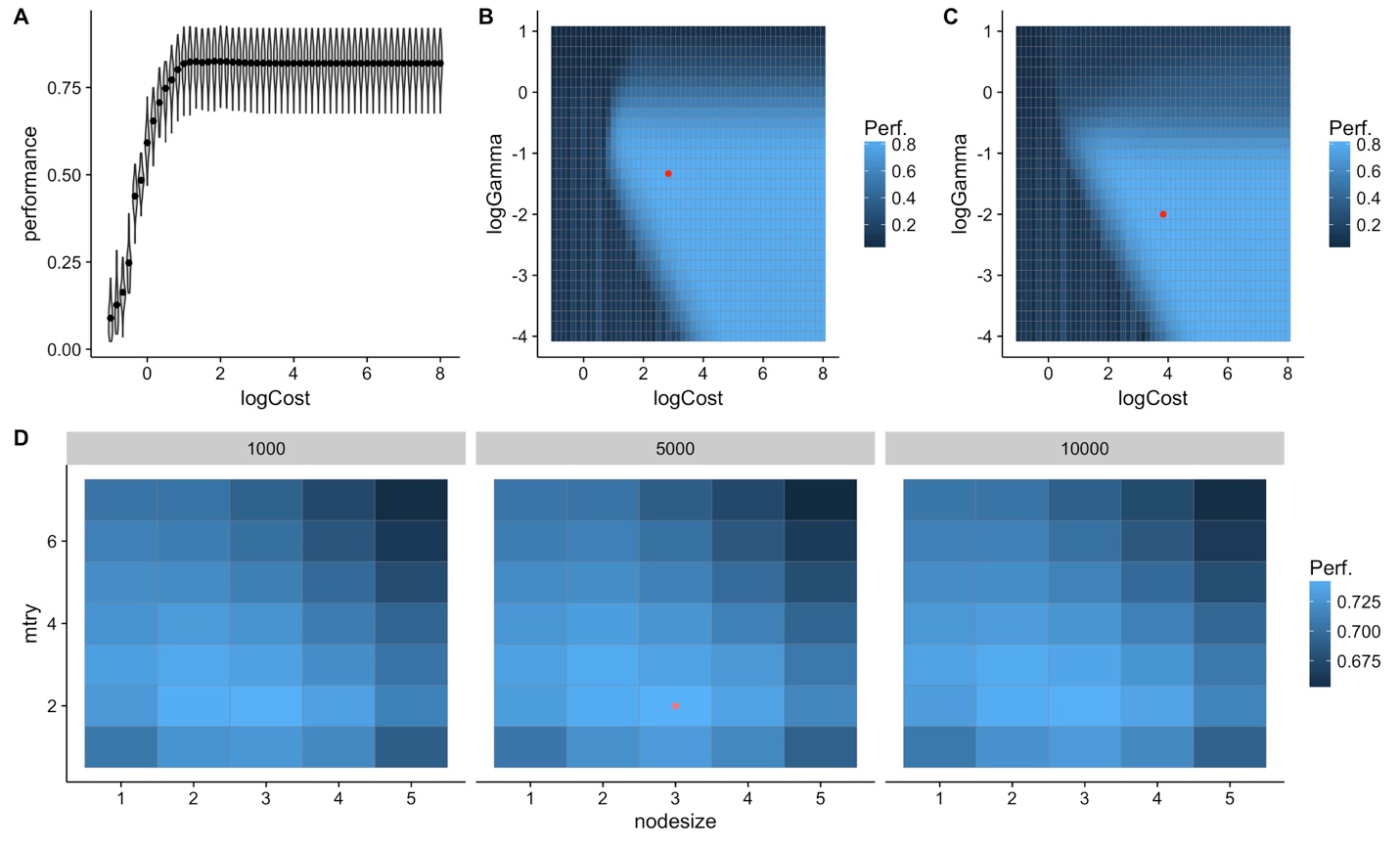
# Predicting bacterial growth conditions from mRNA and protein abundances

