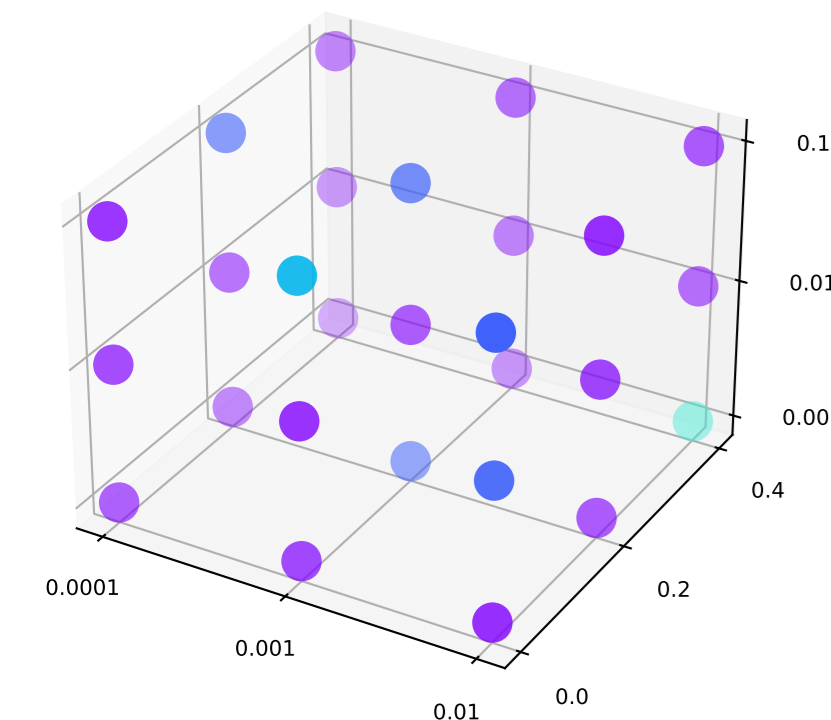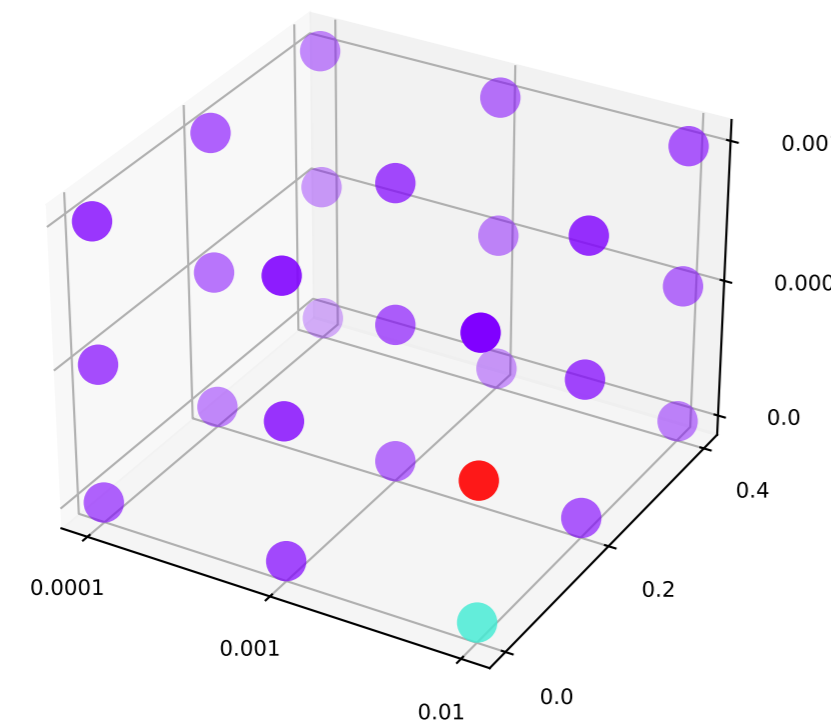Hyperparameter selection for methylation data models