

SUBTYPING PIPELINE

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Quick Guide

Important!

Before you start the pipeline, make absolutely sure that all file names, sequence names, structures of input tables are correct and **follow exactly the patterns** as described in examples.

Pipeline Directory

Locate to **Pipeline** directory:

```
$ cd ~/rki_subtyping/Pipeline
```

Open IDE (Visual Code Studio)

```
$ code ../
```

Input Folders

Make sure you have 5 directories:

```
$ tree -d
```

```
Pipeline/  
├── AllSeqsC020  
├── InputFasta  
├── ManualRega  
├── References  
└── Scripts
```

AllSeqsCO20 Folder

Provide this folder with .xlsx files as listed (from NGS pipeline):

```
AllSeqsC020/  
├── MS95_Seqs_ENV_C020_V5.xlsx  
├── MS95_Seqs_INT_C020_V5.xlsx  
└── MS95_Seqs_PRRT_C020_V5.xlsx
```

Refer to Supplementary part of the guide, if you need more information (Page 21).

InputFasta Folder

Provide this folder with files as listed (from NGS pipeline):

```
InputFasta/  
├── MS95_ENV_20.fasta  
├── MS95_INT_20.fasta  
└── MS95_PRRT_20.fasta
```

Refer to Supplementary part of the guide, if you need more information (Page 22).

Conda Environment

Activate **subtyping_pipeline** environment.

```
$ conda activate subtyping_pipeline
```

Be sure you have change in prompt:

```
(subtyping_pipeline) beast2@Beast2:~/rki_sybttyping/Pipeline$
```

Pipeline with **--outdir** parameter

Parameter **--outdir** determines a name of an output folder. The command will generate four enumerated output folders within **Results** folder. Without specifying an output folder you can get a warning message.

```
$ nextflow Scripts/subtyping_pipeline.nf --outdir Results
```

ManualRega Folder (1)

Provide the folder with **.csv** files (separator: comma) generated by **Rega** using marked **.fasta** files from the folder produced by the pipeline:

~/rki_subtyping/Pipeline/Results/1_marked_fasta

These **.fasta** files have M at the end of the file name:

```
1_marked_fasta/  
├── MS95_ENV_20M.fasta  
├── MS95_INT_20M.fasta  
└── MS95_PRRT_20M.fasta
```

ManualRega Folder (2)

Rega online tool always generates files with the same name **results**, e.g. **results.csv**. Rename these files accordingly, using the pattern as in the example below:

```
ManualRega/  
├── Manual_Rega_MS95_ENV_20M.csv  
├── Manual_Rega_MS95_INT_20M.csv  
└── Manual_Rega_MS95_PRRT_20M.csv
```

Refer to Supplementary part of the guide, if you need more information (Page 23).

Pipeline with **--fullpipeline** parameter

Repeat the previous command with **--fullpipeline** parameter and **-resume** flag. The latter allows for generating an output up to **12_mafft** folder. The complete processes are cached.

```
$ nextflow Scripts/subtyping_pipeline.nf --outdir Results --fullpipeline -  
resume
```

Check the output of **12_mafft** folder before you run iqtree analysis (msa files - multiple sequence alignments)!

Pipeline with **--iqtree** parameter

Parameter **--iqtree** allows for running the iqtree process that produces **13_iqtree** folder within **Results**. The folder contains **.iqtree**, **.treefile**, and **.log** files. The parameter can be added at this point, as the last command with report and plot outputs being produced or not added at all (no **13_iqtree** folder then).

```
$ nextflow Scripts/subtyping_pipeline.nf --outdir Results --fullpipeline -  
-iqtree -resume
```

You can monitor the **.log** file while running iqtree within **work** folder using respective process ID (68), e.g [68/72f0eb].

Decision

Manually modify files (see below) which contain **Manual** tag in PRRT_Subtype, INT_Subtype, and ENV_Subtype columns. Save changes and close **.xlsx** files.

```
9_joint_with_tags/  
├── full_MS95_ENV_20M.xlsx  
├── full_MS95_INT_20M.xlsx  
└── full_MS95_PRRT_20M.xlsx
```

Report and Plot

```
$ nextflow Scripts/subtyping_pipeline.nf --outdir Results --fullpipeline -  
-iqtree -resume
```

Repeating the command above generates **14_report** folder with **MS95_subtype_uploads.xlsx** report file.

