



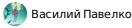
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## Recan: R-based tool for detection of recombination in viral genomes

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## SUBMIT TO PLOS ONE

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Using recan for searching of recombinations.

Command for reading all .fasta files in working directory.

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

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)