

HLA epitopes hands-on session

Eric Spierings (e.spierings@umcutrecht.nl)



Epitope workshop ABHI Curitiba – Friday, December 1, 2023

Where to find the instructions and files?

https://github.com/espierin/cases-workshop



A warm-up: NetSurfP-2.0

- Go to the IPD/IMGT HLA repository and open de MICB protein sequences https://github.com/ANHIG/IMGTHLA/blob/Latest/fasta/MICB prot.fasta
- Pick the full sequence of one of the alleles and copy it.
- Mark the allele.
- Go to the online NetSurf server and paste the sequence https://services.healthtech.dtu.dk/services/NetSurfP-2.0/
- While waiting, select another MICB sequence of choice.
- Mark the allele.
- Go to https://www.ebi.ac.uk/jdispatcher/psa/lalign and use the two protein sequences to align



A warm-up: NetSurfP-2.0

- Check the NetSurf output and mark the polymorphic amino acids
- How many accessible amino acids did you find for your combination?



Case 1: Multiple living related donors for a patient without antibodies

- PIRCHE → SOT → Single patient
- Recipient
- Four candidate donors
- Enter them into the SOT system and calculate the PIRCHE. Compare the outcomes
- Add an uncle and evaluate again
- PM: show the heath plots and hover over the items



Case 2: One DCD donor with multiple candidate recipients (no antibodies)

- PIRCHE → SOT → Donor Allocation
- DCD donor
- Four candidate recipient, create four first
- Enter them into the SOT system and calculate the PIRCHE. Compare the outcomes and store them



Case 3: RAMP evaluation

- PIRCHE → SOT → RAMP
- Use the data from recipient 1, 2, 3, and 4 from case 2 and plot a RAMP
- Evaluate whether this donor is good or bad donor in a relative way. Do this by checking the actual PIRCHE scores from case 2 with the RAMP histograms



Case 4: Adding unacceptables to the RAMP for a patient without antibodies

- PIRCHE → SOT → RAMP
- Enter the typing (recipient 4)
- Create a RAMP
- Select unacceptables to get into a vPRA of ~ 50%
- Check the distribution of the risk classifications



Case 5: Adding unacceptables to the RAMP for a patient with antibodies

- PIRCHE → SOT → RAMP
- Enter the typing
- Add the MFI data → get from file epitopes_class_I.csv
- Select from which run you want to evaluate the data
- Select unacceptables to create a pattern that suits you
- Evaluate the RAMP







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