

Week two 07/02/2022

This week's objective: Learning about the B cell lineage trees

Welcome to week two!

You already know the majority of the concepts and vocabulary for starting to work on your project's research question, ... the « majority » means..., there are still a few concepts to master!

During this week, we will work on the notions related to reconstructing the evolutionary history of a B cell lineage. Once you know why the B cell lineage tree studies can benefit researchers and how they construct it, you will be ready to participate in this ongoing scientific discussion.

I suggest you read about the Clonaltree, a tool that we have developed at LCQB. Clonaltree is an approach to reconstruct BCR lineage trees by incorporating genotype abundances into minimum spanning tree (MST) algorithms.

Reading :

This is the introduction of a chapter about Clonaltree in my thesis dissertation. Soon, we will share with you the article that we have written to represent this method.

Chapter 9: Reconstructing the evolutionary history of a BCR lineage using minimum spanning tree and clonotype abundances. **From the beginning of the chapter until section 9.2.5.**

https://github.com/NikaAb/BCR_intraclonal_diversity/blob/master/doc/Ref_papers/ABDOL_LAHI_Nika_2021.pdf

Study questions :

- What is a B cell lineage?
- How can studying the immune gene sequences be related to the B cell lineage studies? (Hint: what is the relationship between B cell and BCR?)
- Why are the B cell lineage studies potentially valuable in the medical context?
- Why does a "tree" seem a good option to represent a lineage?
- Can we use the classical phylogenetic tree reconstruction algorithms for the B cell lineage? Why? What are the particularities of the B cell lineage trees?
- What are the different steps of the Clonaltree algorithm?
- What is the originality of the clonaltree method?

Write a reflection note answering these questions.

Brenda, Ekaterina, Bon courage!