# SUPPLEMENTARY MATERIAL 2

## DeepMSPeptide: peptide detectability prediction using deep learning.

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**GPMDB test dataset: Statistical comparison of the AUC values obtained using DeepMSPeptide (1D-2C-CNN) with the results of the other approaches based on DeLongs's test (Elisabeth, R. et al. (1988) Comparing the areas under two or more correlated receiver operating characteristic curves: a nonparametric approach'. Biometrics 44, 837-845).**

| | 1D-2C-CNN | 1D-1C-CNN | RF | SvmR | DNN | C5 | Nnet | Rpart | Nb | Pls | Glm | GlmStepAIC | Gaussian | Jrip |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **1D-2C-CNN** | | | | | | | | | | | | | | |
| **1D-1C-CNN** | 0.9214 | | | | | | | | | | | | | |
| **Random Forest** | 2.2E-16 | 2.2E-16 | | | | | | | | | | | | |
| **SvmR1** | 2.2E-16 | 2.2E-16 | 2.2E-16 | | | | | | | | | | | |
| **DNN2** | 2.2E-16 | 2.2E-16 | 2.2E-16 | 0.5858 | | | | | | | | | | |
| **C5** | 2.2E-16 | 2.2E-16 | 2.2E-16 | 0.0007409 | 0.2858 | | | | | | | | | |
| **Nnet** | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 3.078E-06 | 3.021E-11 | | | | | | | | |
| **Rpart** | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | | | | | | | |
| **Nb** | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | | | | | | |
| **Pls** | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 0.000226 | | | | | |
| **Glm** | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 0.000342 | 0.9349 | | | | |
| **GlmStepAIC** | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 0.0003385 | 0.9214 | 0.5423 | | | |
| **Gaussian** | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 6.912E-05 | 0.4028 | 0.3133 | 0.3291 | | |
| **Jrip** | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 2.2E-16 | 5.247E-09 | 0.001483 | 0.00165 | 0.001665 | 0.004665 | |