**Exercise using the Wright-Fisher application**

**Purpose**: The purpose of this exercise is to illustrate the Coalescent process with various extensions in the discrete as well as the continuous form.

Download and open the Wright-Fisher application from [www.coalescent.dk](http://www.coalescent.dk/). It is developed by Anders M. Mikkelsen, Jotun Hein and Mikkel Schierup

It is possible to use the Wright-Fisher animator to follow the reproduction process forward in time and the coalescent process backwards in time one generation at a time. After you have followed the reproduction process a number of generations forwards in time it is possible to “untangle” the genealogy, and then to follow both how many descendants each of the original genes leave over generations (click on upper row), and to follow the ancestors to the sequence in the bottom row (by pressing the circles in the bottom row).

A new simulation is done by setting the parameters and pressing the **new** bottom. The simulation can then be controlled by the buttons in the bottom (right) part of the window, e.g. one generation at a time. One button enables you to untangle the resulting genealogy (i.e. rearranging individuals so that lines do not cross).

1. Try to set **N**=number of genes=10, and **G**=number of generations=15.
   * Forward in time: How many generations does each of the initial genes persist in the population?
     1. What is the mean and the variance in the number of descendants of a given gene?
   * Backwards in time (coalescence). Do all the genes coalesce within this time span?
     1. If so, what is the number of generations to coalescence of the sample?
     2. If not, how many ancestors are there and how large part of the sample are they ancestors to
     3. What would you have expected from theory?
   * Try to repeat this exercise 5 times writing down the number of ancestors and the time to coalescence. This should give you an idea about the variance of the process.
     1. How does the variance in time change when you go from 3 to 2 ancestors compared to going from 2 to 1 ancestor? What do you expect from theory?

1. Try the exercise above with 3 different values of **N** and adjust **G** if necessary. How does the time to coalescence scale with **N**?