

MJOLNIR3:

from raw sequences to manageable data

Adrià Antich

Software used

R / Bash / Python

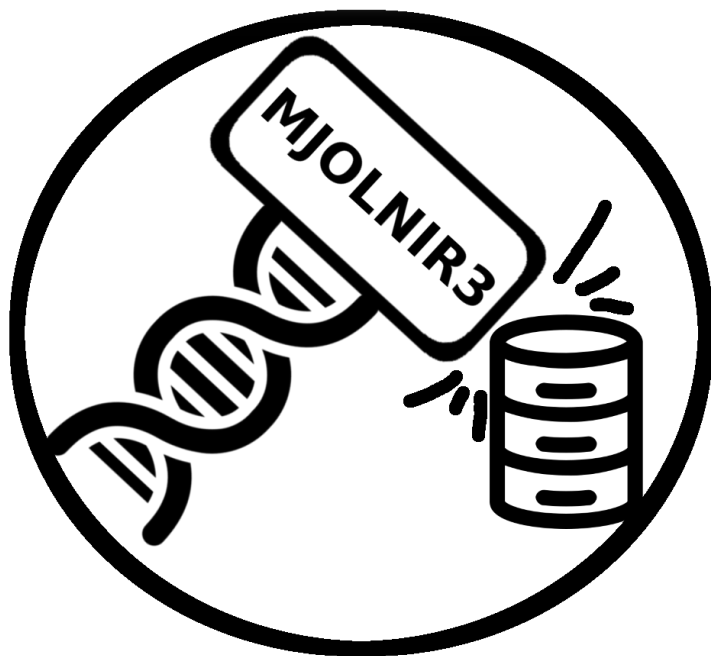
~~OBtools~~ → OBITOOLS3

vsearch

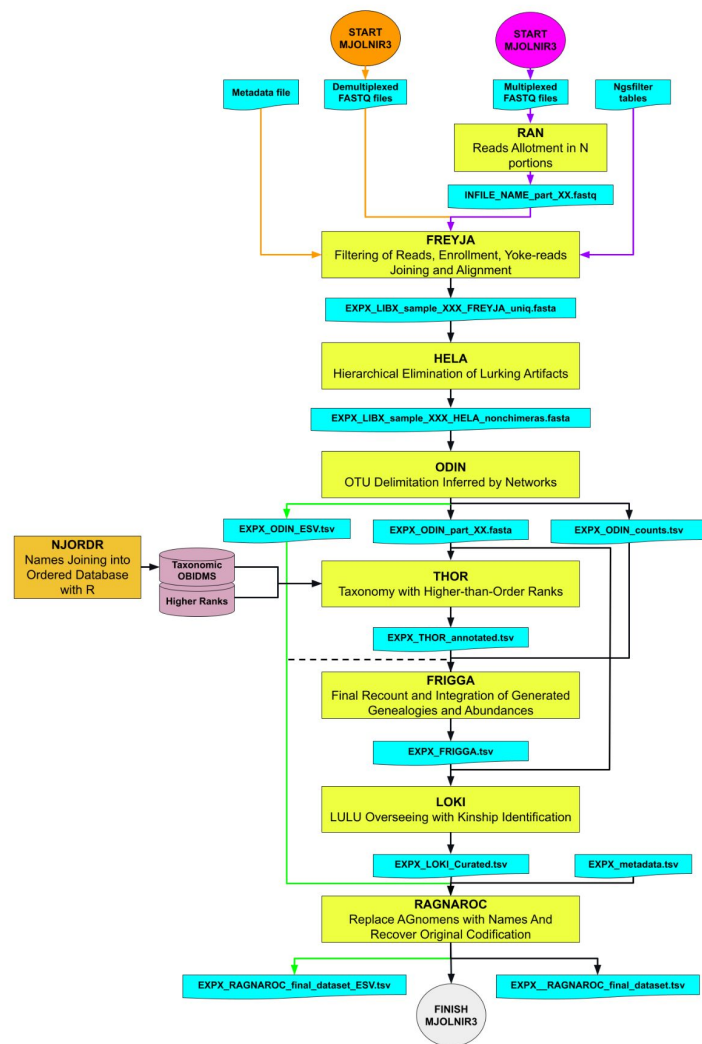
SWARM

DnoiseE

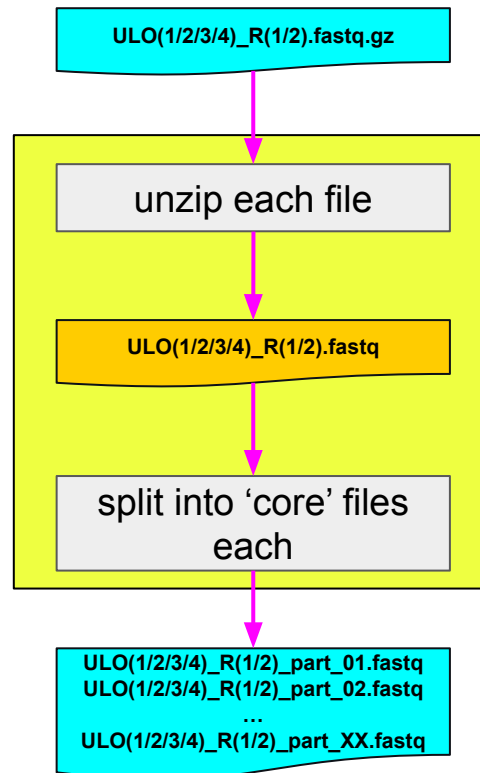
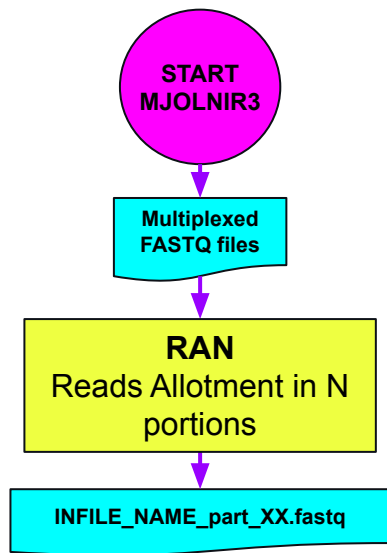
lulu



1. RAN: Reads Allotment in N portions
2. FREYJA: Filtering of Reads, Enrollment, Yoke-reads Joining and Alignment
3. HELA: Hierarchical Elimination of Lurking Artifacts
4. ODIN: OTU Delimitation Inferred by Networks
5. THOR: Taxonomy with Higher-than-Order Ranks
6. FRIGGA: Final Recount and Integration of Generated Genealogies and Abundances
7. LOKI: LULU Overseeing with Kinship Identification
8. RAGNAROC: Replace AGnomens with Names And Recover Original Codification

