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Statistical Models of Adaptive Immune populations ZACHARY SETHNA, CURTIS CALLAN, Princeton University, ALEKSANDRA WALCZAK, THIERRY MORA, Ecole Normale Supérieure — The availability of large (10^4 - 10^6 sequences) datasets of B or T cell populations from a single individual allows reliable fitting of complex statistical models for naïve generation, somatic selection, and hypermutation. It is crucial to utilize a probabilistic/informational approach when modeling these populations. The inferred probability distributions allow for population characterization, calculation of probability distributions of various hidden variables (e.g. number of insertions), as well as statistical properties of the distribution itself (e.g. entropy). In particular, the differences between the T cell populations of embryonic and mature mice will be examined as a case study. Comparing these populations, as well as proposed mixed populations, provides a concrete exercise in model creation, comparison, choice, and validation.

Zachary Sethna
Princeton University

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