

# ANGSD-wrapper: utilities for analyzing next generation sequencing data

Arun Durvasula<sup>1,†</sup>, Paul J. Hoffman<sup>2,†</sup>, Tyler V. Kent<sup>1</sup>, Chaochih Liu<sup>2</sup>, Thomas J. Y.  
Kono<sup>2</sup>, Peter L. Morrell<sup>2</sup> and Jeffrey Ross-Ibarra<sup>1,3,\*</sup>

<sup>1</sup>Department of Plant Sciences, University of California, Davis, CA 95616

<sup>2</sup>Department of Agronomy and Plant Genetics, University of Minnesota, St. Paul, MN  
55108

<sup>3</sup>Center for Population Biology and Genome Center, University of California, Davis, CA  
95616

<sup>†</sup>These authors contributed equally.

<sup>\*</sup>email: rossibarra@ucdavis.edu

April 29, 2016

Running head: ANGSD-wrapper

Keywords: software, visualization, *Zea*, domestication, population genetics

## Abstract

High throughput sequencing has changed many aspects of population genetics, molecular ecology, and related fields, affecting both experimental design and data analysis. The software package ANGSD allows users to perform a number of population genetic analyses on high-throughput sequencing data. ANGSD uses probabilistic approaches to calculate genome-wide descriptive statistics. The package makes use of genotype likelihood estimates rather than SNP calls and is specifically designed to produce more accurate results for samples with low sequencing depth. ANGSD makes use of full genome data while handling a wide array of sampling and experimental designs. Here we present ANGSD-wrapper, a set of wrapper scripts that provide a user-friendly interface for running ANGSD and visualizing results. ANGSD-wrapper supports multiple types of analyses including estimates of nucleotide sequence diversity and performing neutrality tests, principal component analysis, estimation of admixture proportions for individuals samples, and calculation of statistics that quantify recent introgression. ANGSD-wrapper also provides interactive graphing of ANGSD results to enhance data exploration. We demonstrate the usefulness of ANGSD-wrapper by analyzing resequencing data from populations of wild and domesticated *Zea*. ANGSD-wrapper is freely available from <https://github.com/mojaveazure/angsd-wrapper>.

## Introduction

High throughput sequencing has revolutionized evolutionary genetics, allowing researchers to quickly assay large numbers of individuals and interrogate genome-wide variation. Application of these approaches has led to changes in both experimental design and data analysis (Ekblom and Galindo, 2011). Many popular software packages used by researchers for analysis of comparative resequencing data (see Excoffier and Heckel, 2006) were not designed to handle these novel data types or efficiently analyze the large volumes of data now being generated. Despite the decreasing cost of sequencing, researchers must nonetheless allocate finite resources and balance the depth of sequencing and the breadth of a sample. This poses a challenge for population genetics analysis, which generally requires accurate polymorphism calls in a broad sample (Felsenstein, 2006; Pluzhnikov and Donnelly, 1996). While these experimental design challenges in molecular population genetic studies have existed for at least two decades, high throughput sequencing brings the added technical challenges of highly variable coverage, missing data, and high per-nucleotide error rates.

A number of tools have recently been published to estimate population genetic descriptive statistics using high throughput sequencing data (Danecek et al., 2011; Garrigan, 2013; Hutter et al., 2006; Purcell et al., 2007). Korneliussen et al. (2014) recently published the software package ANGSD, which enables users to flexibly perform a large number of common population genetic analyses, including estimation of diversity statistics, admixture analysis including Patterson’s D statistic (Durand et al., 2011), site

frequency spectrum estimation (Nielsen et al., 2012), and calculation of neutrality test statistics (Korneliusson et al., 2013). ANGSD works directly with the alignment formats produced from standard high throughput sequence analysis pipelines, which removes the need for the user to transform the data into a niche format. One of the most important features of ANGSD is that analyses are integrated over per-site genotype likelihoods, rather than only on pre-determined variable sites. This permits ANGSD to calculate common population genetic descriptive statistics on low-coverage sequencing data, and handle missingness due to variation in coverage. Further, this probabilistic framework is appealing to researchers studying non-model organisms where the lack of existing genomic resources or funding prevents the ability to obtain high quality data. Additionally, for many of these non-model organisms, existing tools are not able to take into account biological differences such as non-random mating into their statistical models. Recent use of ANGSD in the study of non-model organisms such as the blue-eyed black lemur (Meyer et al., 2015) and *Ficedula* flycatchers (Burri et al., 2015) has allowed population genetic analysis despite using low coverage resequencing data.