**Supplementary file**

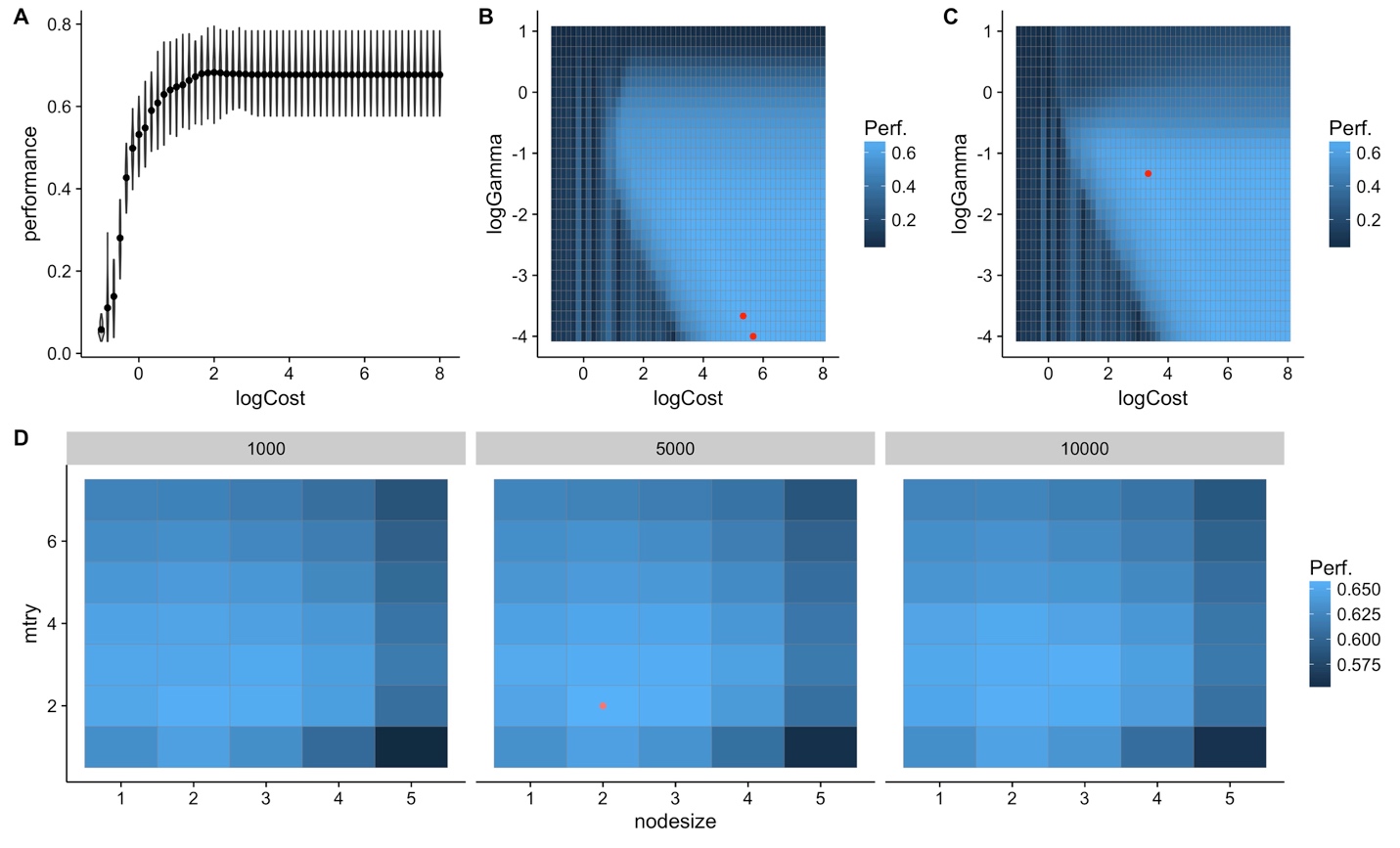
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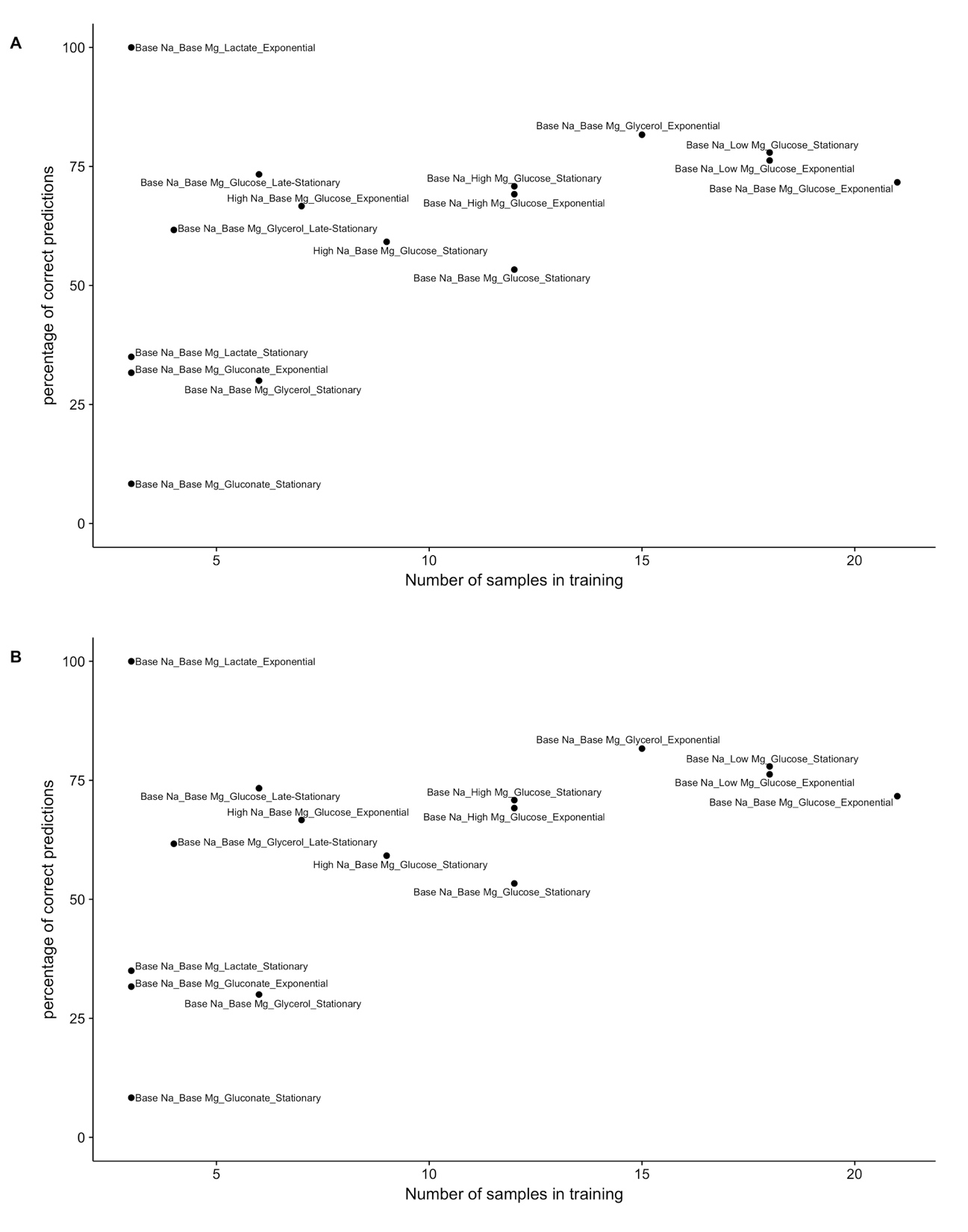
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**Supplementary figure 1.** Tuning results for predictions based on mRNA data. Model performance is measured as the mean *F*1 score over 10 independent tuning runs. Higher performance numbers are better. (A) Tuning results for SVMs with linear kernel. Only the cost parameter was tuned. (B) Tuning results for SVMs with radial kernel. The cost and gamma parameters were tuned. The red dot indicates the winning parameter combination. (C) Tuning results for SVMs with sigmoidal kernel. The cost and gamma parameters were tuned. The red dot indicates the winning parameter combination. (D) Tuning results for random forest models. The mtry, nodesize, and ntrees parameters were tuned. We used three values for ntrees, 1000, 5000, and 10000, shown as three separate panels. The red dot indicates the winning parameter combination.



