

## • Virus Identification + alignment (Genomad, VS2, CT3)

- fasta files

### Method Selection

- `-rdp` : Run RDP method
- `-threeseq` : Run 3Seq method
- `-geneconv` : Run GENECONV method
- `-maxchi` : Run MaxChi method
- `-chimaera` : Run Chimaera method
- `-bootscan` : Run Bootscan method
- `-siscan` : Run Siscan method
- `-all` : Run all methods (default if no method is specified)

## Recombination Detection

### Suit of tools

- input: aligned fasta
- + RDP
- + 3Seq
- + GENECONV

output/

```
|— recombination.log           # log file
|— aligned_sequences.3s.log    # 3Seq output
|— aligned_sequences.3s.pvalHist # 3Seq output
|— aligned_sequences.3s.longRec # 3Seq output
|— aligned_sequences.3s.rec    # 3Seq output
└— output.csv
```