

Sprint Backlog, Iteration # 2

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 visualize the data from the .gfa-file	Connect the Java back end to the web-based front end using the REST API	Kasper	Kasper	4	A
As a user I want to be able to make sense of the data, using smart visualizations	Write algorithm to detect and collapse bubbles in the graph, which is also able to classify the bubbles (e.g. InDel, reversal)	Youp	Youp + Jeffrey	30	B
As a user, I want to be able to visualize the phylogeny of the genomes	Write a class to store the phylogeny data	Matthijs	Matthijs	4	A
	Write a parser to parse the phylogeny data	Matthijs	Matthijs	4	A
	Visualize the phylogeny in the front end	Thomas	Thomas	10	B

Context Project: Programming Life
Group: TagC, PL5

Sprint Retrospective, Iteration # 1

Context Project: Programming Life

Group: TagC, PL5

User Story	Task	Task Assigned To	Estimated Effort per Task <i>(in hours)</i>	Actual Effort per Task <i>(in hours)</i>	Done <i>(yes / no)</i>	Notes
As a developer I want to see the genome on the screen.	Load from database in datastructure (with weighted edges)	Matthijs	10		yes	
	Calculate and add coordinate system to datastructure	Youp	8	12	yes	Also includes work on bubble collapsing
	Visualize the datastructure of the graph and phenotype and add input to filter weights	Thomas	10	12	yes	
	Send the genome to the front end through rest-client	Kasper	10	8	no	Rest API is working, almost done

As a developer I want to upload a genome to the system.	Parse the genome.	Jeffrey	4	4	yes	
	Load the genome in a database	Jeffrey	4	6	yes	

Main Problems Encountered

Problem 1

Description: Phenotype not yet implemented

Reaction: Add to next sprint plan

Adjustments for the next Sprint

We've slightly increased our time estimates.