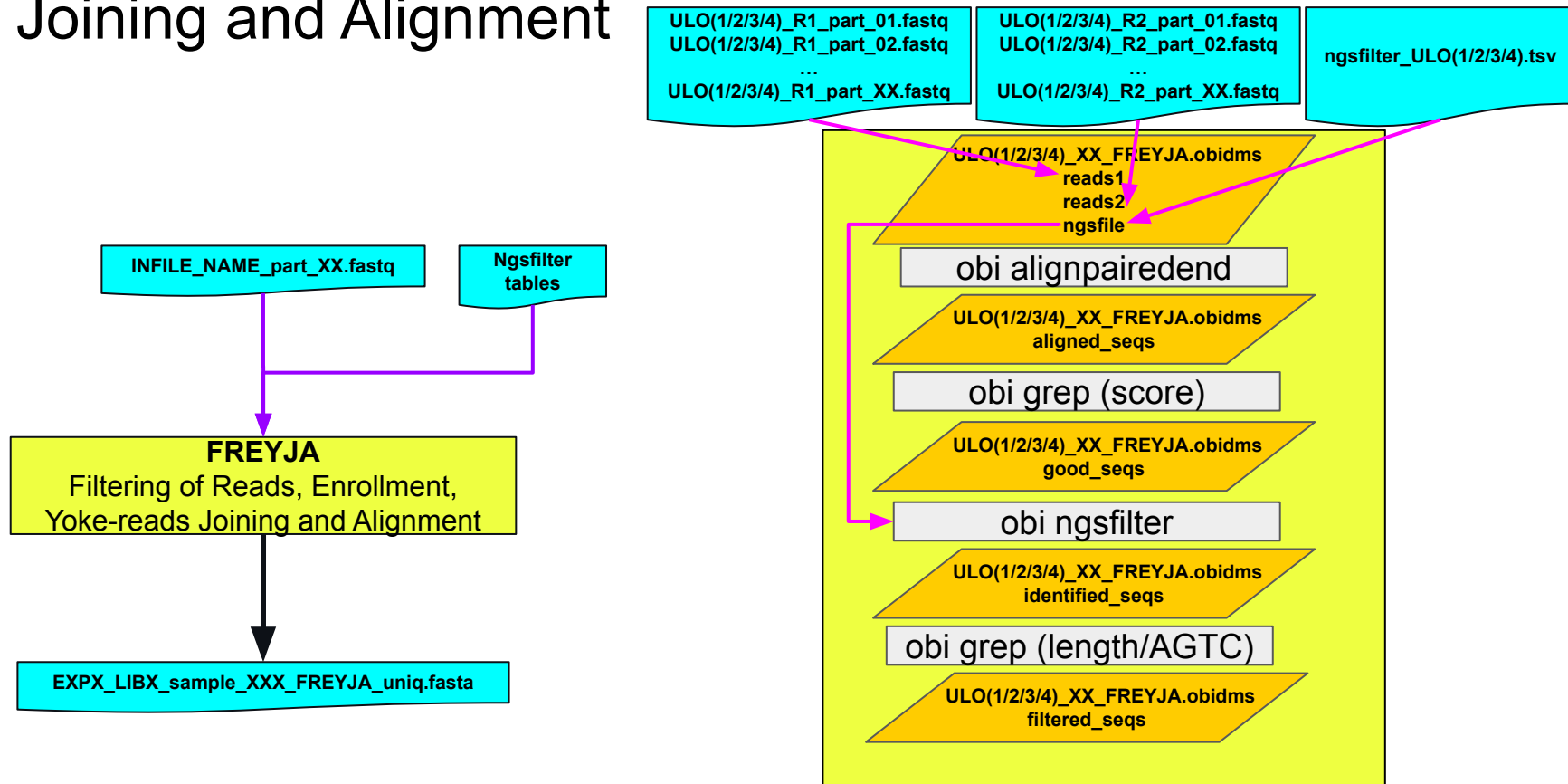


RAN: Reads Allotment in N portions



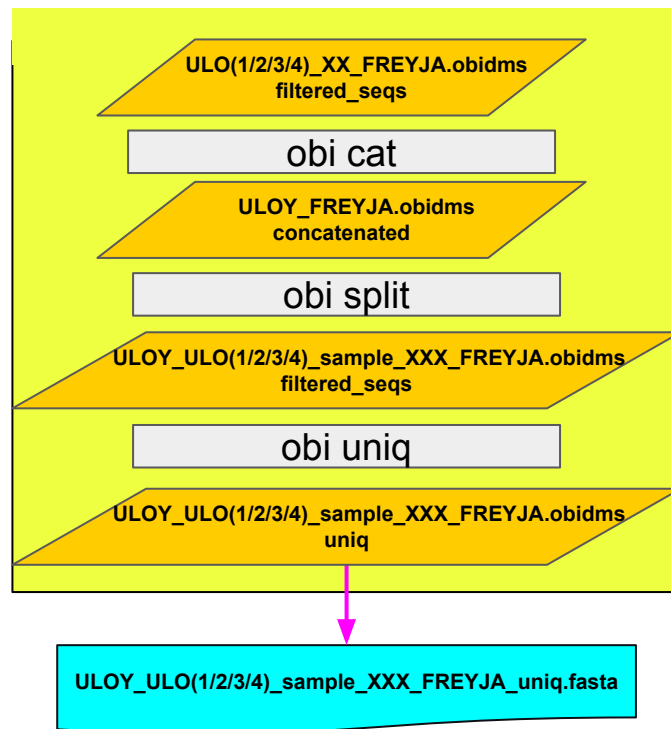
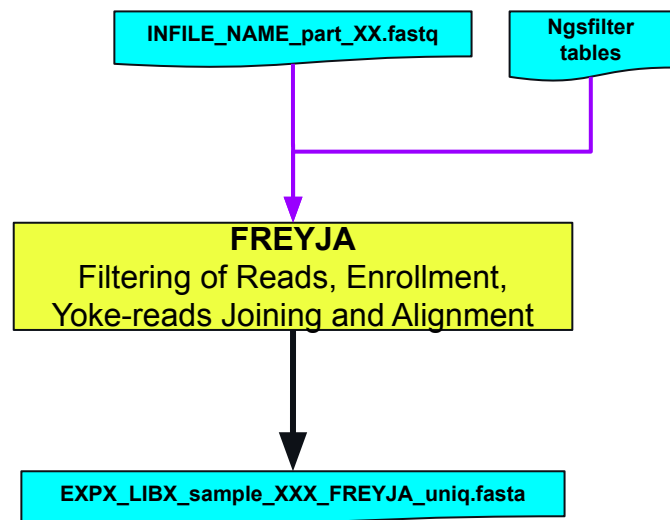


