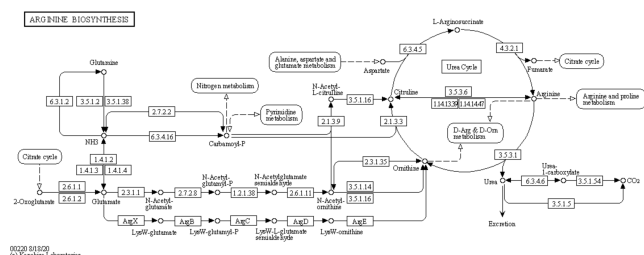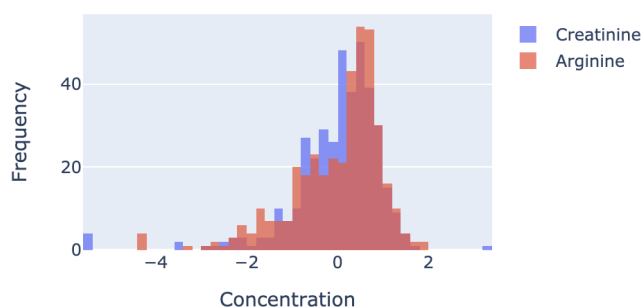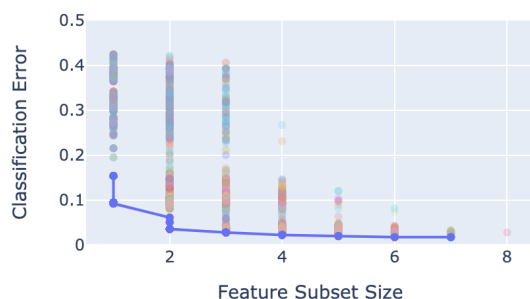# Supplementary Figures

Figure 1: Arginine biosynthesis pathway (https://www.genome.jp/kegg-bin/show_pathway?map00220)
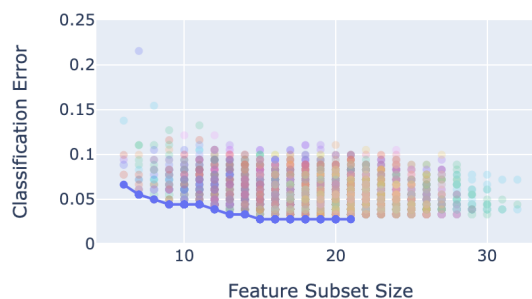

Figure 2: Distribution of Creatinine and Arginine in the metabolomics data set.

Figure 3: Pareto front (indigo line) of a collection of 20,000 feature subsets (all data points), generated by 100 runs of the MOGA on the osteoarthritis data set, where SVM was employed to create testing models.
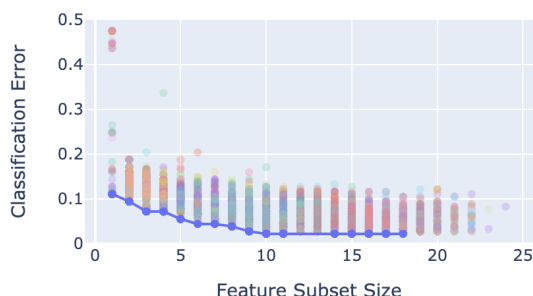

Figure 4: Pareto front (indigo line) of a collection of 20,000 feature subsets (all data points), generated by 100 runs of the MOGA on the climate-change vulnerability data set, where KNN was employed to create testing models.


