



Software

[Users please register](#)

structure

The program *structure* is a free software package for using multi-locus genotype data to investigate population structure. Its uses include inferring the presence of distinct populations, assigning individuals to populations, studying hybrid zones, identifying migrants and admixed individuals, and estimating population allele frequencies in situations where many individuals are migrants or admixed. It can be applied to most of the commonly-used genetic markers, including microsatellites, RFLPs and SNPs. This method was described in an article in *Genetics* 2000 (155: 945-959). [[Abstract](#)], [[Manuscript](#)], [[Example](#)]. [["Time-lapse" plots](#)].

[Download Structure version 2.1](#)

- **NewHybrids**. This implements a Gibbs sampler to estimate the posterior probability that genetically sampled individuals fall into each of a set of user-defined hybrid categories. The method is described in **Anderson, E.C.** and **Thompson, E.A.** (2002) A model-based method for identifying species hybrids using multilocus genetic data. *Genetics* 160: 1217--1229. [[abstract](#)] [[reprint in pdf \(232 K\)](#)].

- A new release is available April 7, 2003. Version 1.1 Beta 3. This has a number of new features including expanded AFLP support, options for specifying species origins of select individuals, facilities for setting allele frequency priors, a non-graphical user interface version, etc. Download the documentation below for more info.



This program uses my GFMCMC visualization library. Click on the icon to see a full-size screen shot.

Program	Platform/Description	Size	Download
VERSION			

BayesAss+ : Bayesian Estimation of Recent Migration Rates Using Multilocus Genotypes.

Version 1.1 Release Date 8 May 2003. Note: This release fixes a bug in version 1.01 that would cause underflows (and program crashes) when using the Windows version.

[Linux](#)|[Mac OS X](#)|[Windows](#)|[Source Code](#)|[Documentation](#)|[Input File](#)

Reference: G.A. Wilson and **B. Rannala** 2003. Bayesian inference of recent migration rates using multilocus genotypes. *Genetics* 163: 1177-1191. [Reprint\(PDF format for Adobe Acrobat\)](#)

Important Message (May 8, 2003): All non-Windows distributions are currently command line, but we are developing a Java GUI that will be available for all platforms within the next month.