FREYJA: Filtering of Reads, Enrollment, Yoke-reads Joining and Alignment



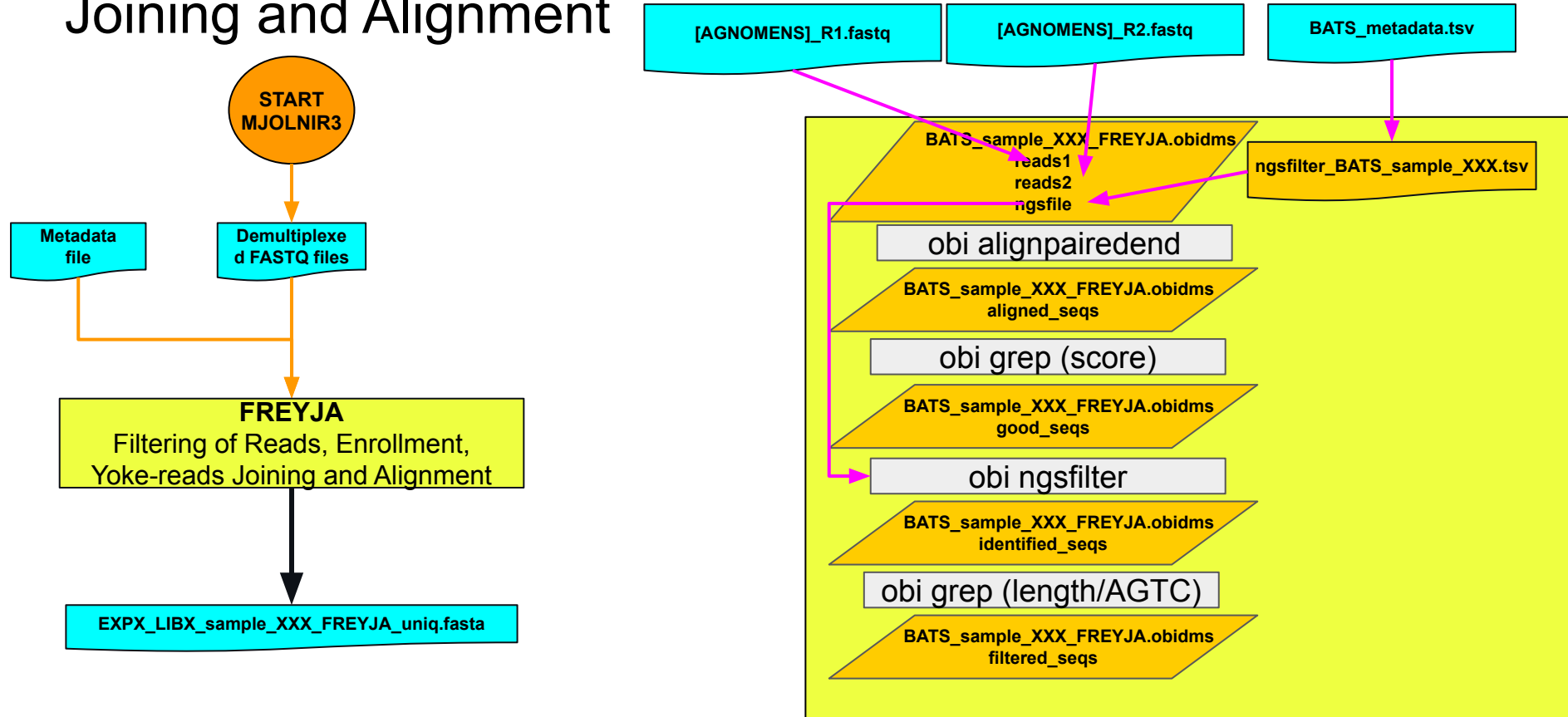


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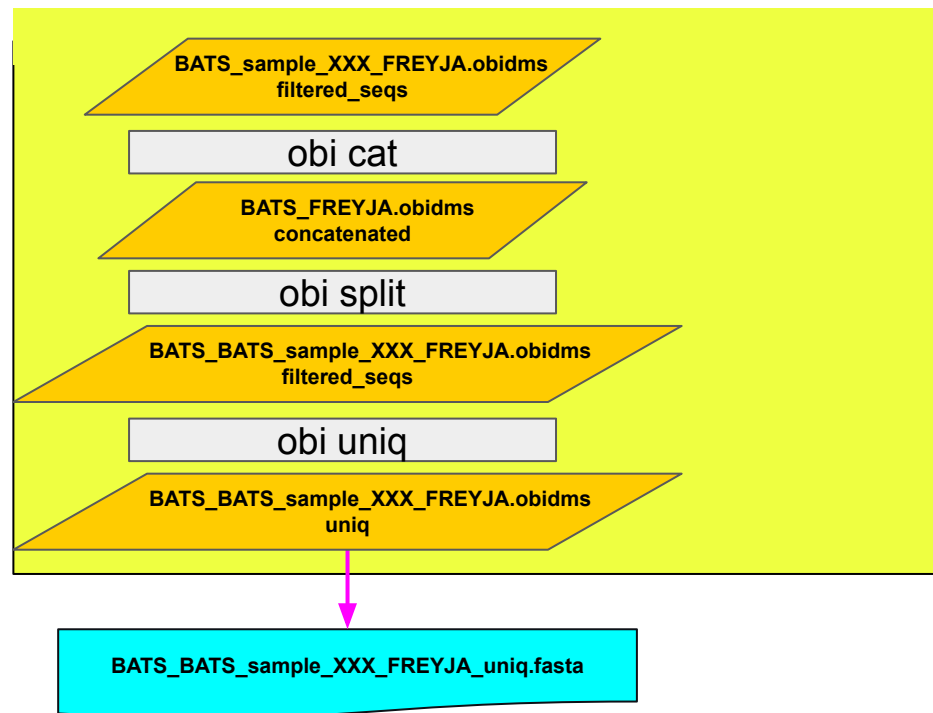
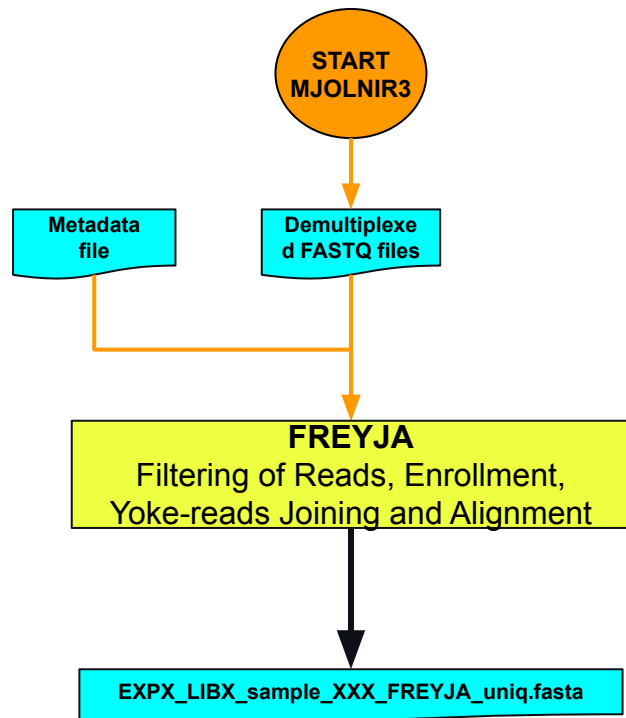


