Assignment 2

- **Calculate the transcript half lives for the yeast genes using the 60 minute time series data provided in the file 'DecayTimecourse.txt'. There are three sets of time series data (one data set is shown below and the rest are provided as additional columns in the same file)**

Time course	timecourse1								
YORF	0	5	10	15	20	30	40	50	60
YAL026C	1	0.70303208				0.71308819	0.33221819	0.21532545	0.22649514
YDR148C									
YIL125W	1	1.1766388	0.82316981	0.55652807		0.71267772	0.42796191	0.32020411	0.2765778
YLR240W									
YCL009C	1	0.62675044	0.44743	0.4869724			0.41871941	0.18346187	0.23364639
YMR108W	1	0.74864715	0.69063903	0.55242479		0.51310847	0.39007258	0.40292287	0.15819191
YNR044W									
YGL032C	1				0.79540411	0.47498061	0.62537554		0.0161048

Since there are three replicates the final half life can be calculated as the average of the three calculated half lives for each transcript.

- **Identify the genes/transcripts with very high (top 10%) and very low (bottom 10%) half lives and perform a simple functional enrichment analysis using GO annotations from http://biit.cs.ut.ee/gprofiler/ and http://go.princeton.edu/cgi-bin/GOTermFinder and report the results of your analysis.**