Here we present ANGSD-wrapper, a user-friendly interface to ANGSD. ANGSD-wrapper takes the form of a set of configuration files and wrapper scripts (Figure S1) that streamline the execution of multi-step pipelines required for data analysis in ANGSD. ANGSD-wrapper also eases the configuration of ANGSD-related programs such as ngsTools (Fumagalli et al., 2014), ngsF (Vieira et al., 2013), ngsAdmix (Skotte et al., 2013), and PCA (Fumagalli et al., 2013). As in ANGSD, ANGSD-wrapper allows users to perform whole genome analysis or analyze a set of user-defined windows across the genome. The wrapper scripts are written against a frozen versions of ANGSD (v [INSERT VERSION]) and supporting tools for consistency of analysis. Because the large volume of data associated with high throughput sequence analysis is often difficult to visualize, ANGSD-wrapper also provides a suite of interactive visualization tools to plot results and explore patterns at multiple scales. We demonstrate some of the analyses possible using ANGSD-wrapper when applied to low-coverage resequencing using data from domesticated maize and two related wild teosinte subspecies. ANGSD-wrapper is freely available from <https://github.com/mojaveazure/angsd-wrapper>.

## Methods

ANGSD-wrapper is a set of configuration files and scripts written primarily in the Bash scripting language. The scripts can be run either on a standalone computer with a UNIX terminal, or on computing clusters where they can be submitted to a queuing system such as SGE (Gentzsch, 2001), Slurm (Jette et al., 2002) or TORQUE (Staples, 2006). A Python installation (van Rossum, 2016) is required for some light, dynamic pre-processing of the data, and the statistical software R (R Core Team, 2014) is required to make use of the visualization tools incorporated in ANGSD-wrapper. The visualization portion of

Table 1: Table of methods implemented in ANGSD-wrapper

Method	Calculations	Interactive Graphing
SFS	Site frequency spectrum	Yes
2DSFS	Joint site frequency spectrum, $F_{ST}$	Yes
ABBA/BABA	Patterson’s D statistic	Yes
Ancestral	Extract ancestral sequence from BAM file	No
Genotypes	Genotype likelihood estimations	No
PCA	Principal component analysis	Yes
Thetas	Diversity statistics ( $\theta_w$ , $\theta_\pi$ , Fu and Li’s $\theta$ , Fay’s $\theta$ ) and neutrality tests (Tajima’s D, Fu and Li’s D, Fu and Li’s F, Fay and Wu’s H, Zeng’s E )	Yes
Inbreeding	Calculate per-individual inbreeding coefficients with ngsF	No
Admixture	Perform admixture analysis	Yes

ANGSD-wrapper also requires installation of the R packages **Shiny** (Chang et al., 2015), **APE** (Paradis et al., 2004), **Lattice** (Sarkar, 2008), **Hmisc** (Jr et al., 2015), **data.table** (Dowle et al., 2015), **DT** (Xie, 2015), and **shinythemes** (Chang, 2015), as well as **genomeIntervals** (Gagneur et al., 2015) from Bioconductor (Huber et al., 2015). These dependent packages are installed automatically upon first run of the visualization interface.

ANGSD-wrapper is divided into scripts associated with analytical approaches implemented in ANGSD and associated software. It provides a common configuration file, **Common.Config**, which holds variables that are likely to remain constant across analyses, including identifiers for chromosomal regions and the paths to project directories. In ANGSD-wrapper, each method is self-contained in a shell script which uses information from the common configuration file and a method-specific configuration file. Each analysis is run using a simple command:

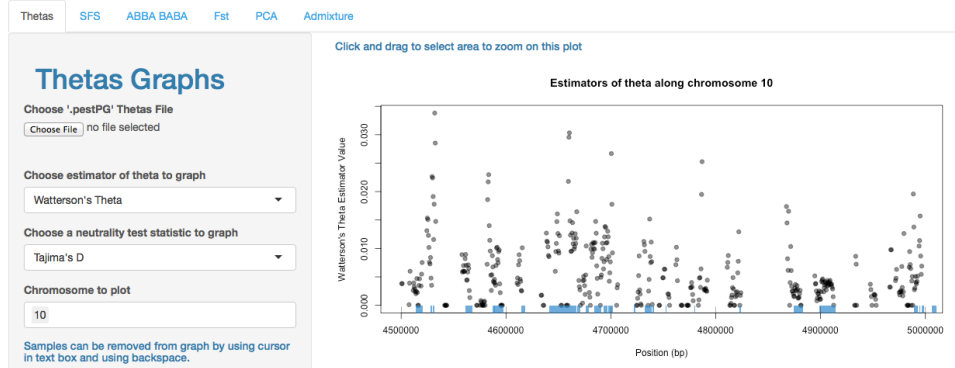
```
$ angsd-wrapper <method> <configuration_file>
```

Analyses supported by ANGSD-wrapper are shown in Table 1. A detailed flowchart of each of these workflows is shown in Figure S1, and additional details, documentation, a tutorial, and a wiki can be found on the GitHub page: <https://github.com/mojaveazure/angsd-wrapper/wiki>.

The visualization software included with ANGSD-wrapper is contained in a directory called ‘shiny-Graphing.’ This application is started from within ANGSD-wrapper and launched locally from a standard web browser. This software provides a graphical user interface (GUI) to quickly and interactively plot results obtained from ANGSD-wrapper. Each tab in the GUI contains plots for different ANGSD methods. In order to use the plotting software, the user navigates to the desired tab and uploads the appropriate

Figure 1: Visualization of Watterson's  $\theta$  estimated by ANGSD across a 1.5Mb region of chromosome 10 in *Zea mays* ssp. *mays* using ANGSD-wrapper. Darker colors indicate a higher density of points. Blue boxes indicate gene annotations provided by a GFF file.

#### ANGSD-wrapper graph



results file. The Shiny server automatically parses ANGSD output files and creates the resulting plot(s) (Figure 1), which can be saved using the browser's built-in image saving capabilities.

## Results and Discussion

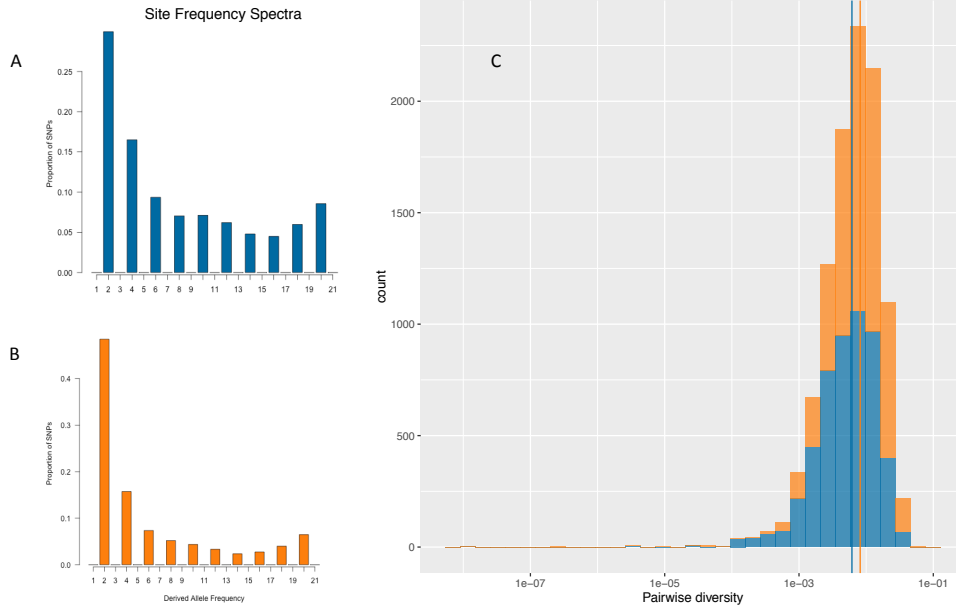
As a demonstration of analyses in ANGSD-wrapper, we explore patterns of pairwise nucleotide diversity in a single genomic region of domesticated maize and wild teosinte. We used a subset of the resequenced samples from the Maize HapMap2 project (Table S1) and calculated summary statistics using a 10Mb region on chromosome 10 (Chia et al., 2012). The data are available at [https://figshare.com/articles/Example\\_Data\\_tar\\_bz2/2063442](https://figshare.com/articles/Example_Data_tar_bz2/2063442) and can be downloaded from within ANGSD-wrapper using the command

```
$ angsd-wrapper setup data
```

