| Code file name (/lib) | Purpose |
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| *libraries.py* | External libraries used for computation |
| *data.py* | Compiling data of the DHFR empirical landscape |
| *math\_functions.py* | Mathematical functions defined to assist in computation or to work as foundation blocks in complex functions. |
| *bio\_functions.py* | All range of functions defined to assist in computation, ranging from calculating hamming distance to finding paths in a landscape. |
| *\_peaks.py* | Functions defined to assist in assessment of peaks of a fitness landscape. |
| *peak\_count\_functional.py* | Code used to collect data of number of functional peaks in all available landscapes |
| *peak\_count.py* | Code used to collect data of all peaks present in all available landscapes |
| *peak\_probability\_functional.py* | Code used to collect data of probability of encountering a functional peak in all available landscapes |
| *peak\_probability.py* | Code used to collect data of probability of encountering any peak in all available landscapes |
| *peak\_plots.py* | Code used to generate all ‘peak probability’ and ‘peak count’ plots using the collected data. |
| *Joint\_peak\_plots.py* | Code used to generate plots with overlapping empirical and NK expected peaks in landscapes. |
| *\_mutation\_effect.py* | Functions designed to assist in collecting data regarding fitness effects of mutations |
| *mutation\_effect.py* | Code used to collect data of fitness effects of a mutation |
| *mutation\_effect\_plots.py* | Code used to generate all plots of variation of fitness effects of mutation(s) with change in background fitness |
| *\_DFE.py* | Functions used in segregating data into bins, useful while creating and analysing the DFEs |
| *DFE.py* | Code used to collect and save all phenotypic DFE probability distributions. |
| *DFE\_mwu\_test.py* | Code used to collect data of Mann-Whitney U test performed on DFEs of genotypes with similar fitness. |
| *DFE\_ks\_test.py* | Code used to collect data of Kolmogorov-Smirnov test performed on DFEs of genotypes with similar fitness. |
| *DFE\_stat\_test\_plots.py* | Code used to generate box plots for the KS and MWU tests performed on DFEs of different background bins. |
| *DFE\_3D\_data.py* | Code used to generate data for a 3D surface plot of the phenotypic DFE. |
| *DFE\_2d\_plot.py,*  *DFE\_3d\_plot\_functional.m,*  *DFE\_3d\_plot\_non\_functional.m* | Codes used to generate DFE probability distribution plots. |
| *\_Epistasis\_functions.py* | All additional functions required for epistasis and epistasis change computations. |
| *Epistasis\_change\_data.py* | Code used to collect all data for epistasis change due to a single mutation at a different locus. |
| *Epistasis\_plots.py* | Code used to generate box plots for epistasis present in the empirical landscape |
| *Epistasis\_change\_plot.py* | Codes to generate box plots to quantify epistatic interactions changing due to a mutation at a different loci. |
| *Epistasis\_change\_3d\_data.py* | Code used to collect data for 3D representations |
| *Epistasis\_change\_background\_all\_3d\_plot.m,*  *Epistasis\_change\_background\_functional\_3d\_plot.m,*  *Epistasis\_change\_background\_non\_functional\_3d\_plot.m* | Codes used to plot 3D representations of epistatic interaction changing from particular epistatic backgrounds with functional/non functional/all genetic backgrounds. |
| *Epistasis\_change\_mutation\_all\_3d\_plot.m,*  *Epistasis\_change\_mutation\_functional\_3d\_plot.m,*  *Epistasis\_change\_mutation\_non\_functional\_3d\_plot.m* | Codes used to plot 3D representations of epistatic backgrounds changing to particular epistatic interactions with functional/non functional/all genetic backgrounds. |
| *\_paths.py* | Functions used to assist in analysing paths in a landscape from one variant to another |
| *peak\_accessibility\_data.py* | Code used to find data of accessibility of the highest peak in the fitness landscape from its neighbouring variants |
| *path\_plots.py* | Code used to generate statistical distributions of paths leading to the highest peak from a certain distance from the peak. |
| *mutation\_evolvability\_data.py* | Code used to collect data of neutral mutations which lead to change in evolvability (shift in fitness effect of beneficial mutations) |
| *evolvability\_plots.py* | Code used to generate box plots of relative change in evolvability of a genotype brought upon by neutral mutation. |
| *beta\_lactamase\_epistasis\_change.py* | Code used to compute the epistasis change by a mutation at different loci observed in beta lactamase fitness landscape. |
| *beta\_lactamase\_epistasis\_change\_plots.py* | Code used to generate box plots of epistasis change observed in beta lactamase landscape |