

# ggmsa Pipeline



## 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
- .....

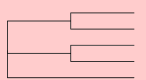
## MSA Visualization



## Annotation Modules

MSA annotations containing  
colored labels and symbols

## Diagrams Combination



- Trees
- Structures
- .....



## External data

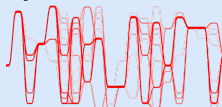
Associated molecular data  
(RNA Structrue data,  
phylogenetic tree, genes maps)

## Other Features

### Sequence logos



### Sequence Bundles



### Sequence Recombination



### RNA Secondary Structures

