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Statistical Models of Adaptive Immune populations ZACHARY
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THIERRY MORA, Ecole Normale Supérieure — The availability of large (10⁴-10⁶
sequences) datasets of B or T cell populations from a single individual allows re-
liable 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 hid-
den 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. Com-
paring these populations, as well as proposed mixed populations, provides a concrete
exercise in model creation, comparison, choice, and validation.

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