

User Story	Task	Member responsible for tas	Member assigned to tas	Estimated Effort (hours)	Priority	Actual effort	Done
When the user opens a DNA sequence, he will be able to zoom in and get more details visible	Visualize the zooming levels	Daphne	Ties, Daphne	16	A.1	Daphne: 1 Ties: 12	Yes
	Improve node collapsing	Niek	Niek	16	A.1	Niels: 0.5	No
	Arrow Edge	Ties	Arthur	10		Arthur: 11	No
	Testing	Niels	Niels	20	B.1	Niek: 8 (Controllers) Niels: 10 (Core	Partially
As a user, I want to wait as little time as possible while using the application.	Code enhancement						
When the user opens a DNA sequence, the phylogenetic tree will be shown	Rendering enhancement	Arthur	Ricardo	15	B.2	Ties: 2	Partially
	Improve Phylogenetic tree	Niels	Niels	4	C.1	Ties: 0.5	Yes
When the user scrolls through the DNA sequence, there will be a box indicating the position in the sequen	ZoomBox						
	Alter the zoombox so that it scroll with the genome and indicates where we are in the genome	Daphne	Daphne/Ricardo	12	C.1	Daphne: 8	Yes
	GUI testing	Ricardo	Arthur/Ricardo	20	C.1		0 No
	Node info	Ties	Ties, Arthur	15	B.2	Ties: 8, Arthur: 6	Yes

Other Tasks:	Hours:
Arthur: Bugfixes, Code review, Meetings	12
Ties: Checkstyle, code review	9
Niels: Code fixes, Code Review	13
Daphne: Code review, Meetings	5
Ricardo: Code review, Meetings, Loading bar	11
Niek: Code review, Meetings	5

Main problems encountered

We've wasted a lot of time trying to implement the loading bar and arrows, and did not succeed in doing so.

We've got some scaling issues with the infobox, but will fix this next week.

When loading the graph, we still reparse the file, which should not be done. Ties will fix this next week.