

* Balance classes of directions due to coefficients close to zero are resolved with sign = 0

Figure 1: Heatmap showing the performance of 12 machine learning models across 100 genes. The models are CYT, IS, IPS, IMPRES, RohIS, chemokine, IS_Davoli, Proliferation, IFny, ExpandedImmune, T_cell_inflamed, TIDE, and MSI. The genes are listed on the x-axis. The y-axis for each model shows three metrics: Elastic_Net_all (red), L21_all (green), and L21_all_top (orange). The heatmap shows that the models generally perform well on the Elastic_Net_all metric, while the L21_all and L21_all_top metrics show more variation across genes.

Analysis  Elastic_Net_all  L21_all  L21_all_top