



THE UNIVERSITY
OF QUEENSLAND
AUSTRALIA

School of
Biomedical Sciences

ESTIMATES OF EFFECTIVE POPULATION SIZE (N_E) IN THE GENOMICS ERA

Effective population size (N_e) is the evolutionary analogue to census size (N). Whereas ecological/demographic processes such as competition, predation, and population dynamics depend primarily on N , evolutionary processes such as the rate of loss of genetic variability and the relative influence of natural selection and genetic drift depend on N_e . Because collecting the detailed life-history information necessary to calculate N_e directly is hard, genetic methods to estimate N_e are widely used. We are now firmly in the genomics era, which presents both promises and challenges for estimation of N_e . Join me as I discuss ways to deal with these challenges presented by genomics-scale datasets. I will also show that, for the growing subset of species for which detailed information about gene architecture is available, knowledge about linkage relationships can be leveraged to provide a window into the past, in the form of a time-series of estimates of N_e that extend back in time for tens, hundreds, or even thousands of generations.

Seminar details

Speaker: Robin Waples,
NOAA Fisheries, Seattle WA, USA

Date: 11 April 2017

Time: 12:00pm till 1:00pm

Venue: Building 68 room 214