FREYJA: Filtering of Reads, Enrollment, Yoke-reads Joining and Alignment

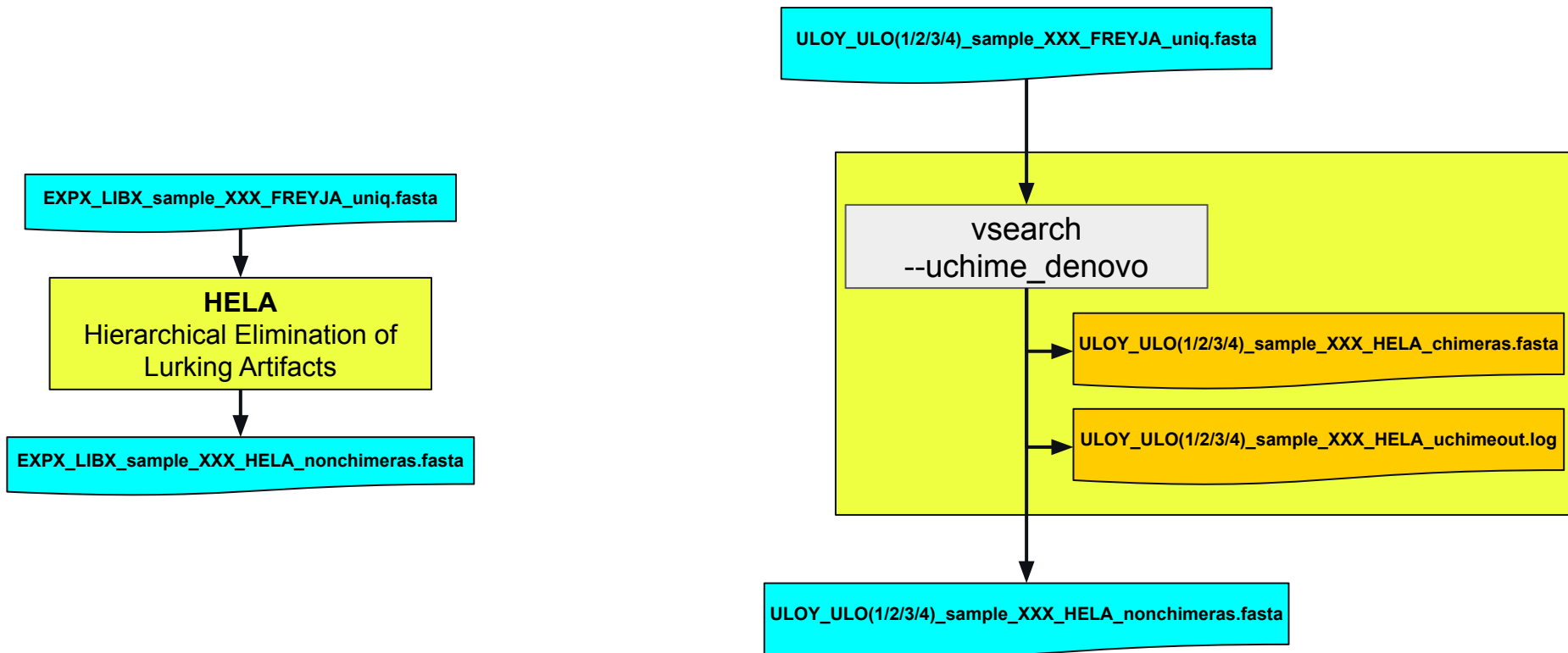




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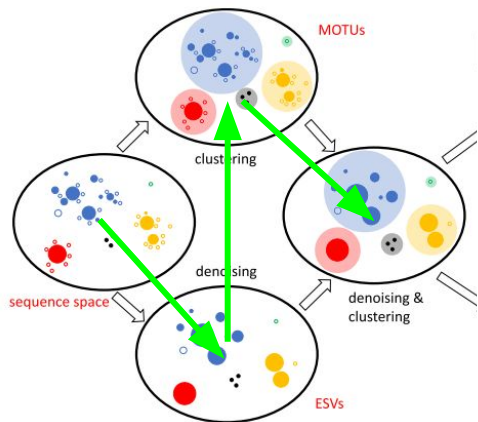


