

12th Summer Academy “Infection and Immunity”
Lecture 8 on Wednesday, 20 July, 2022**Prof. Dr. Daniel Hoffmann**

Faculty of Biology
Department of Bioinformatics and Computational Biophysics
University of Duisburg-Essen
Daniel.Hoffmann@uni-due.de
<https://www.uni-due.de/zmb/members/hoffmann/overview.shtml>

Member of



www.uni-due.de/sgvivi

Computational discovery of HLA associated mutations in viral genomes**Publications for seminar preparation:**

Borrow, P., Lewicki, H., Wei, X., Horwitz, M. S., Peffer, N., Meyers, H., Nelson, J. A., Gairin, J. E., Hahn, B. H., Oldstone, M. B. and Shaw, G. M. (1997), ‘Antiviral pressure exerted by HIV-1-specific cytotoxic T lymphocytes (CTLs) during primary infection demonstrated by rapid selection of CTL escape virus.’, *Nat Med* 3, 205–11.
<https://pubmed.ncbi.nlm.nih.gov/9018240/>

Amrhein, V., Greenland, S. and McShane, B. (2019), ‘Scientists rise up against statistical significance.’, *Nature* 567, 305–307.
<https://pubmed.ncbi.nlm.nih.gov/30894741/>

Kruschke, J. K. and Liddell, T. M. (2018), ‘The Bayesian New Statistics: Hypothesis testing, estimation, meta-analysis, and power analysis from a Bayesian perspective.’, *Psychon Bull Rev* 25, 178–206.
<https://pubmed.ncbi.nlm.nih.gov/28176294/> (up to page 186)

O’Donnell, T. J., Rubinsteyn, A. and Laserson, U. (2020), ‘MHCflurry 2.0: Improved Pan-Allele Prediction of MHC Class I-Presented Peptides by Incorporating Antigen Processing.’, *Cell Syst* 11, 42–48.e7.
<https://pubmed.ncbi.nlm.nih.gov/32711842/>

Habermann, D., Kharimzadeh, H., Walker, A., Li, Y., Yang, R., Kaiser, R., Brumme, Z. L., Timm, J., Roggendorf, M. and Hoffmann, D. (2022), ‘Hamdetector: A bayesian regression model that integrates information to detect hla-associated mutations’, *Bioinformatics* .
<https://pubmed.ncbi.nlm.nih.gov/35238330/>