



Input data

Raw MSA data
(fasta files, Biostrings objects,
ape objects, phangorn objects)



Data pre-processing

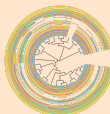
Reads in MSA data into
a formal data frame



Predefined data calling

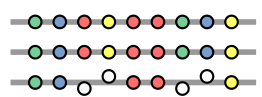
Calling predefined
color schemes and
polygon characters

MSA Layout



- segments
- circles
-

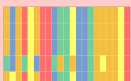
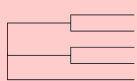
MSA Visualization



Annotation Modules

MSA annotations containing
colored labels and symbols

Diagrams Combination



- Trees
- Structrues
-



External data

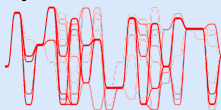
Associated molecular data
(RNA Structrue data,
phylogenetic tree, genes maps)

Other Features

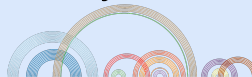
Sequence logos



Sequence Bundles



RNA Secondary Structures



Sequence Recombination

