

Supporting information to “2018 YPIC challenge: A case study in characterizing an unknown protein sample”

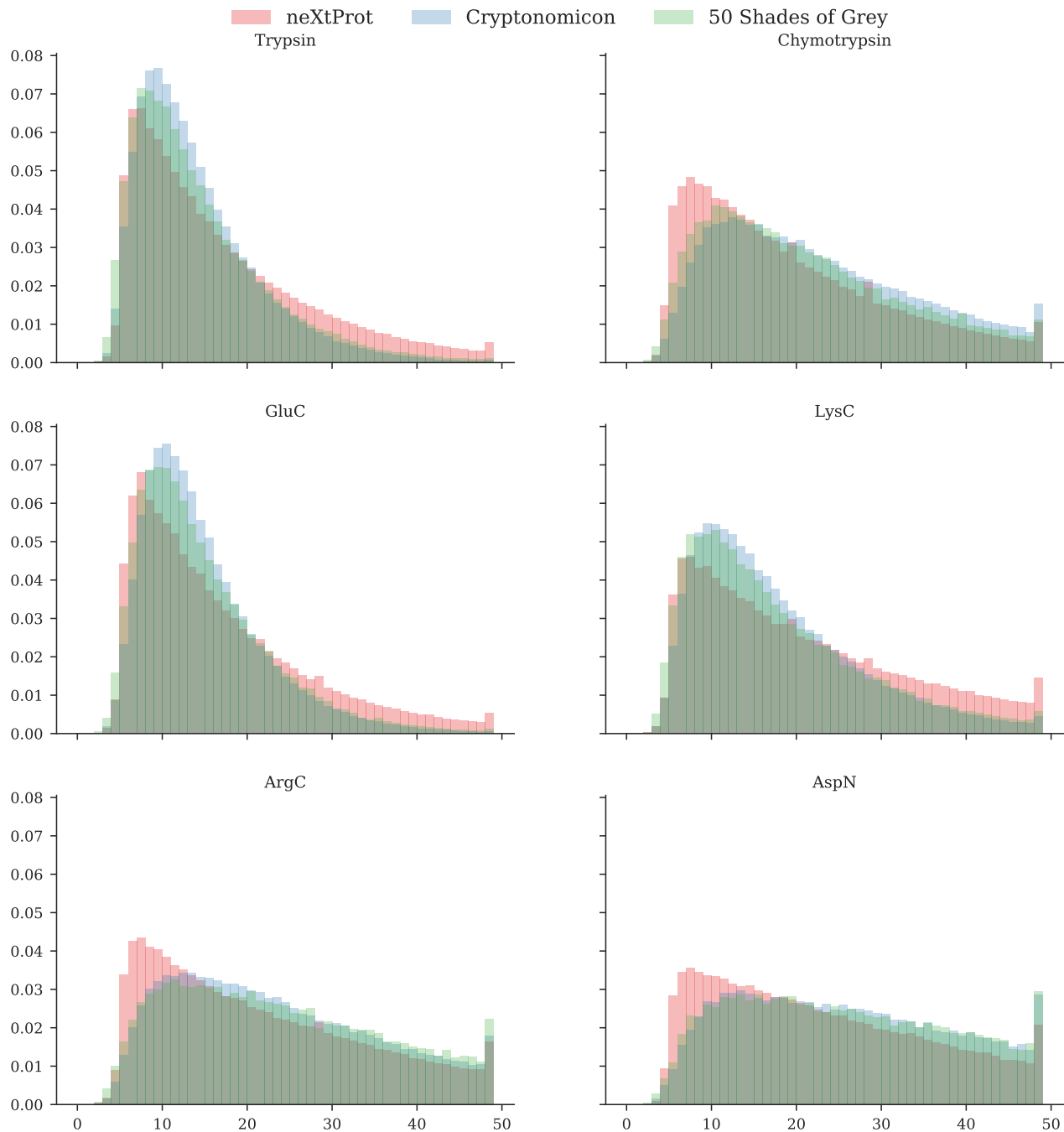
Lindsay Pino¹, Andy Lin¹, Wout Bittremieux^{*,1,2,3}

¹Department of Genome Sciences, University of Washington, Seattle WA 98195, USA; ²Department of Mathematics and Computer Science, University of Antwerp, 2020 Antwerp, Belgium; ³Biomedical Informatics Network Antwerpen (biomina), 2020 Antwerp, Belgium

