ChemicalSequence

commands
bind_unit (bound chemical)
unbind_unit (bound chemical)
replace_bound_unit (old chemical, new chemical)
move_bound_unit (chemical, step size)
add_termination_site (termination site)
watch_site_availability (first, last, observer)

accessors
is_out_of_bounds (first, last)
is_termination_site (position, TS families)
length ()
sequence ()
sequence (first, last)

SequenceOccupation

commands
add_element (chemical, first, last)
remove_element (chemical, first, last)
add_sequence (quantity)
remove_sequence (quantity)
add_watcher (first, last, observer)