# Subsystem 1: README

**Folder structure (Alphabetical order)**

* alpha\_force\_polynomial.png: Plot alpha vs Force and fitted polynomial curve of degree 2.
* beam\_mass\_fmincon.m: Mass of the beam used as objective function in fmincon. Parameters are R, r and .
* beam\_mass\_ga.m: Mass of the beam used as objective function in genetic algorithm. Parameters are R, r, , rhoI (index of which takes values 1,2,3,4).
* beam\_mass\_surf.m: Mass of the beam used to generate contour plot. Inputs are and
* contour\_mass.png: Contour plot of mass for various and
* forcevsalpha.m: Reads data file inputs\_outputs\_regression.m. Fits polynomial regression model . Stores model parameters to modelpars.csv.
* inputs\_outputs\_regression.csv: Data file containing radii, angle, density and stress values based on a sample size of 40 obtained using latin hypercube sampling. Stress obtained using Solidworks model.
* latinhypersample.m: Generates latin hypercube random sample of R, r, and values. Saves file to LHsam.csv. LHsam.csv had R and r in cm. This was converted to meters and saved as inputs\_outputs\_regression.csv.
* modelpars.m: polynomial model parameters as determined in forcevsalpha.m.
* Nonlin\_con\_fmincon.m: Nonlinear constraints for fmincon. Parameters are R, r and .
* Nonlin\_con\_ga.m: Nonlinear constraints for genetic algorithm. Parameters are R, r, , rhoI (index of which takes values 1,2,3,4).
* opt\_script\_fmincon.m: Script that runs fmincon optimisation. Calls modelpars.csv, beam\_mass\_fmincon.m and Nonlin\_con\_fmincon.m. Also creates a contour plot for which it calls beam\_mass\_surf.m
* opt\_script\_ga.m: Script that runs genetic algorithm. Calls modelpars.csv, beam\_mass\_ga.m, and Nonlin\_con\_ga.m.

**Main Scripts**

*For Optimisation:*

* opt\_script\_fmincon.m
* opt\_script\_ga.m

*For Regression:*

* forcevsalpha.m

**Execution Time**

* All scripts approx. 5 – 10 seconds
* Intel Core i7-7500U CPU @2.7 GHz, 16GB RAM

For further details, please refer to the final report.