HELA: Hierarchical Elimination of Lurking Artifacts

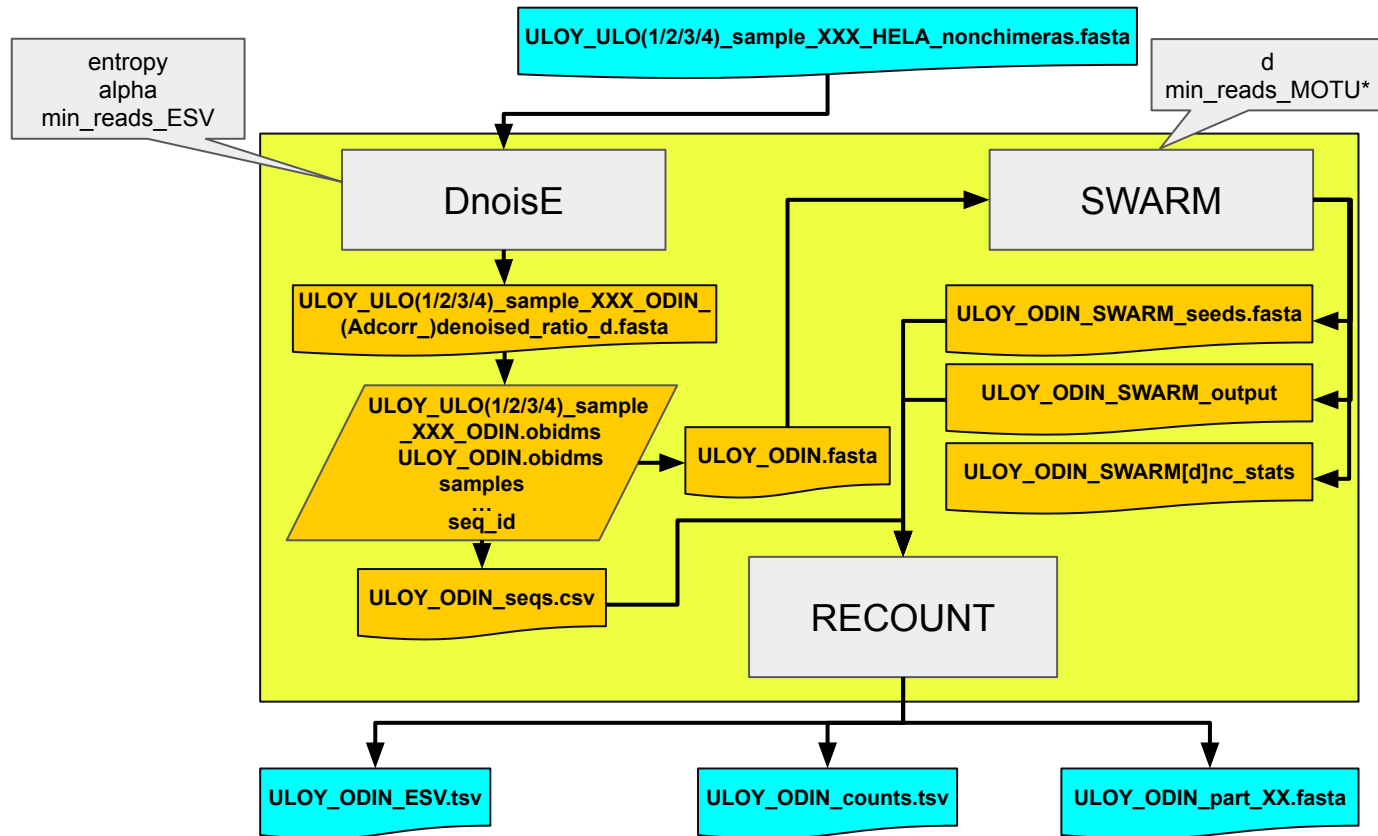




ODIN: OTU Delimitation Inferred by Networks

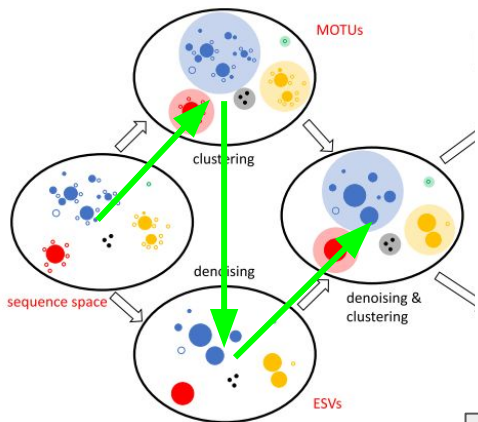


algorithm = “DnoisE_SWARM”



