Thesis outline and status

Chapter		Programs	Draft	Remaining
Num	Title			
I	Introduction	na	NO	draft
II	An algorithm for aligning genomic and expressed DNA sequences (*sim4*)	YES	NO	draft
	- algorithm and implementation	YES	NO	draft
	- evaluation and results	YES	NO	draft
III	Evaluation of programs for finding conserved regions in multiple alignments and unaligned DNA sequences	YES	YES	-
	- collection of data for annotation	YES	YES	-
	- selection of cost functions	YES	YES	-
	- program evaluation and calibration of parameters	YES	YES	-
IV	Visualization tools for annotated multiple alignments	In progress	In progress	draft + tools
	- bacterial system	YES	In progress	draft
	- Hox clusters	NO	NO	draft+tools
	- *meta*-framework	NO	NO	draft+tools
	- application to the fungal system	NO	NO	draft+tools
V	Conclusions	na	NO	draft

Color codes:

Red = Completed (small adjustments)   Green = In progress   Blue = Not started