

# Sprint Retrospective, Iteration # \_7\_

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 read an annotation file	Be able to read .gff-files	Lex	6	6	yes	
As a Mac User, I want to be able to open the app.	Fix the bug that the UI closes instantly on Mac	Jip	2	2	yes	
As a user i want to have a laptop to run the program	Buy a new laptop and reinstall software.	Marc	3	3	yes	My laptop broke down so I had to spend a morning setting things up again.
As a user I want the panning to be smooth	Make panning faster	Marc, Lex, Eric	6	6	yes	files were being opened and closed repeatedly which slowed down everything. Optimized graph loading structure
As a user I don't want to encounter bugs	Fix tests for refactor	Marc, Eric	2	4	yes	Null pointer exceptions in columns
As a user I want the graph to display properly	Fix some edge cases for rendering the graph with specific ranged	Marc	10	15	yes	Changed the implementation of hashmap to a treemap which solved the problem.

						Implemented singleton pattern in the gui , parser and refactored / optimized sequencegraph
As a user, I want to be able to view annotations from a gff file	View annotations	Jip and Lex	15	15	yes	Also with a button and tableView to choose annotations
As a user I want to pan through the whole sequence	Fix all issues with dynamic panning	Jasper	6	10	yes	
As a user, when viewing different genomes, I want to see rainbow-esque nodes	Rainbow nodes	Jip	10	10	yes	
As a user I want to know where I am in the sequence while navigating	Create a minimap to show the user of the location in the sequence	Jasper	4	4	yes	
As a user I want to select genomes to highlight	Implement a genome menu where genomes can be selected through checkboxes	Jasper	3	3		
As a user I want to see how genomes go through edges	Make the thickness of edges relative to the	Jasper	5	5		

	number of genomes going through it					
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Context Project: \_\_\_\_ Programming Life \_\_\_\_

Group: \_\_\_\_ Dynamite and Butterflies \_\_\_\_

## Main problems encountered

### Problem 1

This week, we started merging our new features on Wednesday, which solved a lot of the problems we had in earlier sprints and made the day of release a lot less stressful.

### Problem 2

We were a bit holding back on starting new features as we wanted to wait for the refactor of graph drawer to be merged. In the future we think we should just start the new features anyway. This is possible when we take the time for the merges as stated in Problem 1.