**Supplementary figure 2.** Tuning results for predictions based on protein data. Model performance is measured as the mean *F*1 score over 10 independent tuning runs. Higher performance numbers are better. (A) Tuning results for SVMs with linear kernel. Only the cost parameter was tuned. (B) Tuning results for SVMs with radial kernel. The cost and gamma parameters were tuned. The red dots indicate the winning parameter combinations. (C) Tuning results for SVMs with sigmoidal kernel. The cost and gamma parameters were tuned. The red dot indicates the winning parameter combination. (D) Tuning results for random forest models. The mtry, nodesize, and ntrees parameters were tuned. We used three values for ntrees, 1000, 5000, and 10000, shown as three separate panels. The red dot indicates the winning parameter combination.

**Supplementary figure 3**. Percentage of correct predictions as a function of the number of samples during training. (A) Predictions based on mRNA abundances. (B) Predictions based on protein abundances.



**Supplementary figure 4.** The error count distribution for mRNA (A) and protein (B) confusion matrixes. *This needs some more text to explain that 4 correct predictions means 0 errors, 3 mean 1 error, etc. Maybe better to write “number of false predictions” along the x axis.*



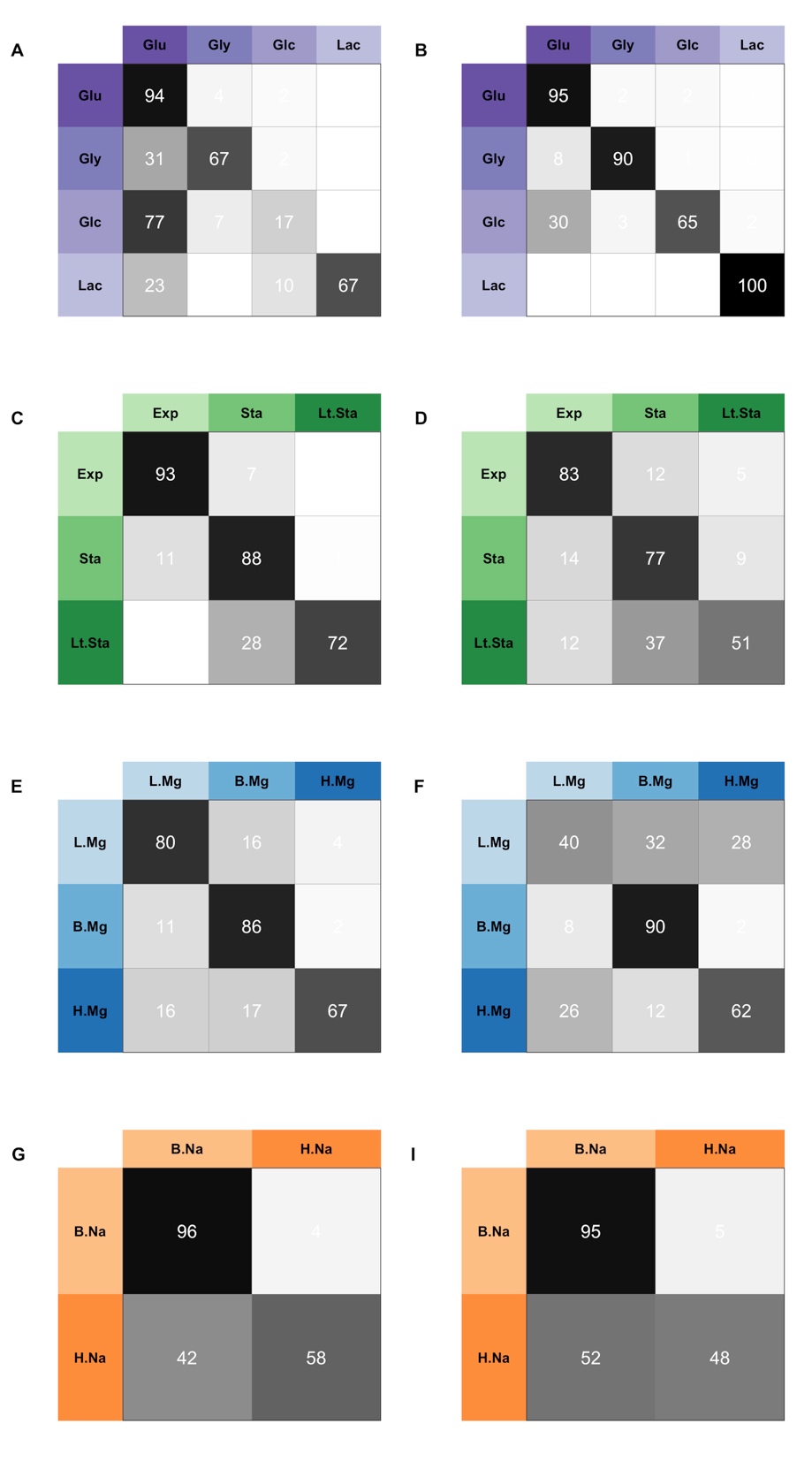
**Supplementary figure 5.** Complex predictions with intersection mRNA data. Corresponding multivariate F1 score is xx