Figure 5: Pareto front (indigo line) of a collection of 20,000 feature subsets (all data points), generated by 100 runs of the MOGA on the climate-change vulnerability data set, where SVM was employed to create testing models.
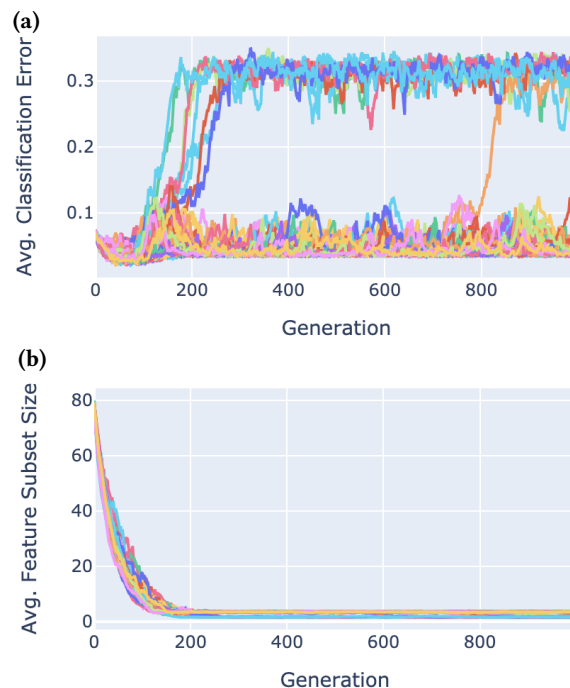
Figure 6: Convergence of mean population classification error (a) and feature subset size (b) throughout 1000 generations and 100 runs of the MOGA on the osteoarthritis data set, where SVM was employed to create testing models.

(a)

(b)
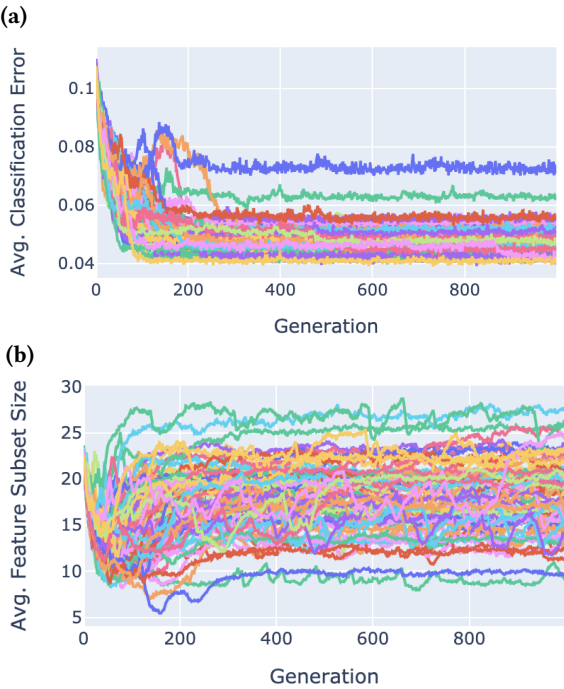
Figure 8: Convergence of mean population classification error (a) and feature subset size (b) throughout 1000 generations and 100 runs of the MOGA on the climate-change vulnerability data set, where SVM was employed to create testing models.

(a)

(b)
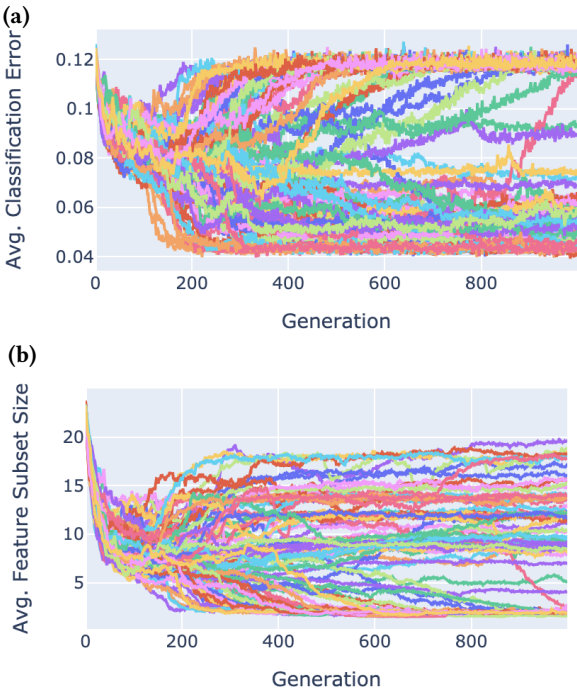
Figure 7: Convergence of mean population classification error (a) and feature subset size (b) throughout 1000 generations and 100 runs of the MOGA on the climate-change vulnerability data set, where KNN was employed to create testing models.