Benedict Matern, PhD

Bioinformatician

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SUMMARY

As a bioinformatician in the field of immunology, I am an expert in exploring scientific questions in the context of HLA polymorphism and immunogenicity. I use computational strategies to examine HLA polymorphism in the context of T-cell and B-cell epitopes, and elucidate how this may lead to an immune response. By analyzing polymorphism of HLA amino acid sequences, especially in the context of world populations, I work to predict the biological and immunological determinants of the HLA molecules and apply these concepts in the practical and scientific settings.

PROFESSIONAL APPOINTMENTS

PIRCHE AG., Berlin, DE

Director of Bioinformatics

February 2023 - Present

- Created an AI prediction model for T-cell epitope presentation model
- Directing projects for developing bioinformatic tools and performing scientific analysis
- Simulated swine transplantation to predict epitope immunogenicity and immune memory
- Investigated the effects of HLA imputation on epitope analysis in world populations
- Promotion from Senior Bioinformatics Scientist to Director of Bioinformatics in October 2023
- Liaison with UMC Utrecht CTI for scientific collaborations

University Medical Center Utrecht, Utrecht, NL

Bioinformatics Postdoctoral Researcher

February 2020 - February 2023

- Defined epitope-focused HLA immunogenicity models
- Developed the cloud-based Workshop Database for the 18th IHIW
- Collected and Analyzed Data with 18th IHIW Project Leaders
- Simulated T-cell and B-cell epitopes in a ULISES Tumor Therapy model
- Developed sequence analysis techniques for implementation of a genome-wide CRISPR knockout assay

Maastricht University Medical Center, Maastricht, NL

Bioinformatics PhD Candidate

February 2016 - February 2020

- Thesis: Prospecting the MHC: A Bioinformatic View of HLA Polymorphism and Gene Organization - Defended June 2020
- Elucidated patterns in class II HLA gene organization.
- Analyzed and interpreted nanopore sequencing data.
- Explored patterns in HLA peptide sequences.
- PhD Promoter: Em. Prof. Dr. M.G.J Tilanus
- PhD Co-Promoter: Dr. M. Groeneweg

NMDP - BeTheMatch, Minneapolis, MN, USA

Student Researcher

February 2015 - September 2016

- Explored concepts in HLA matching for Stem Cell Transplantation.
- Developed MIRING validator for high-quality genotyping data.

EDUCATION

University of Minnesota, Minneapolis, MN, USA
M.S. Biomedical Informatics & Computational Biology
September 2013 - December 2015

- Courses in Biostatistics, Statistics for Human Genetics, Database Design, Machine Learning, Metagenomics
- Bioinformatics Journal Club

University of Wisconsin - Stout, Menomonie, WI, USA
B.S. Applied Mathematics & Computer Science
Concentrations in Bioinformatics & Software Development
September 2004 - May 2009

- Implemented BLAST algorithm for a database of oligonucleotides
- Molecular Cell Biology, Microbiology, Computer Science, Data Structures, Database Design

TEACHING EXPERIENCE

UMC Utrecht CTI Theme Meeting Presentation

Nov 10 2022

Modeling Linked Recognition of HLA: Allele-Specific Definitions of B-Cell Epitopes

Sept 16 2021

HLA Immunogenicity as a Targeted Tumor Therapy

Educational Session - EFI 2022

May 2022 : Amsterdam NL

Tools for analysis of HLA epitopes in transplantation.

