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Recan: R-based tool for detection of recombination in viral genomes

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Using recan for searching of recombinations.

- 1 Command for reading all .fasta files in working directory.

```
library(bio3d)
ls <- list.files(path = ".")
mult <- read.fasta(ls[1])
for (i in ls[2:8]) {
  f <- read.fasta(i)
  mult <- seqbind(mult, f)
}
mult$id
```

- 2 Performed multiple sequence alignment using MSA.

```
ali <- seqaln(mult, exefile="msa")
ali$id
```

Using recan for building plots.

```
library(recan)
seqSim.ali, ref = 6)
scanSeqSim.ali, ref = 6, rec_detect = TRUE)
```