Repeating it again generates a **MS95_subtype_counts.png** plot and adds it to the **14_report** folder.

Clean Up

Once the pipeline has generated **Results** folder with all desired output files (**save** all needed outputs first), the input files can be removed from the input folders.

```
$ rm -rf InputFasta/* AllSeqsCO20/* ManualRega/* Results/
```

The same is true for dot and nextflow temp files/folders:

```
$ rm -rf .nextflow work .nextflow.log .nextflow.log.*
```

Processes Overview

[1b/f2f10a]	process > mark_fasta (2)	[100%]	3 of 3, cached: 3	✓
[a9/dd644a]	process > get_tags (3)	[100%]	3 of 3, cached: 3	✓
[97/70bbdd]	process > comet (3)	[100%]	3 of 3, cached: 3	✓
[73/a28f41]	process > stanford (3)	[100%]	2 of 2, cached: 2	✓
[e6/e4af1d]	process > json_to_csv (3)	[100%]	2 of 2, cached: 2	✓
[65/e0eb90]	process > clean_rega (3)	[100%]	3 of 3, cached: 3	✓
[87/4d2fcf]	process > join_env (1)	[100%]	1 of 1, cached: 1	✓
[34/36991e]	process > join_int (1)	[100%]	1 of 1, cached: 1	✓
[62/e59285]	process > join_prprt (1)	[100%]	1 of 1, cached: 1	✓
[8d/dad394]	process > make_decision (1)	[100%]	1 of 1, cached: 1	✓
[d8/983216]	process > join_with_tags	[100%]	1 of 1, cached: 1	✓
[e6/ceaa42]	process > fasta_for_mafft (2)	[100%]	3 of 3, cached: 3	✓
[54/89322b]	process > env_concat_panel (1)	[100%]	1 of 1, cached: 1	✓
[a4/b7aaee]	process > int_concat_panel (1)	[100%]	1 of 1, cached: 1	✓
[f7/9e1ccf]	process > prprt_concat_panel (1)	[100%]	1 of 1, cached: 1	✓
[c0/786bcd]	process > mafft (3)	[100%]	3 of 3, cached: 2	✓
[68/72f0eb]	process > iqtree (3)	[100%]	3 of 3, cached: 3	✓
[3c/0fb71f]	process > report	[100%]	1 of 1, cached: 1	✓
[c5/462a18]	process > countplot (1)	[100%]	1 of 1	✓

Supplementary

Example of .xlsx within AllSeqsCO20

Scount	Fragment	Cutoff	Header	Lauf	NGS-ID	Index
GenBank-ID	Sequenz					
20-02944	PRRT	20	20-02944_PRRT_20	95	1	
CCCCCT...						
20-02945	PRRT	20	20-02945_PRRT_20	95	2	
CCCCCT...						
20-02947	PRRT	20	20-02947_PRRT_20	95	3	
CCCCCT...						
20-02949	PRRT	20	20-02949_PRRT_20	95	4	

```
CCCCCT...
20-02950    PRRT          20      20-02950_PRRT_20    95      5
CCCCCT...
```

Example of .fasta within InputFasta

```
>20-02955_ENV_20
GGAATTAGGCCAGTGGTGTCAACCCAACTATTGTAAATGGCAGCCTAGCAGAAGAAGAT
GTGGTCATTAGATCTGAAAATTTACAAACAATGCTAAAACCATAATAGTACAGCTTAAT
GAAACAGTAGTGATTAATTGTACAAGACCCGGCAACAATACAAGAAAAAGTATACATATA
GGACCAGGAAAAGCATGGTATGCAACAGGAGAGATAATAGGAGATATAAGACAAGCACAT
TGTAACCTTAATAAAACACAATGGGAAAAAACTTTAAAAAGGGTAGCTAGTAAATTAAGG
AAACAATCCAACCTTACAACAGTAATCTTTAAGAACTCCTCAGGGGGGGACCCAGAAATT
GTAATGCACAGTTTTAACTGTGGAGGGGAATTTTTCTATTGTAACACAACACAGTTGTTC
AATAGTATTTGGAATGACACTACTAATAGTACTGACACAAATGAACTATCACACTCCCA
TGCAGAATAAAACAAATTATAAATAGATGGCAGGAAGCAGGAAGGG
```