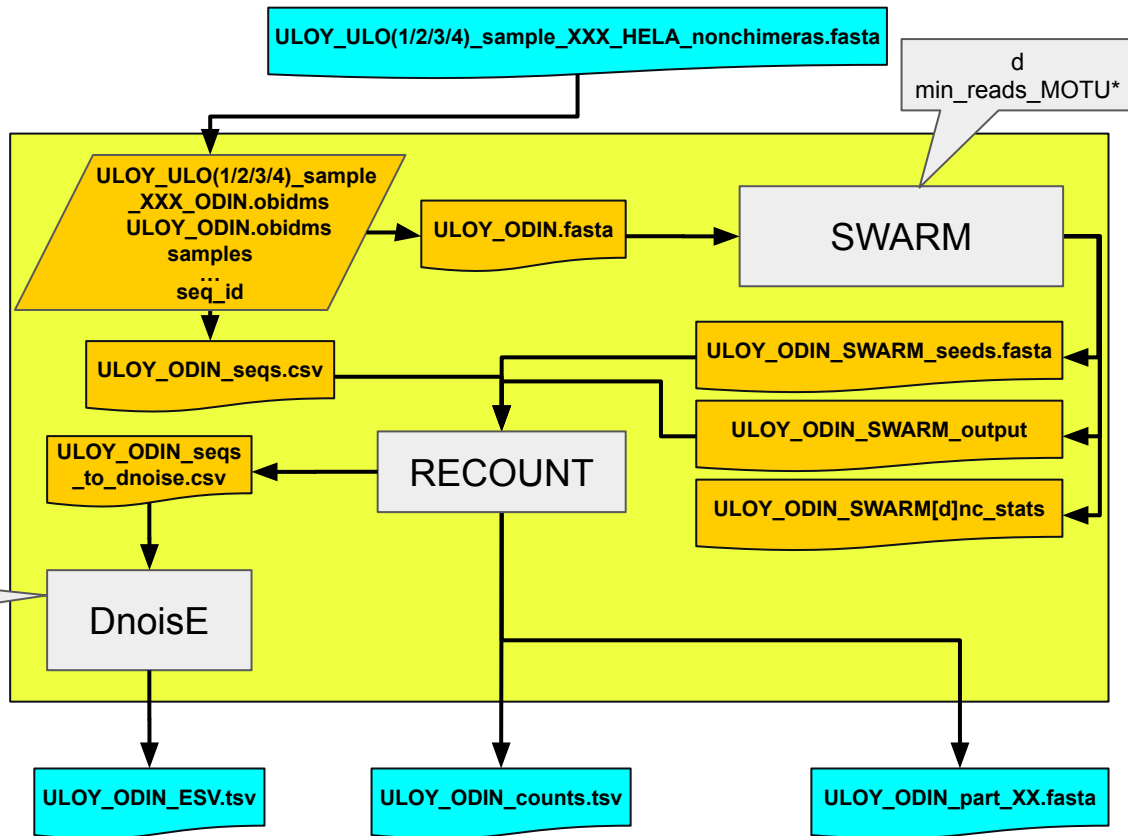


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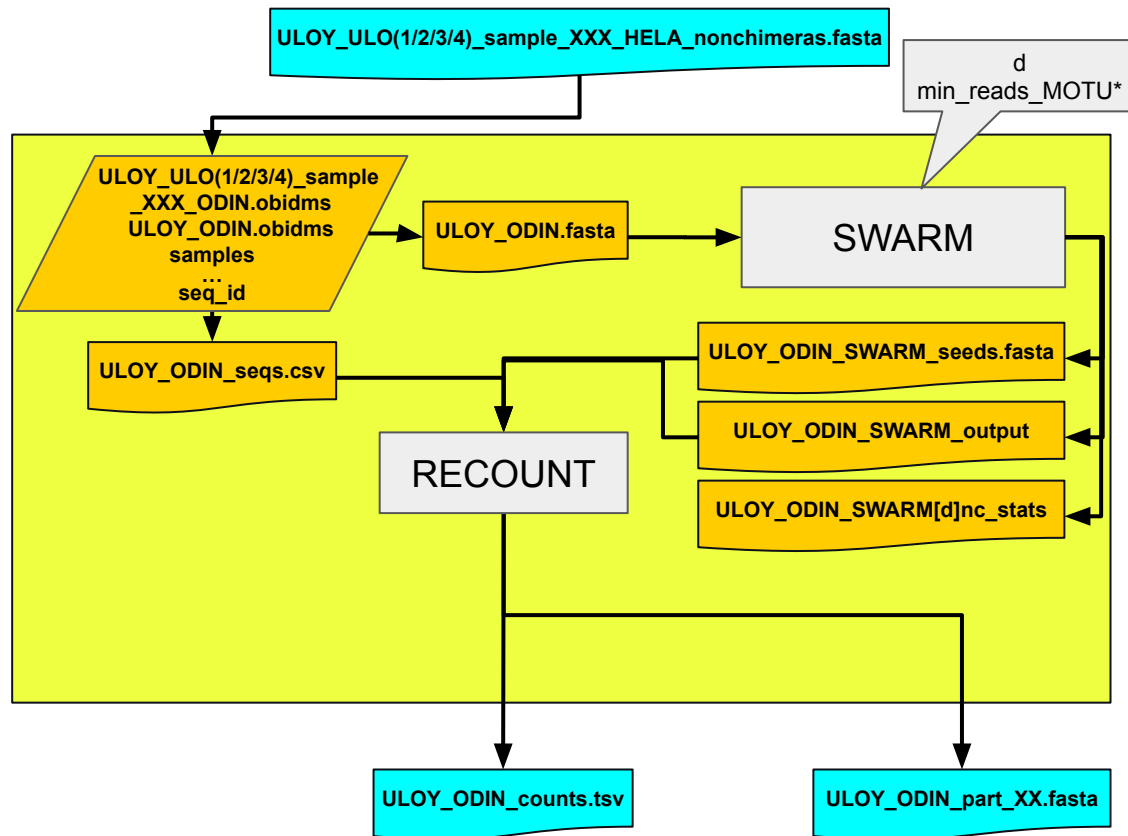
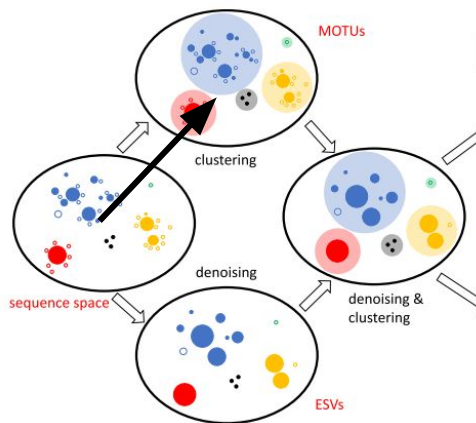


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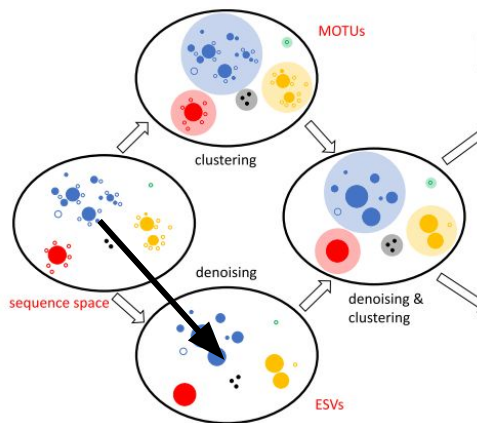
entropy
alpha
min_reads_ESV



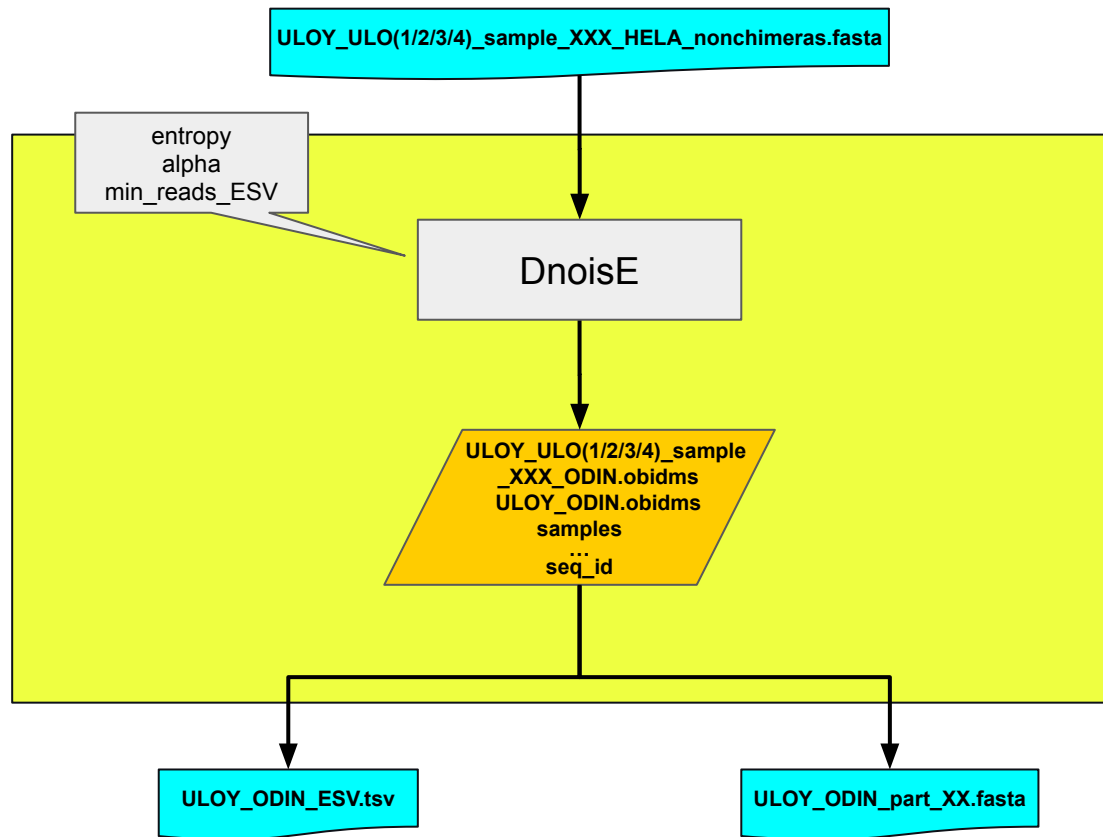
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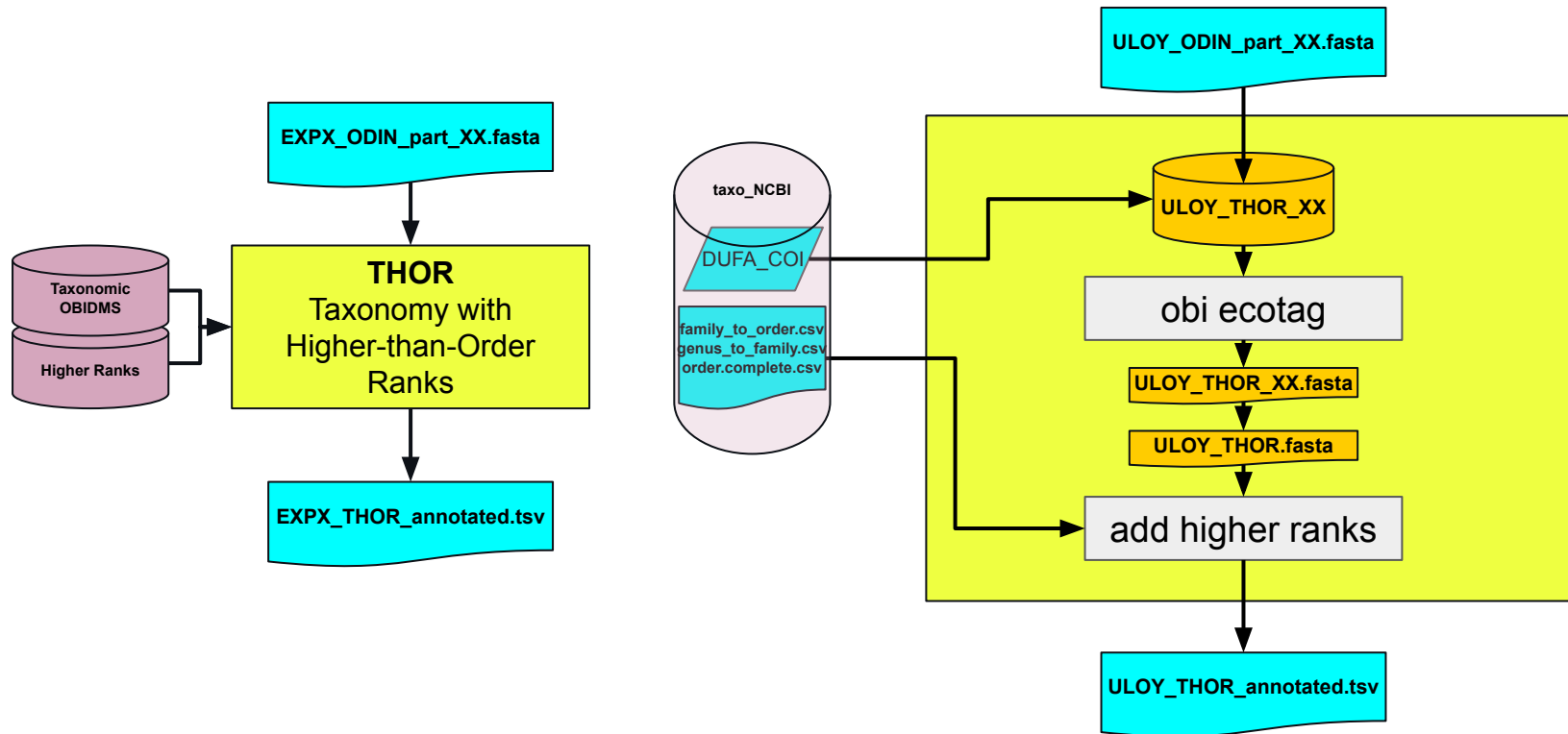
algorithm = "DnoisE"



