Sprint Plan 6

User Story	Task	Member responsible for the task	Task Assigned To	Estimated Effort per Task *(in hours)*	Priority (A—E) *(A is highest)*
As a user I want to be able to load the 328 genomes	Remove empty leaves	Jeffrey	Jeffrey	10	A
As I user I want to visualize the genomes in a clear and concise way	Improve positioning of the ribbon nodes	Matthijs	Matthijs	6	B
	Improve the bubble collapsing algorithm	Matthijs	Matthijs	6	B
	Draw edges if nodes are offscreen	Matthijs	Matthijs	2	B
As a user I want to be able to see the strands when zoomed in and mutations when less zoomed in	Update and send ribbon labels to the frontend	Matthijs	Matthijs	5	C

	Create backend method for useful minimap	Matthijs	Matthijs	8	C
	Make algorithm to recognize mutations (SNP, duplications)	Jeffrey	Jeffrey	15	B
As a developer I want to have maintainable code.	Use SIG to improve code quality	Kasper	Kasper	24	B
As a user I want the program to be fast, even with large datasets	Change constructors from database	Youp	Youp	4	C
	Finish coupling to database	Youp	Youp	4	A
	Implement caching algorithm	Youp	Youp	20	C
As a user I want a user-friendly program	Make zooming view draggable	Thomas	Thomas	6	C
	Show labels on mouse-over	Thomas	Thomas	5	D

As a user I want to navigate and select genomes from the Phylogenetic tree in an easy way	Visualize the phylogenetic tree	Thomas	Thomas	8	A
	Collapse the phylogenetic tree and give a heatmap	Thomas	Thomas	8	A