Example of .csv within ManualRega

An example of a **.csv** file produced by Rega online tool (names of columns and only one sample for demonstration)

```
"name","length","assignment","rule","support","begin","end","type","pure",
"pure_support","pure_inner","pure_outer","scan_best_support","scan_assigned_support",
"scan_assigned_nosupport","scan_best_profile","scan_assigned_profile","crf",
"crf_support","crf_inner","crf_outer","crfscan_best_support",
"crfscan_assigned_support","crfscan_assigned_nosupport","crfscan_best_profile",
"crfscan_assigned_profile","major_id","minor_id"
"20-02944_PRRT_20","1026.0","HIV-1 CRF
06_CPX","4","98.0","1823.0","2848.0","Human
immunodeficiency virus 1","HIV-1 Subtype
G","93.0","0.0","93.0","0.5","0.357","0.643",
"G K A1 A1 A1 G A1 A1 G G G G G","G - - - - - G G G G -","HIV-1
CRF 06_CPX",
"98.0","0.0","98.0","1.0","1.0","0.0","06_CPX 06_CPX 06_CPX 06_CPX 06_CPX
06_CPX
06_CPX 06_CPX 06_CPX 06_CPX 06_CPX 06_CPX 06_CPX 06_CPX","06_CPX 06_CPX
06_CPX 06_CPX
06_CPX 06_CPX 06_CPX 06_CPX 06_CPX 06_CPX 06_CPX 06_CPX 06_CPX
06_CPX","","
```

References Folder

This folder contains reference panels and does not need any change unless reference panels should be replaced.

```
References/  
├── Reference_ENV_Panel_Stanford.fas  
├── Reference_INT_Panel_Stanford.fas  
└── Reference_PRRT_Panel_Stanford.fas
```

Scripts Folder

This folder contains the scripts and does not need any change.

```
Scripts/  
├── comet_rest.py  
├── decision.py  
├── fasta_for_mafft.py  
├── full_join.py  
├── json_parser.py  
├── nexflow.config  
├── plot.py  
├── rega_cleanup.py  
├── repeat_marking.py  
├── report.py  
├── subtyping_pipeline.nf  
└── tag_parser.py
```

Conda

Conda Info

List available conda environments.

```
$ conda info --envs  
# conda environments:  
#  
base * /home/beast2/anaconda3  
subtyping_pipeline /home/beast2/anaconda3/envs/subtyping_pipeline
```

Conda Version

Pipeline's version of conda **4.14.0**

```
$ conda --version
```

Deactivation of Environment

This command is used to deactivate the current environment.

```
$ conda deactivate
```

Be sure you have change in prompt:

```
(base) beast2@Beast2:~/rki_sybtyping/Pipeline$
```

GitHub Repo

Repo Link

The project is hosted [here](#). Use this link to clone the repo in case of data loss.

How to Clone

Locate to home directory

```
$ cd
```

Clone the repo

```
$ git clone https://github.com/vera-rykalina/rki_subtyping.git
```

Modify path of **ProjectDir** within **subtyping_pipeline.nf**

```
projectDir = "/home/beast2/rki_subtyping/Pipeline"
```

Notes

Keep in Mind (1)

- The pipeline does not take into account subsubtypes. If there are subsubtypes they are converted to subtypes. For instance, A1 is converted to A, F2 is converted to F etc.
 - The pipeline does not perform a full quality check of **.fasta** sequences. Illegal characters should be excluded (the pipeline takes care only of underscores so far). Sequences with illegal characters are not accepted by Rega online tool.
-

Keep in Mind (2)

- Make sure that sample names do not exceed 30 characters in length. Long sample names get shorten by Rega online tool that can cause issues. E.g, this sequence name **PK105_F482_23_MiS84_S86_20consensus_PRRT_20** is too long and gets shortern by Rega to **PK105_F482_23_MiS84_S86_20cons**. In such cases a manual change is necessary.
-

Keep in Mind (3)

- Be sure you are connected to the Internet
- You can always delete the whole **Results** folder or individual subfolder/subfolders within **Results** and repeat the commnand with **-resume**.