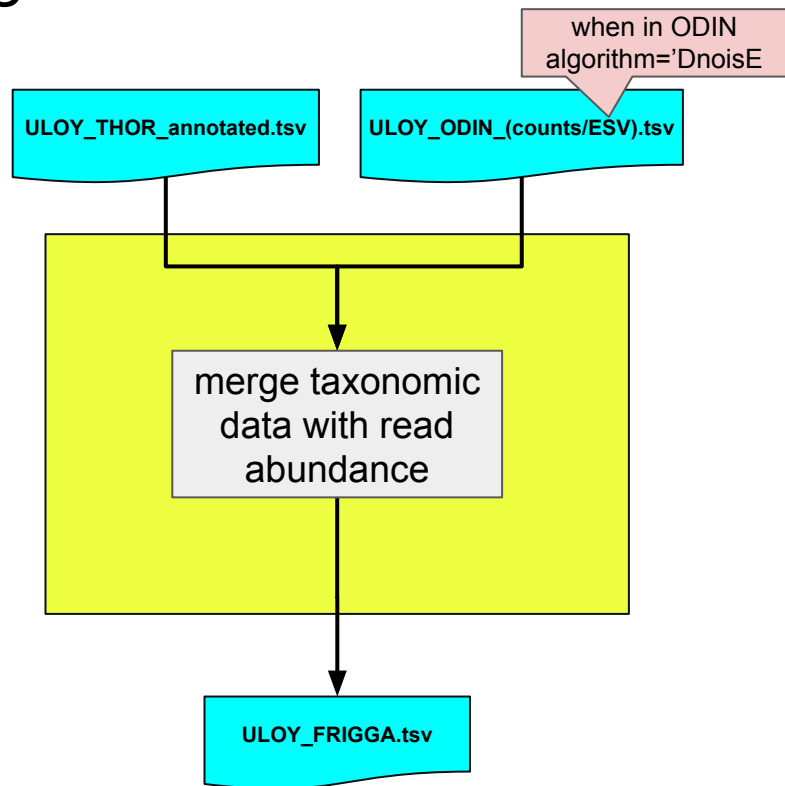
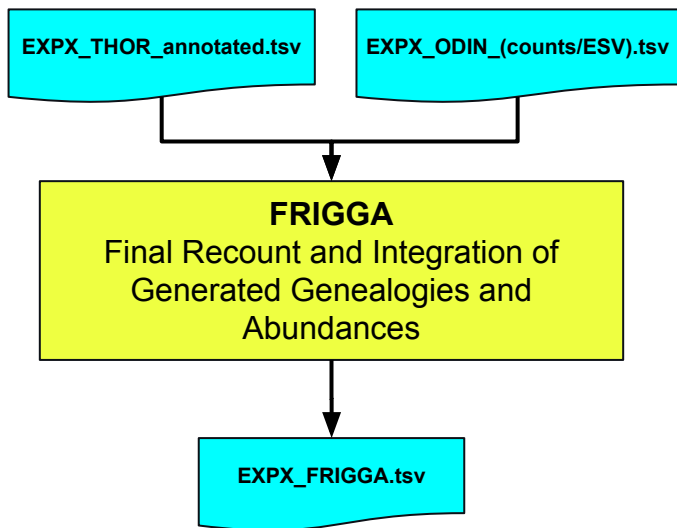
NJORDR: Names Joining into Ordered Database with R for MJOLNIR3 pipeline