Advisement of Master's Students - UMCU

Feb 2020 - Feb 2022

Typing of Eplets from SSO Genotyping Assays
HLA Genotyping from WES/WGS
HLA Genotyping from RNA-Seq

SLPHS Presentation - Spring Lake Park High School, MN, USA

Dec 20, 2018

Oral Presentation: Transplantation, with the help of a MinION

Advisement of Master's Student - MUMC

November 2017 - June 2018

Advised Master's Thesis: The identification of intronic polymorphism in HLA-DRA

BICB Journal Club, University of Minnesota, Minneapolis, MN

October 6, 2016

Oral Presentation: Rules and Tools of N-NGS

Lunch & Learn, BeTheMatch, Minneapolis, MN

September 23, 2016

Oral Presentation: Analysis of Nanopore Sequencing Data, or How Ben Learned to Stop Worrying and Love the MinION

CONFERENCES

DASH Data Standards Hackathons

October 2024 : Utrecht, Netherlands (Organizer)
September 2022 : Online
Feb 2022 : Online
April 2021 : Online
April 2020 : Online
August 2019 : Minneapolis, MN, USA
October 2018 : Baltimore, MD, USA
November 2017 : Utrecht, Netherlands
September 2017 : Pacific Grove, CA, USA
May 2017 : Heidelberg, Germany
November 2016 : Vienna, Austria
January 2016 : Minneapolis, MN, USA

Organizer, Participant and Contributor

American Transplant Congress

June 1-5, 2024 : Philadelphia, PA, USA
Oral Presentation: Swine Xenografts Share Few Predicted Indirectly Recognizable SLA-Derived Epitopes with HLA-Derived Epitopes from Human Kidney Grafts

EFI Conference

May 20-23, 2024 : Geneva, Switzerland
Poster: PIRCHE application versions 3 and 4 lead to equivalent T cell epitope mismatch scores in solid organ and stem cell transplantation modules

April 26-29, 2023 : Nantes, France

May 17-20, 2022 : Amsterdam, NL

Oral Presentation: The Role of HLA Epitope Mismatches in Antibody Development and Refractoriness to Optimize Allocation in Platelet Transfusion
Organized Educational Session: Bioinformatics & HLA
Organized Hands-On Session: Tools for analysis of HLA epitopes

April 22-25 2021 : Glasgow, UK (Online)

May 8-11, 2019 : Lisbon, Portugal

Poster: Multiple lineages of DRB1*13~DRB3~DQB1 haplotypes identified by HLA-DRA polymorphism (Best Poster Prize)

May 9-12, 2018 : Venice, Italy

May 30-June 2, 2017 : Mannheim & Heidelberg, Germany

Poster: Nanopore sequencing is coming of age: a new analysis platform for HLA allele assignment based on full length de novo assembly.
Poster : ABO blood group typing with Oxford Nanopore MinION sequencing

May 15-16, 2016 : Kos Island, Greece

ASHI Annual Meeting

October 21-25, 2024 : Anaheim, CA, USA
Workshop Moderator: Roadmap for Laboratory Data Standards

October 16-20, 2023 : San Antonio, TX, USA
Abstract Session Chair: Data Alchemy: Translating HLA Insights through Bioinformatics

October 23-28, 2022 : Las Vegas, NV, USA

September 26-October 1, 2021 : Orlando, FL, USA (Online)

October 19-21 2020 : Online

September 23-27, 2019 : Pittsburg, PA, USA
Poster: HLA-DRA POLYMORPHISM DEFINES MULTIPLE LINEAGES OF DRB1*13~DRB3~DQB1 HAPLOTYPES

October 1-5, 2018 : Baltimore, MD, USA
Oral Presentation: The Highly Polymorphic HLA-DRA Gene: Conserved and Diverse Regions within the HLA-DRA Gene imply Haplotypes of DRA~DRB3/4/5~DRB1~DQB1

Sept 11-15, 2017 : San Francisco, CA, USA

Oct 26-30, 2016: St. Louis, MO, USA

18th International Histocompatibility and Immunogenetics Workshop

May 11-15, 2022 : Noordwijkerhout, Netherlands
Developed IHIW database & interfaced with project leaders to coordinate data collection and analysis. Participant of several components

17th International Histocompatibility and Immunogenetics Workshop

September 6-10, 2017 : Pacific Grove, CA, USA
Participated in Component: Extension of HLA allele sequences by full-length HLA allele-specific hemizygous Sanger sequencing (SSBT)

