WBS	Name	Start	Finish	Work	Slack	% Complete
1	Learn how to use SNP tools to get information from VCF files	Jan 9	Jan 13	5d		100
2	Design how to make pipeline/tools to store SNP frequency	Jan 16	Jan 20	5d		100
3	Develop tools to add SNP frequency to the database from VCF files	Jan 23	Feb 3	10d		100
4	Develop tools to retrieve data from database in the format that can be used with filtering tools	Feb 13	Feb 17	5d		0
5	Develop tools to merge 2 database and install all application on UPPMAX	Feb 20	Feb 24	5d		0
6	Learn how to use filtering tools	Feb 27	Feb 29	3d		0
7	Develop a pipeline to filter out as many SNP as possible for certain diseases	Mar 1	Mar 2	2d		0
8	Learn how to use variant effect predictors (PolyPhen 2, Logre, MAPP, Massesor, SIFT, GERP)	Mar 5	Mar 16	10d		0
9	Develop combiner to combine the result from many variant effect predictor using supervise learning	Mar 19	Mar 23	5d		0
10	Calibrate and test the combiner using known variant dataset	Mar 26	Mar 30	5d		0
11	Use calibrated combiner to filter out variants for certain disease	Apr 2	Apr 6	5d		0
12	Write thesis documents	Apr 16	May 18	20d		0
13	Prepare presentation	May 21	May 25	5d		0