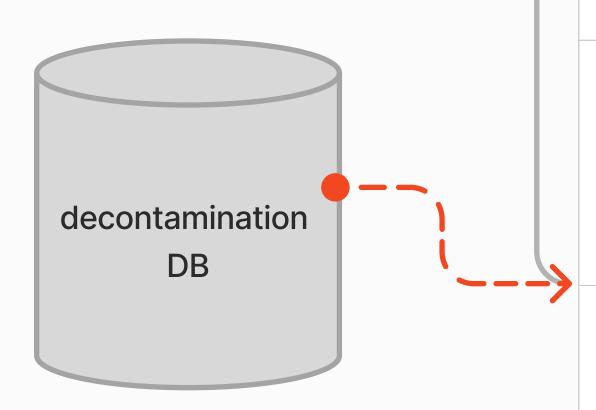
Virus Identification (Genomad, VS2, CT3)

fasta files



Preprocessing

Dereplication

- input: fasta
- output: directory
- + CheckV and BLAST

Decontamination

- input: fasta
- output: clean fasta
- + BLAST

Adjust seq

- input: fasta
- output: adjusted fasta
- + Biopython

Recombinaiton

- input: fasta
- output: filtered fasta
- + RDP, 3Seq, GENECONV,

MaxChi, Chimaera, Bootscan,

Siscan

```
results/

clean_sequences.fasta  # Decontaminated sequences

clean_sequences_stats.txt  # Decontamination statistics

clean_sequences_blast.tsv  # BLAST results (if keep-temp is used)

clean_sequences_decontamination.log  # Detailed log file
```