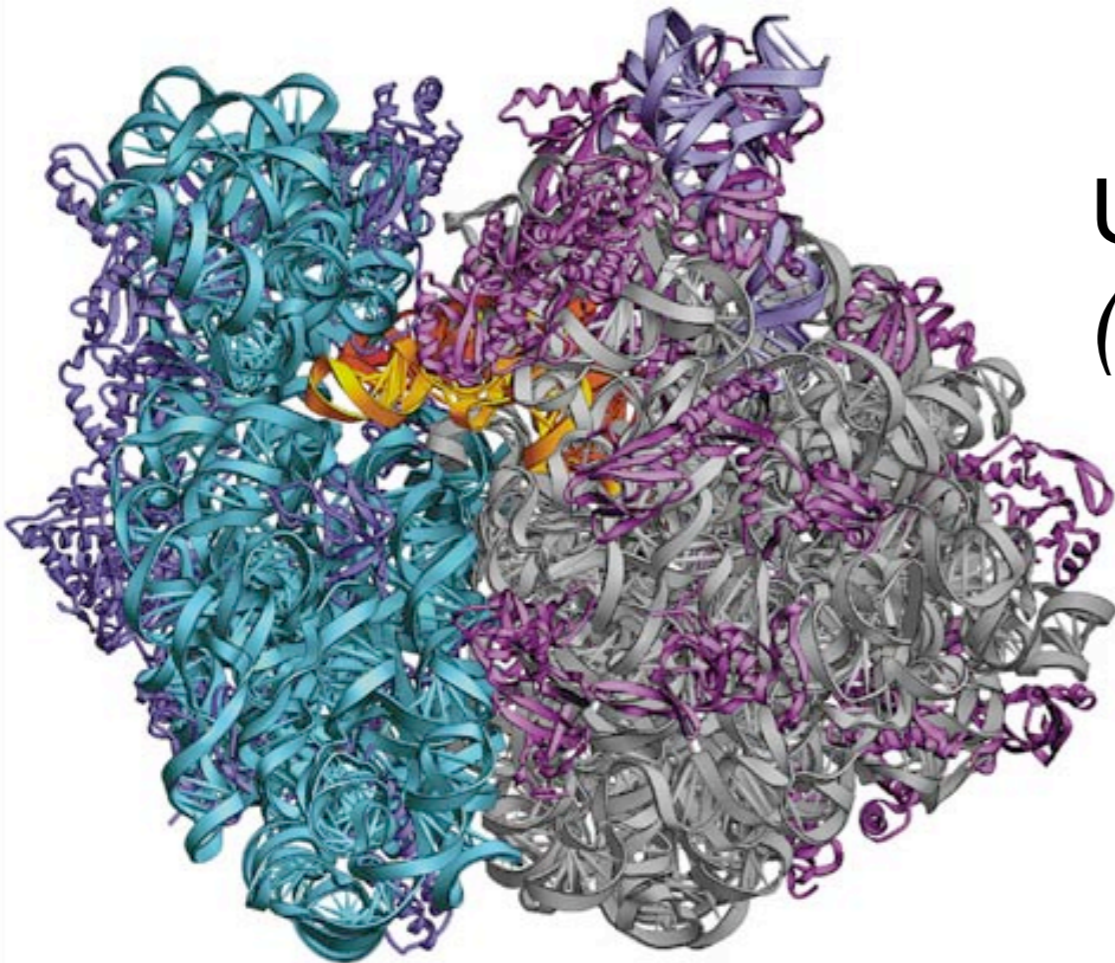




DART

Tools?
Trees?

