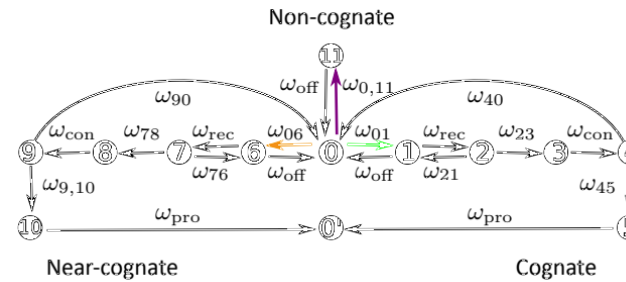


„Mathematik/Theorie“

- ◆ Identifying coding regions of RNA via a scaling approach
- ◆ Classification of Cytochrome P450 Monooxygenases with machine learning

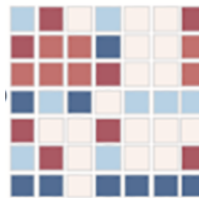
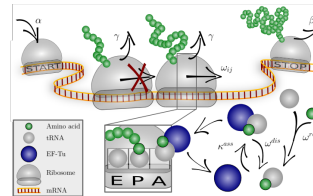


„Forschungssoftwareentwicklung“

- ◆ Dynamic KD-Trees
- ◆ Ribosome density pipeline
- ◆ Developing a reproducible GUI

„Simulationen“

- ◆ Creation of a Ribo-seq benchmark data set



„Datenanalyse“

- ◆ No current topic available