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This work reflects sixteen hours of lectures delivered by the author at the 2009 St Flour summer school in probability. It provides a rapid introduction to a range of mathematical models that have their origins in theoretical population genetics. The models fall into two classes: forwards in time models for the evolution of frequencies of different genetic types in a population; and backwards in time (coalescent) models that trace out the genealogical relationships between individuals in a sample from the population. Some, like the classical Wright-Fisher model, date right back to the origins of the subject. Others, like the multiple merger coalescents or the spatial Lambda-Fleming-Viot process are much more recent. All share a rich mathematical structure. Biological terms are explained, the models are carefully motivated and tools for their study are presented systematically.