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Inferring population history from DNA sequences: Methods, models and challenges. And spatial statistics?

I plan to discuss basic methodology and recent results for inferring the population history of humans and other species. Population history has traditionally been inferred from the site frequency spectrum, but in recent years methods based on complete genomic sequences have emerged. These methods are based on the coalescent process with mutation and recombination. I also plan to talk about model checking. In particular I will draw attention to connections between summaries of mutation patterns in genomics and point processes in spatial statistics.