## **Sprint Retrospective, Iteration # \_6\_**

User Story	Task	Members worked on task	Estimated Effort per Task (in hours)	Actual Effort per Task (in hours)	Done (yes / no)	Notes
As a user, I want to be able to see genome information	Parse the genome information from the .gfa-file	Lex	5	9	yes	We wanted to do this right, so we thought a lot about the implementation before implementing. This worked really well.
As a user, And I am not the admin on my PC, I want to have cross-session information	Rewrite preferences	Jip	5	7	Yes	We cannot test due to not having easy access to MAC.
As a user, I want to be able to choose a genome to view	Colour nodes of a chosen genome	Jip, Lex, Marc	50	50	Yes	
As a user, I want to be able to save genome views in a bookmark like manner	Make bookmarks for the genomes	Jip	5	3	Yes	
As a user, I want some visual representation	Implement edge thickness	Jip	1	1	Yes	

of the amount of genomes going through an edge						
As a user I want to dynamically pan across the graph.	Dynamic panning	Jasper, Eric, Marc	20	40	Partially	Dynamic panning proved to be more difficult than expected. the scrollbar implementation proved to be too difficult, so we scrapped that.
As a developer, I want to have good decoupling between data and visuals	Decouple GraphDrawer	Eric	20	17	Partially	Proved difficult and not ready for master yet.

Context	Project:	Progran	nming Li	fe
Group:	Dynan	nite and Bu	ıtterflies_	

## Main problems encountered

## Problem 1

Estimating workload wrong.

This is something we are continuously trying to improve. From now on we will converse with eachother and ask others opinions on the time estimation. After doing that and spending more time on choosing the time I think that these estimations will improve.