DNA, Amino acid, RNA Tests



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Packages in DART

- **XRate**
 - estimate substitution rates
 - *Expectation Maximization for cts-time Markov chains*
- **Handel**
 - statistical alignment & indel-history reconstruction
 - *finite-state transducer composition, MCMC phylo-alignment*
- **StemLoc**
 - statistical alignment & folding of structured RNA
 - *Pair Stochastic Context-Free Grammars, posterior decoding*

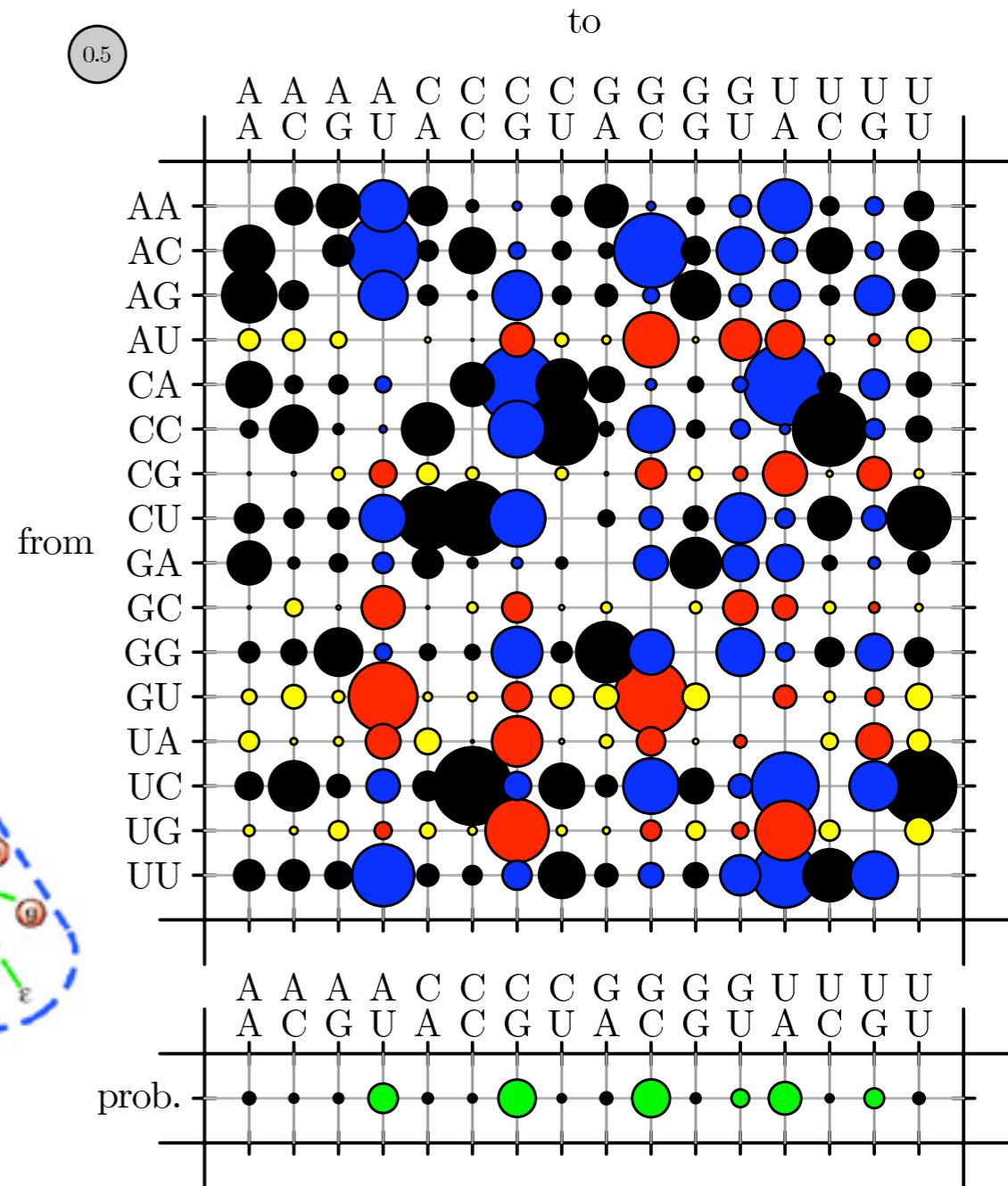
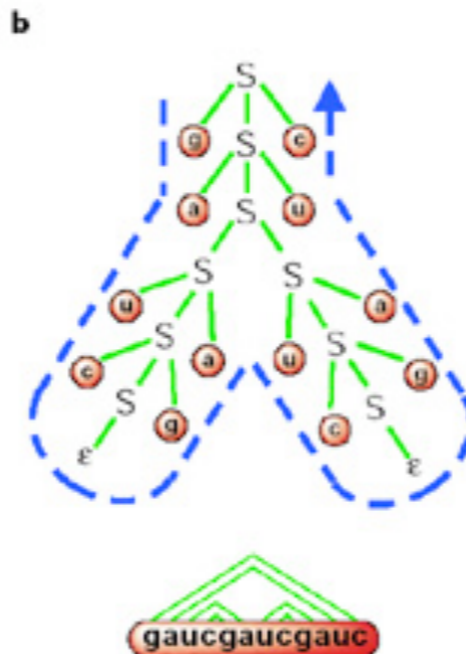
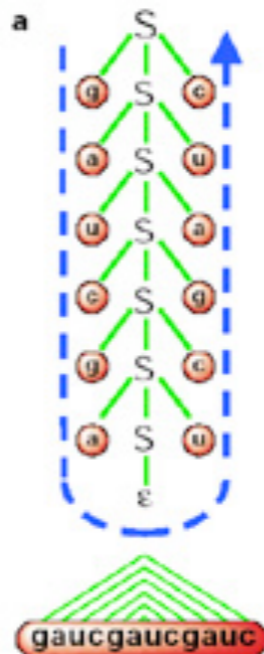
Common features

