data=HybPhyloMaker/HybSeqCourse2023
22 tree=FastTree
23 OUTGROUP="Zingiber-officinale_S242"
24 probes=curcuma_HybSeqProbes_first958.fa
25 raxmlperjob=1
26
27 5. Prepare pseudoreference
28 qsub HybPhyloMaker0b_preparereference.sh
29
30 6. Install appropriate R packages (and wait until this and previous jobs are finished)
31 qsub HybPhyloMaker0c_Rsetup_MetaCentrum.sh
32
33 7. Filter the raw data
34 qsub HybPhyloMaker1a_rawprocessParallel.sh
35
36 8. Run this submitter created by the previous job (this script submits 35 jobs)
37 cd HybSeqCourse2023/20filtered/ && ./submitRawProcessJobs.sh && cd ../..
38
39 9. Run the summary script (after all jobs are finished)
40 qsub HybPhyloMaker1a2_rawprocessParallel_summary.sh
41
42 10. Map reads to pseudoreference
43 qsub HybPhyloMaker2a_readmappingParallel.sh
44
45 11. Run this submitter created by the previous job (this script submits 35 jobs)
46 cd HybSeqCourse2023/exons/21mapped_bwa/ && ./submitMappingJobs.sh && cd ../../..
47
48 12. Run the summary script (after all jobs are finished)
49 qsub HybPhyloMaker2a2_readmappingParallel_summary.sh
50
51 13. Generate PSLX files
52 qsub HybPhyloMaker3_generatepslx.sh
53
54 14. Copy PSLX files
55 mkdir pslx_AmomumCourse
56 cp HybSeqCourse2023/exons/50pslx/*.pslx pslx_AmomumCourse
57
58 15. Edit file settings.cfg
59 nano settings.cfg
60 otherpslx=HybPhyloMaker/pslx_AmomumCourse
61
62 16. Generate exon assemblies
63 qsub HybPhyloMaker4a_processpslx.sh
64
65 17. Filter missing data
66 qsub HybPhyloMaker5_missingdataremoval.sh
67
68 18. Generate FastTree trees
69 qsub HybPhyloMaker6b_FastTree_for_selected.sh
70
71 19. Create tree files
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70 qsub HybPhyloMaker7_roottrees.sh
71
72 20. Create diverse species trees (run all three, no need to wait...)
73 qsub HybPhyloMaker8a_astral.sh
74 qsub HybPhyloMaker8b_astrid.sh
75 qsub HybPhyloMaker8c_mrl.sh
76 qsub HybPhyloMaker8e_concatenatedFastTree.sh
77
78 21. After all jobs are finished run these additional scripts
79 qsub HybPhyloMaker8h_neighbourNetwork.sh
80 qsub HybPhyloMaker8k_quartetsampling.sh
81 qsub HybPhyloMaker11_phyparts.sh
82
83 22. Create a XLSX-formatted report (no need to wait for previous scripts to finish)
84 qsub HybPhyloMaker_reports.sh
85
86
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