In the following we refer to methods listed in Table 1 when describing analyses.

We first use the “SFS” method to estimate the site frequency spectrum (SFS) of both maize and its wild progenitor *Zea mays* ssp. *parviglumis*, assuming an inbreeding coefficient of  $F = 1$  for these highly inbred samples. The SFS and diversity statistics were calculated using ancestral states inferred by the “Ancestral Sequence” method from a single resequenced genome of *Tripsacum dactyloides*. We show that the maize SFS is skewed towards more intermediate-frequency variants (Figure 2A-B, Tajima's D of 0.2 and 0.0085 in maize and teosinte, respectively), likely a result of the bottleneck associated with maize domestication (Beissinger et al., 2015; Eyre-Walker et al., 1998). Using the “Thetas” method we find further evidence of the domestication bottleneck, with mean levels of pairwise nucleotide diversity in this region in maize  $\approx 25\%$  lower than in teosinte (0.0061 and 0.0082, respectively; Figure 2C). Using the “2DSFS method,” which includes an  $F_{ST}$  calculation, we find a mean  $F_{ST}$  in this region of 0.116, nearly

Figure 2: Summary statistics for *Zea mays*. Derived site frequency spectra for A. maize and B. teosinte. C. distribution of pairwise nucleotide diversity for maize (blue) and teosinte (orange). Mean values for each taxon are represented by corresponding vertical lines. Pairwise nucleotide diversity results are visualized separately from the interactive graphics and colors were added to A and B using a custom script.



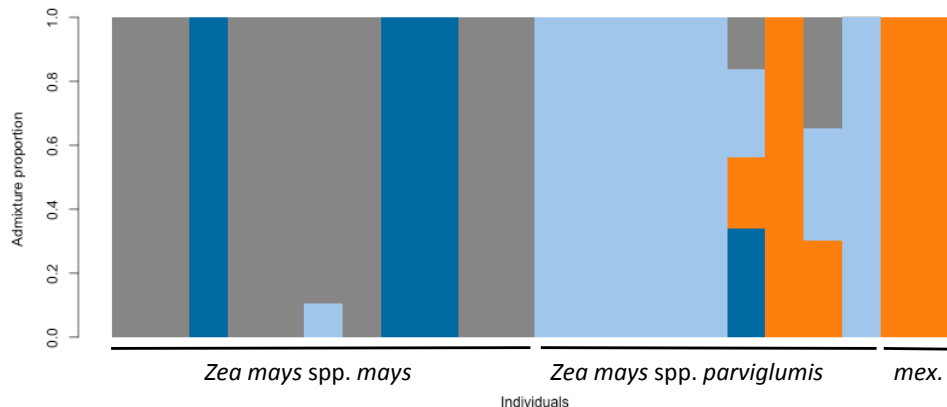
identical to the genome-wide value of 0.11 reported in Hufford et al. (2012). None of the genes in this region have been identified as potential domestication candidates Hufford et al. (2012), consistent with the lack of extended regions of high  $F_{ST}$  in our analysis (Figure S3).

