NetMHCpan-3.0: improved prediction of binding to MHC class I molecules integrating information from multiple receptor and peptide length datasets - DTU Orbit (25/12/2018)

NetMHCpan-3.0: improved prediction of binding to MHC class I molecules integrating information from multiple receptor and peptide length datasets

Background: Binding of peptides to MHC class I molecules (MHC-I) is essential for antigen presentation to cytotoxic T-cells.

Results: Here, we demonstrate how a simple alignment step allowing insertions and deletions in a pan-specific MHC-I binding machine-learning model enables combining information across both multiple MHC molecules and peptide lengths. This pan-allele/pan-length algorithm significantly outperforms state-of-the-art methods, and captures differences in the length profile of binders to different MHC molecules leading to increased accuracy for ligand identification. Using this model, we demonstrate that percentile ranks in contrast to affinity-based thresholds are optimal for ligand identification due to uniform sampling of the MHC space.

Conclusions: We have developed a neural network-based machine-learning algorithm leveraging information across multiple receptor specificities and ligand length scales, and demonstrated how this approach significantly improves the accuracy for prediction of peptide binding and identification of MHC ligands. The method is available at www.cbs.dtu.dk/services/NetMHCpan-3.0.

General information
State: Published
Organisations: Immunological Bioinformatics, Department of Systems Biology, Center for Biological Sequence Analysis, Universidad Nacional de San Martin
Contributors: Nielsen, M., Andreatta, M.
Number of pages: 9
Publication date: 2016
Peer-reviewed: Yes

Publication information
Journal: Genome Medicine
Volume: 8
Issue number: 1
Article number: 33
ISSN (Print): 1756-994X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 6.61 SJR 4.537 SNIP 1.426
Web of Science (2017): Impact factor 8.898
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 5.48 SJR 3.966 SNIP 1.328
Web of Science (2016): Impact factor 7.071
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.03 SJR 2.899 SNIP 1.052
Web of Science (2015): Impact factor 5.846
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.79 SJR 2.873 SNIP 1.082
Web of Science (2014): Impact factor 5.809
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.31 SJR 2.059 SNIP 0.922
Web of Science (2013): Impact factor 4.942
ISI indexed (2013): ISI indexed yes
Scopus rating (2012): CiteScore 3.43 SJR 1.683 SNIP 1.067
Web of Science (2012): Impact factor 3.906
ISI indexed (2012): ISI indexed no
Scopus rating (2011): CiteScore 3.33 SJR 1.668 SNIP 0.934
ISI indexed (2011): ISI indexed no