Living Donor Abdominal Organ Transplantation: State of the Art

August 29-31, 2024 : Rome, Italy

SIP Symposium: Evolution and Characterization of the Immune System

October 7-10, 2024 : Sassenheim, Netherlands

ISHLT Annual Meeting

April 10-13, 2024 : Prague, Czech Republic
Poster: Interplay and Divergent Effects of PIRCHE-II Scores & Eplet Mismatch Loads on De Novo DSA Development and Clinical Parameters in Lung Transplantation

Bootcongres

March 6-7, 2024 : Utrecht, Netherlands

APHIA Conference

November 11-14, 2018 : Sydney, Australia
Oral Presentation: The highly polymorphic HLA-DRA gene: an implication for DRA~DRB3/4/5~DRB1 haplotypes

Dutch Hematology Congress 2018

January 24, 2018 : Arnhem, Netherlands

Oral Presentation: The power of nanopore MinION single molecule sequencing for HLA and ABO typing.

EFI Summer School

July 24-26, 2017 : Dublin, Ireland

Participant, and Oral Presentation: MinION Sequencing: Research and Applications in HLA

ULISES Annual Meeting

November 17, 2022 : Barcelona, Spain

London Calling Nanopore Sequencing Conference

May 4-5, 2017 : London, England

Oral Presentation: Identification of Human Leukocyte Antigen Splice Variants by MinION cDNA Sequencing

May 26-27, 2016 : London, England

Oral Presentation: De novo Assembly of HLA Nanopore Reads

PUBLICATIONS

Matern B, Spierings E, Bandstra S, et al. Quantifying uncertainty of molecular mismatch introduced by mislabeled ancestry using haplotype-based HLA genotype imputation. Front Genet. 2024;15. doi:10.3389/fgene.2024.1444554

Matern BM, Niemann M. PIRCHE application major versions 3 and 4 lead to equivalent T cell epitope mismatch scores in solid organ and stem cell transplantation modules. Hum Immunol. 2024;85(3):110789. doi:10.1016/j.humimm.2024.110789

Niemann M, Matern BM, Spierings E. PIRCHE-II Risk and Acceptable Mismatch Profile Analysis in Solid Organ Transplantation. In: Boegel S, ed. HLA Typing: Methods and Protocols. Springer US; 2024:171-192. doi:10.1007/978-1-0716-3874-3_12

Niemann M, Matern BM, Spierings E. Repeated local ellipsoid protrusion supplements HLA surface characterization. HLA. 2024;103(1):e15260. doi:10.1111/tan.15260

Truong L, Matern BM, El-Lagta N, et al. Report from the extended HLA-DPA1 ~ promoter ~ HLA-DPB1 haplotype of the 18th international HLA and immunogenetics workshop. HLA. 2023;102(6):690-706. doi:10.1111/tan.15155

Matern BM, Niemann M, Nemparis I, et al. Using cloud infrastructure to facilitate data collection and conversion of HLA diagnostic data for the 18th International HLA and Immunogenetics Workshop. HLA. 2023;101(5):484-495. doi:10.1111/tan.14989

Niemann M, Strehler Y, Lachmann N, et al. Snowflake epitope matching correlates with child-specific antibodies during pregnancy and donor-specific antibodies after kidney transplantation. Front Immunol. 2022;13. Accessed November 7, 2022. https://www.frontiersin.org/articles/10.3389/fimmu.2022.1005601

Niemann M, Matern BM, Spierings E. Snowflake: A deep learning-based human leukocyte antigen matching algorithm considering allele-specific surface accessibility. Front Immunol. 2022;13:937587. doi:10.3389/fimmu.2022.937587

Peereboom ETM, Matern BM, Spierings E, Geneugelijk K. The Value of Single-cell Technologies in Solid Organ Transplantation Studies. Transplantation. 2022;106(12):2325-2337. doi:10.1097/TP.0000000000004237

