ChemicalSequence commands add (number) PartialStrand remove (number) commands bind unit (first, last) SequenceOccupation start segment (position) unbind unit (first, last) extend segment (position) commands add termination site (termination site) add element (first, last) register site (binding site) accessors remove element (first, last) set appariated strand (chemical sequence, completed() add sequence (quantity) free end factory) 0..n remove sequence (quantity) start appariated strand (position) 1..n register site (binding site) extend appariated strand (strand id, position) register moving site (binding site) create left end binding site (position) deregister moving site (binding site) create right end binding site (position) Segment start segment (position) remove free end binding site (position) commands extend segment (strand id, position) extend right() accessors extend left() number sites (first, last) accessors absorb right (other segment) number sites (first, last) number available sites (first, last) set first() number available sites (first, last) is out of bounds (first, last) set last() is termination site (position, TS families) length () accessors sequence () first() sequence (first, last) last() relative (absolute position) complementary (position)