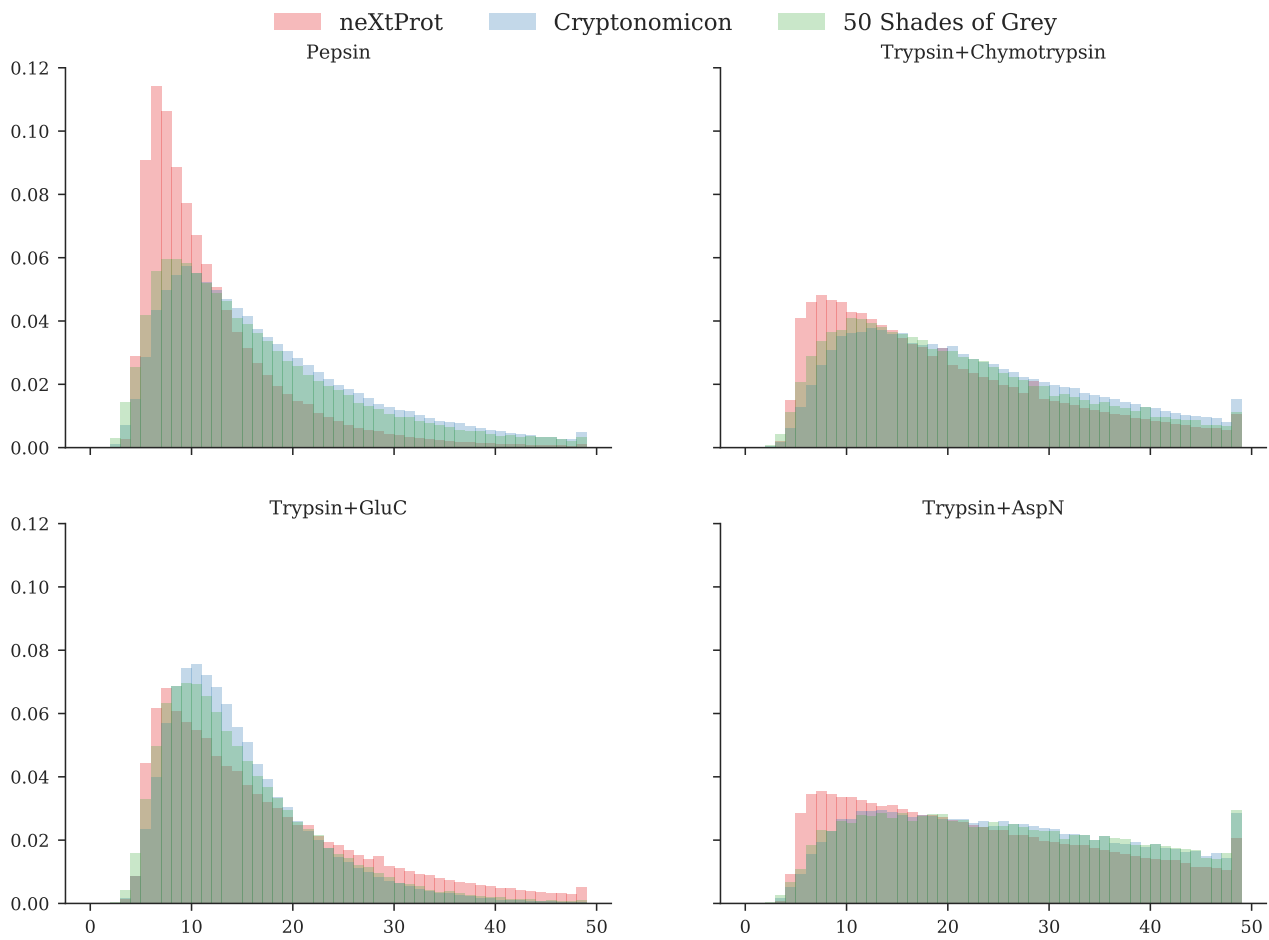
*Corresponding author: wout.bittremieux@uantwerpen.be, +32 3 265 34 07.

List of Figures

| | | |
|---|--------------------------------------------------------------|---|
| 1 | Simulated peptide length for alternative proteases | 2 |
|---|--------------------------------------------------------------|---|



Supplementary Figure 1: Length of simulated peptides for various corpuses using alternative proteases including chymotrypsin, Glu-C, Lys-C, Arg-C, Asp-N, pepsin, and a combined digestion with trypsin. NeXtProt is a database of human proteins, whereas Cryptonomicon and 50 Shades of Grey are two English fiction novels.



Supplementary Figure 1: Length of simulated peptides for various corpuses using alternative proteases including chymotrypsin, Glu-C, Lys-C, Arg-C, Asp-N, pepsin, and a combined digestion with trypsin. NeXtProt is a database of human proteins, whereas Cryptonomicon and 50 Shades of Grey are two English fiction novels.