Carapito R, Aouadi I, Verniquet M, et al. The MHC class I MICA gene is a histocompatibility antigen in kidney transplantation. Nat Med. 2022;28(5):989-998. doi:10.1038/s41591-022-01725-2

Niemann M, Matern BM, Spierings E, Schaub S, Hönger G. Peptides Derived From Mismatched Paternal Human Leukocyte Antigen Predicted to Be Presented by HLA-DRB1, -DRB3/4/5, -DQ, and -DP Induce Child-Specific Antibodies in Pregnant Women. Front Immunol. 2021;12. Accessed April 25, 2022. https://www.frontiersin.org/article/10.3389/fimmu.2021.797360

Peereboom ETM, Matern BM, Tomosugi T, et al. T-Cell Epitopes Shared Between Immunizing HLA and Donor HLA Associate With Graft Failure After Kidney Transplantation. Front Immunol. 2021;12. Accessed April 27, 2022. https://www.frontiersin.org/article/10.3389/fimmu.2021.784040

Matern BM, Mack SJ, Osoegawa K, et al. Standard reference sequences for submission of HLA genotyping for the 18th International HLA and Immunogenetics Workshop. HLA. 2021;97(6):512-519. doi:10.1111/tan.14259

Duygu B, Matern BM, Wieten L, Voorter CEM, Tilanus MGJ. Specific amino acid patterns define split specificities of HLA-B15 antigens enabling conversion from DNA-based typing to serological equivalents. Immunogenetics. 2020;72(6-7):339-346. doi:10.1007/s00251-020-01172-8

Truong L, Matern BM, Groeneweg M, et al. Polymorphism clustering of the 21.5 kb DPA-promoter-DPB region reveals novel extended full-length haplotypes. HLA. 2020;96(3):299-311. doi:10.1111/tan.13975

Matern BM, Olieslagers TI, Groeneweg M, et al. Long-Read Nanopore Sequencing Validated for Human Leukocyte Antigen Class I Typing in Routine Diagnostics. J Mol Diagn JMD. 2020;22(7):912-919. doi:10.1016/j.jmoldx.2020.04.001

Matern BM, Olieslagers TI, Voorter CEM, Groeneweg M, Tilanus MGJ. Insights into the polymorphism in HLA-DRA and its evolutionary relationship with HLA haplotypes. HLA. Published online October 16, 2019. doi:10.1111/tan.13730

Truong L, Matern B, D’Orsogna L, Martinez P, Tilanus MGJ, De Santis D. A novel multiplexed 11 locus HLA full gene amplification assay using next generation sequencing. HLA. Published online October 16, 2019. doi:10.1111/tan.13729

Voorter CEM, Matern B, Tran TH, et al. Full-length extension of HLA allele sequences by HLA allele-specific hemizygous Sanger sequencing (SSBT). Hum Immunol. 2018;79(11):763-772. doi:10.1016/j.humimm.2018.08.004

Matern BM, Groeneweg M, Voorter CEM, Tilanus MGJ. Saddlebags: A software interface for submitting full-length HLA allele sequences to the EMBL-ENA nucleotide database. HLA. 2018;91(1):29-35. doi:10.1111/tan.13179

Duygu B, Matern BM, Groeneweg M, Voorter CEM, Tilanus MGJ. Polymorphism at residue 156 of the new HLA-A*02:683 allele suggests immunological relevance. HLA. 2017;90(2):107-109. doi:10.1111/tan.13059

AWARDS

Best Poster Award - EFI 2019 - Multiple lineages of DRB1*13~DRB3~DQB1 haplotypes identified by HLA-DRA polymorphism

EFI Education & Training Bursary - 2018 - MUMC / PathWest Perth Collaboration

EFI Travel Bursary - 2017 - 13th International Summer School on Immunogenetics