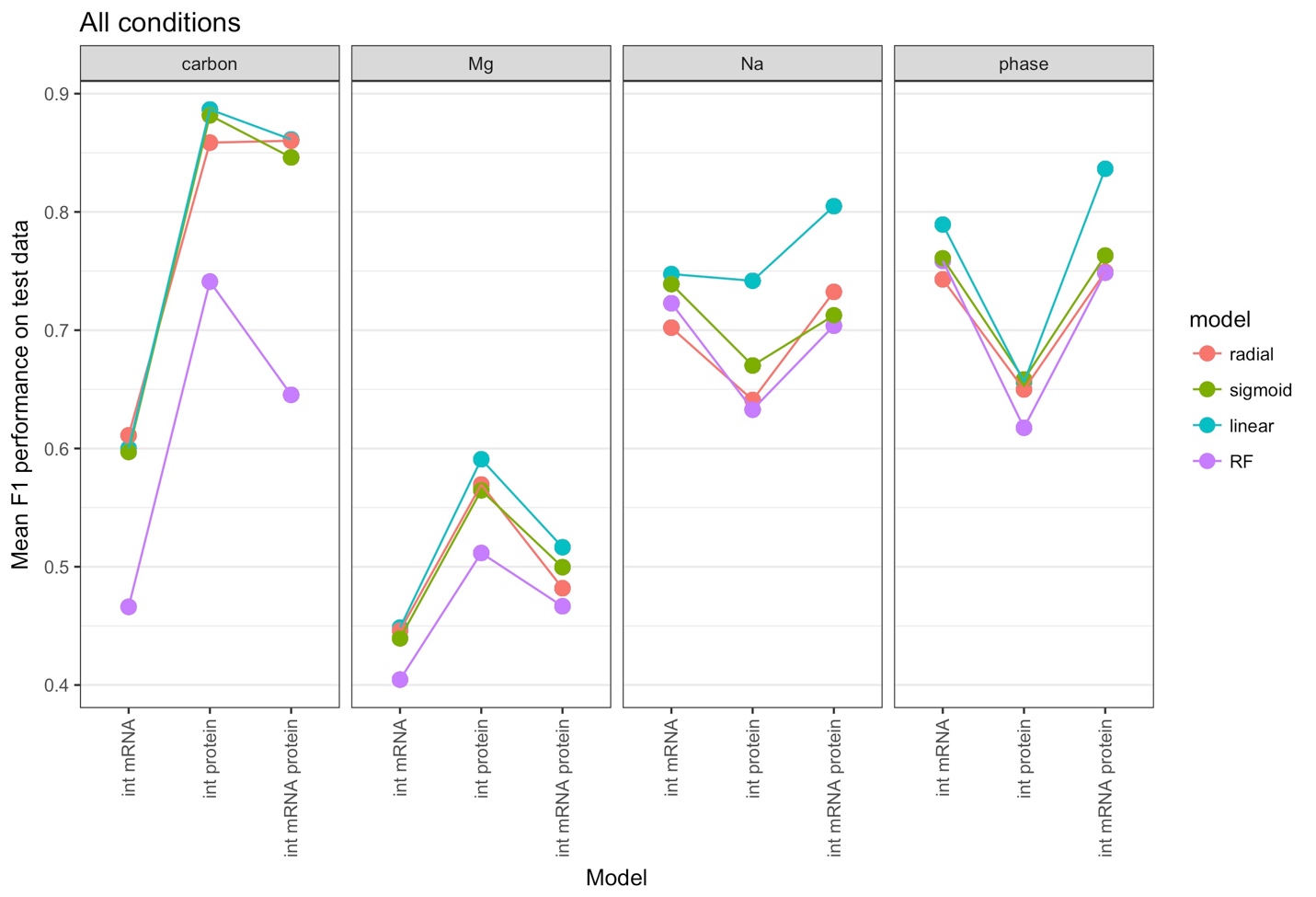
**Supplementary figure 6.** Complex predictions with intersection protein data. Corresponding multivariate F1 score is xx

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**Supplementary figure 7.** Complex predictions with intersection combined mRNA and protein data. Corresponding multivariate F1 score is xx



**Supplementary figure 8.** Prediction accuracy for univariate predictions. (A) Prediction of carbon source from mRNA abundances. (B) Prediction of carbon source from protein abundances. (C) Prediction of growth phase from mRNA abundances. (D) Prediction of growth phase from protein abundances. (E) Prediction of Mg2+ levels from mRNA abundances. (F) Prediction of Mg2+ levels from protein abundances. (G) Prediction of Na+ levels from mRNA abundances. (H) Prediction of Na+ levels from protein abundances.



**Supplementary figure 9.** Prediction accuracy for univariate predictions based on only mRNA abundances, only protein abundances, or the combination thereof. All predictions were done on the intersection of samples that contain both mRNA and protein data. Protein abundances are more predictive for carbon source and Mg2+ levels, and mRNA abundances are more predictive for Na+ levels and growth phase.

**Supplementary Table 1:** Number of distinct values each parameter takes during tuning process for each model. Each model with each parameter combination is trained with 10 distinct train-tune divisions of train&tune subset. To find the best model mean score of those 10 independent runs are averaged.

A

|  |  |  |
| --- | --- | --- |
|  | cost | gamma |
| SVM, linear kernel | 55 | NA |
| SVM, radial kernel | 55 | 31 |
| SVM, sigmoidal kernel | 55 | 31 |

B

|  |  |  |  |
| --- | --- | --- | --- |
|  | mtry | ntree | nodesize |
| Random Forest | 7 | 3 | 5 |