

Darwin's inheritance

Modern evolutionary research from a mathematical point of view

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Target Session(s): Genome evolution

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In my talk, I will briefly sketch the development of evolutionary research from Darwin till today. Basically, there are two main aims in phylogenetic research: The reconstruction of evolutionary relationships between different species, which are often represented by a tree, as well as the reconstruction of ancestral sequences (as normally only data for present-day species are given). Both of them are based on the idea that a common ancestor evolved into multiple species today, which assumes a combination of various random processes like speciation to form the tree and mutations along the tree. Biomathematicians try to find ways to reconstruct precisely these processes.

While Darwin was still strongly dependent on morphological data for his evolutionary research, the abundance of DNA, RNA and protein data requires mathematical methods in order to infer the correct tree. Several methods and criteria can be used to solve this problem, and I will introduce three basic concepts in my talk and also discuss their typical drawbacks, like statistical inconsistency. I will also present some modern-day challenges like how to extend the traditional tree based methods to non-treelike data (i.e. phylogenetic networks that can represent hybridisation or horizontal gene transfer).

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