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
Publication status: 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 (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
Original language: English
Electronic versions:
NetMHCpan_3.0.pdf
DOIs:
10.1186/s13073-016-0288-x

Bibliographical note
© 2016 Nielsen and Andreatta. Open Access This article is distributed under the terms of the Creative Commons Attribution 4.0 International License (http://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The Creative Commons Public Domain Dedication waiver (http://creativecommons.org/publicdomain/zero/1.0/) applies to the data made available in this article, unless otherwise stated.
Source: FindIt
Source ID: 2303167531
Research output: Contribution to journal › Journal article – Annual report year: 2016 › Research › peer-review