- **Fast** algorithms
- Unix **command-line** tools
- Newick, FASTA, Stockholm
- Scheme-like **model description** formats
- Detailed **logfile** system & analysis tools

biowiki.org/XRATE

```
(alphabet (token ... ))
(grammar
  (chain (terminal (L R))
    (initial...) (rate...))
  (nonterminal (name S))
  (transform (prob ... )
    (from (S))
    (to (L S R)) ... )
  ...
)
```

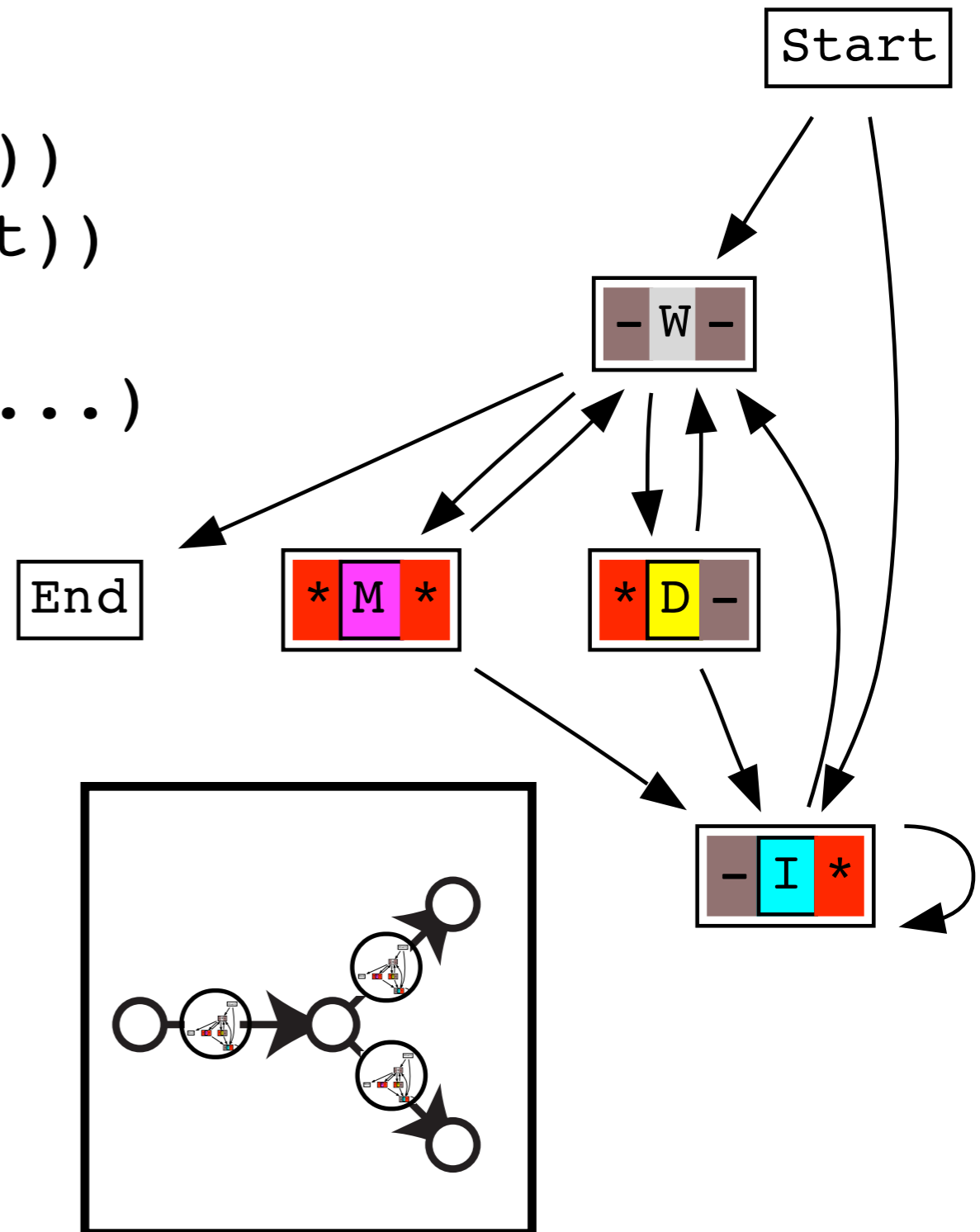
S → L S R



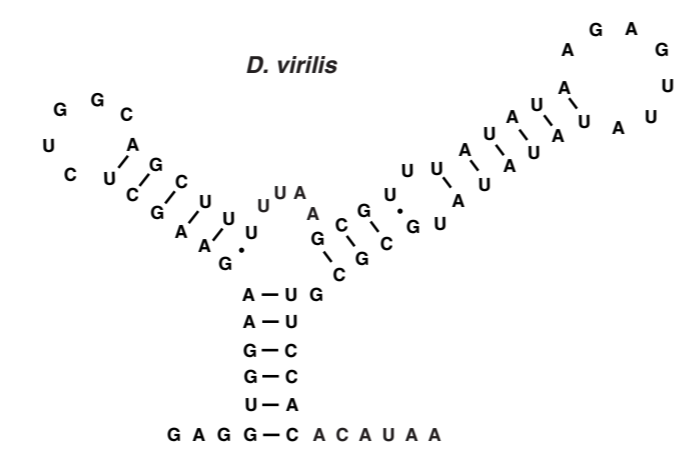
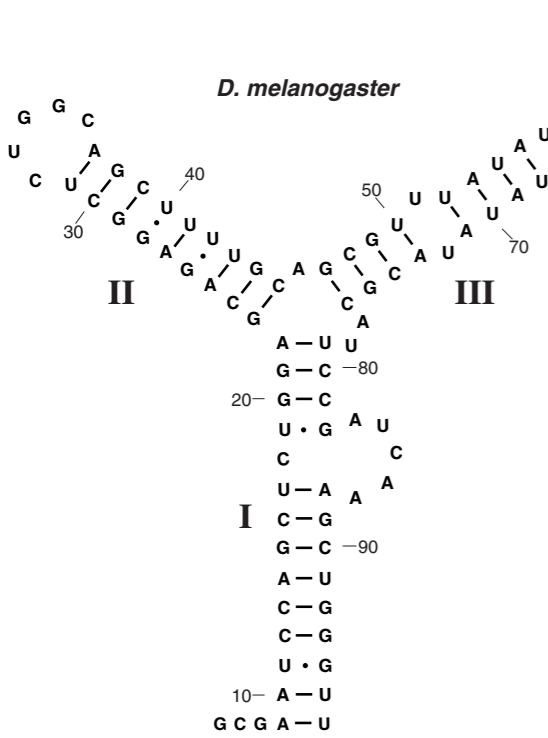
biowiki.org/HANDEL

```
(transducer (name TKF91)  
  (state (name S) (type start))  
  (state (name I) (type insert))  
  ...  
  (transition (from S) (to I)...)  
  ...  
)
```