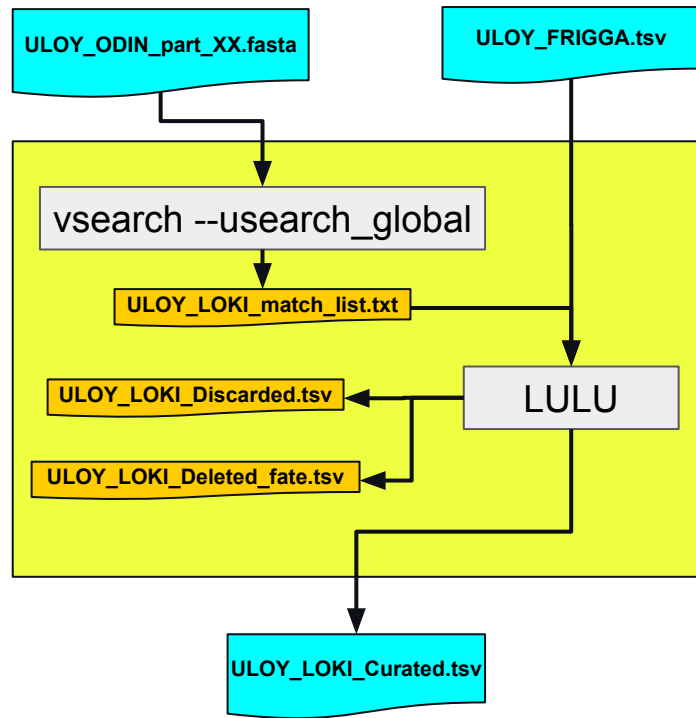
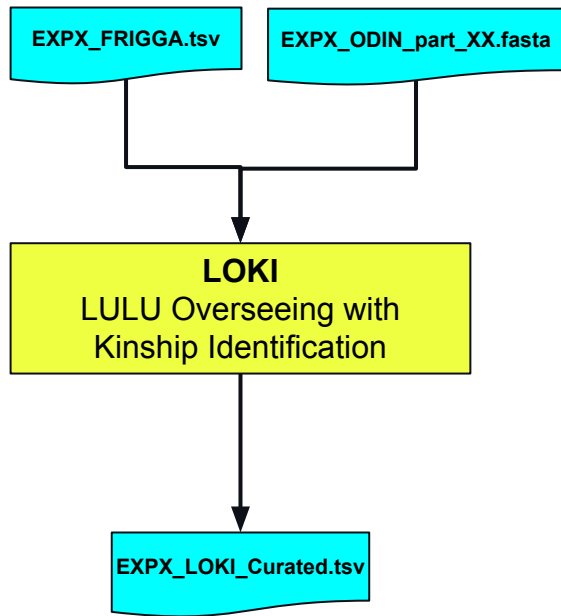
THOR: Taxonomy with Higher-than-Order Ranks



FRIGGA: Final Recount and Integration of Generated Genealogies and Abundances

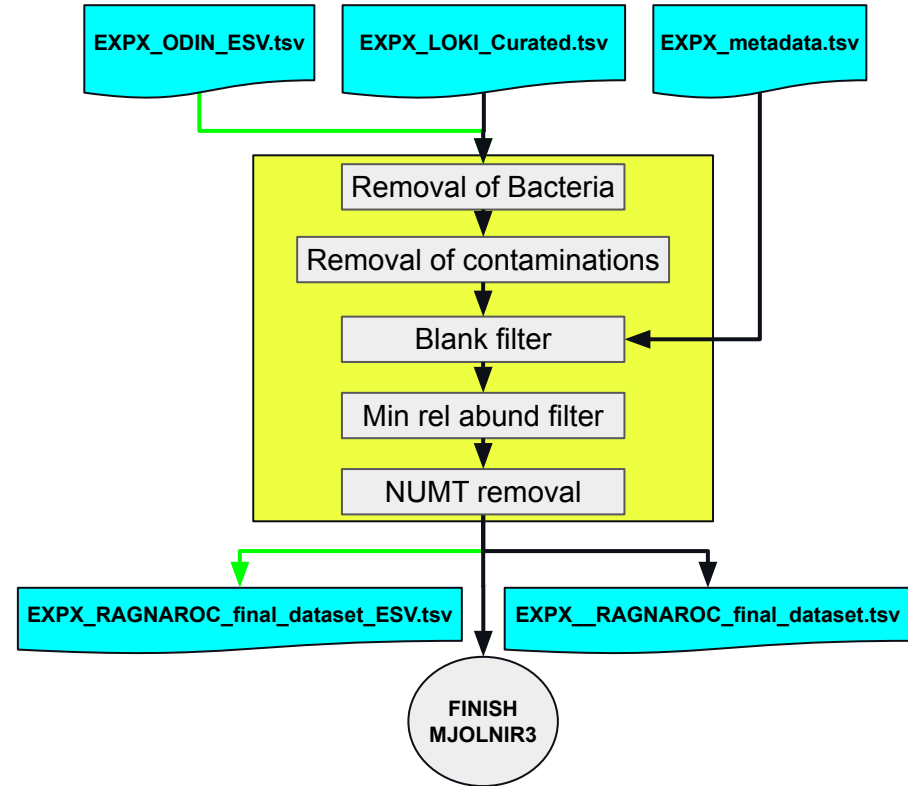
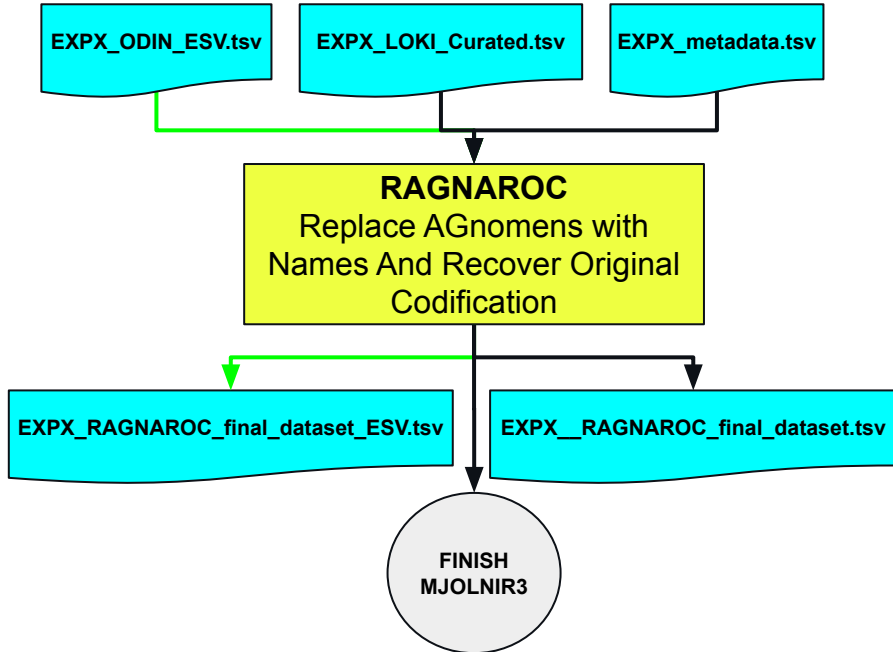


LOKI: LULU Overseeing with Kinship Identification





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