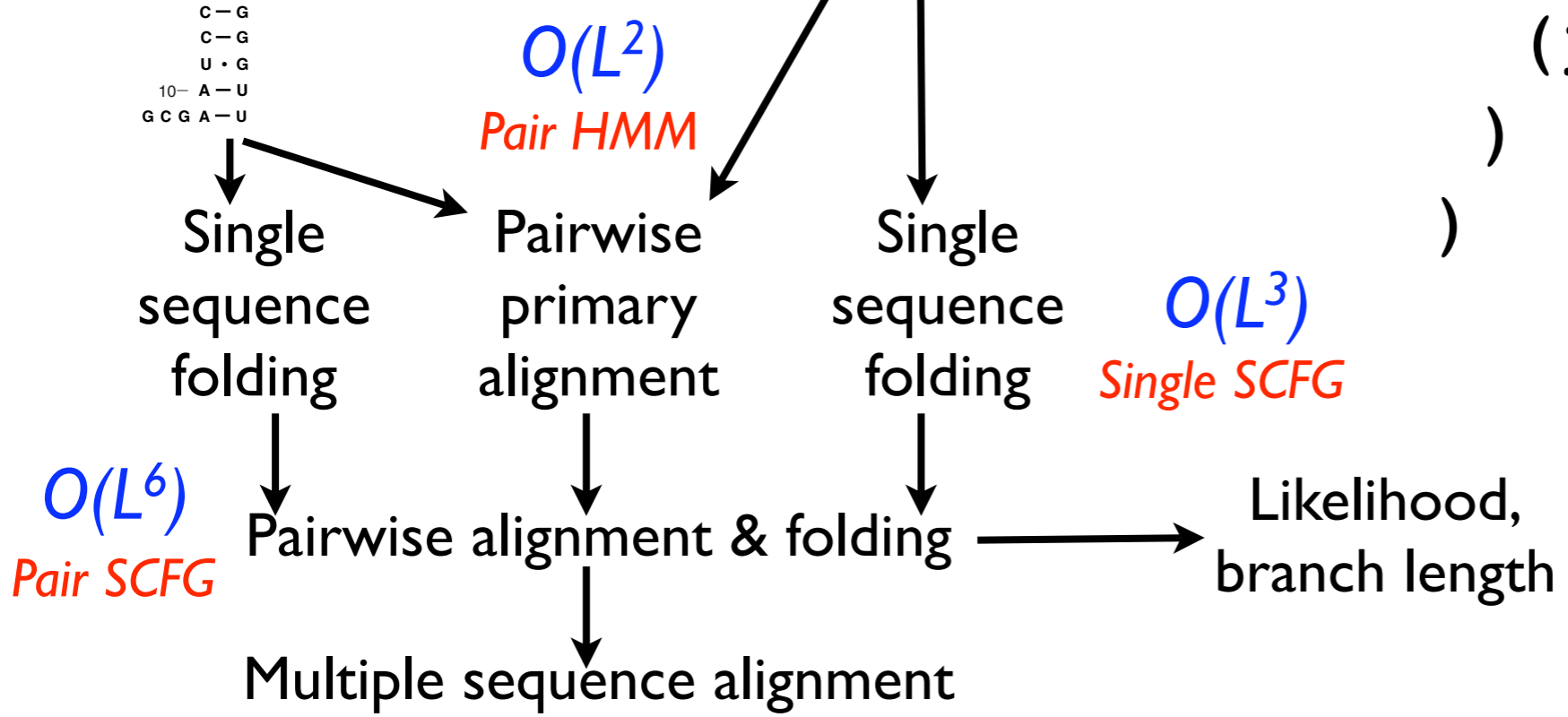
```
(branch (transducer TKF91)  
  (branch (transducer TKF91))  
  (branch (transducer TKF91))  
)
```



biowiki.org/STEMLOC



```
(model-set
  (single-scfg ... )
  (model-pair
    (pair-hmm ... )
    (pair-scfg ... )
  )
)
```



URLs

- **biowiki.org/DART**
- biowiki.org/XRATE
- biowiki.org/HANDEL
- biowiki.org/STEMLOC