Finally, we include two samples of the related wild teosinte *Zea mays* ssp. *mexicana* to assess evidence for admixture. We ran the “Admixture” method, which implements an estimate of admixture proportion from genotype likelihoods (Skotte et al., 2013). We identify structure within domesticated maize separating three high-latitude temperate landraces from the other tropical accessions (Figure 3). *Zea mays* ssp. *mexicana* clusters into its own group (orange), along with a single accession of ssp. *parviglumis* collected from a region in which many teosinte populations appear to be the result of admixture between the two subspecies (Fang et al., 2012). Consistent with an independent analysis from SNP genotyping (Hufford et al., 2013), the lowland maize samples included here show no evidence of admixture with ssp. *mexicana*. Most ssp. *parviglumis* accessions fall primarily into a single (light blue) cluster, but two accessions show assignment to multiple clusters, perhaps due to the limited resolution resulting from analysis of a single genomic region and restricted geographic sampling.

## Conclusions

ANGSD-wrapper provides an easy-to-use interface that simplifies many population genetic analyses implemented in ANGSD (Korneliussen et al., 2014) and permits the exploration of genome-scale results

Figure 3: Admixture analysis for *Zea mays* ssp. *mays*, *Zea mays* ssp. *parviglumis*, and *Zea mays* ssp. *mexicana* (*mex*). Colors represent the proportion of each individual's genome assigned to one of the  $K=4$  source populations. Individuals are shown in the same order as Table S1. For results using other values of  $K$  see Figure S2.



through interactive visualization. ANGSD-wrapper is under active development to incorporate updates to the ANGSD software package.

## Acknowledgments

We acknowledge funding support from the US National Science Foundation (IOS-1238014 to JRI and IOS-1339393 to PLM), from a University of Minnesota Doctoral Dissertation Fellowship supporting TJYK, and from the University of California Davis Plant Sciences Department. We thank members of the Ross-Ibarra and Morrell Labs for discussion and software testing. We thank the authors of ANGSD and related programs for answering questions, particularly Matteo Fumagalli and Filipe Vieira. Finally, we would like to thank Felix Andrews for statistical advice, although we did not follow it.

## References

- Beissinger, T. M., Wang, L., Crosby, K., Durvasula, A., Hufford, M. B., and Ross-Ibarra, J. (2015). Recent demography drives changes in linked selection across the maize genome. *bioRxiv*.
- Burri, R., Nater, A., Kawakami, T., Mugal, C. F., Olason, P. I., Smeds, L., Suh, A., Dutoit, L., Bureš, S., Garamszegi, L. Z., et al. (2015). Linked selection and recombination rate variation drive the evolution of the genomic landscape of differentiation across the speciation continuum of ficedula flycatchers. *Genome research*, 25(11):1656–1665.
- Chang, W. (2015). *shinythemes: Themes for Shiny*. R package version 1.0.1.
- Chang, W., Cheng, J., Allaire, J., Xie, Y., and McPherson, J. (2015). *shiny: Web Application Framework for R*. R package version 0.11.1.
- Chia, J.-M., Song, C., Bradbury, P. J., Costich, D., de Leon, N., Doebley, J., Elshire, R. J., Gaut, B., Geller, L., Glaubitz, J. C., et al. (2012). Maize hapmap2 identifies extant variation from a genome in flux. *Nature Genetics*, 44(7):803–807.
- Danecek, P., Auton, A., Abecasis, G., Albers, C. A., Banks, E., DePristo, M. A., Handsaker, R. E., Lunter, G., Marth, G. T., Sherry, S. T., et al. (2011). The variant call format and vcftools. *Bioinformatics*, 27(15):2156–2158.
- Dowle, M., Srinivasan, A., Short, T., with contributions from R Saporta, S. L., and Antonyan, E. (2015). *data.table: Extension of Data.frame*. R package version 1.9.6.
- Durand, E. Y., Patterson, N., Reich, D., and Slatkin, M. (2011). Testing for ancient admixture between closely related populations. *Molecular Biology and Evolution*, 28(8):2239–2252.
- Eklblom, R. and Galindo, J. (2011). Applications of next generation sequencing in molecular ecology of non-model organisms. *Heredity*, 107(1):1–15.
- Excoffier, L. and Heckel, G. (2006). Computer programs for population genetics data analysis: a survival guide. *Nature Reviews Genetics*, 7(10):745–758.
- Eyre-Walker, A., Gaut, R. L., Hilton, H., Feldman, D. L., and Gaut, B. S. (1998). Investigation of the bottleneck leading to the domestication of maize. *Proceedings of the National Academy of Sciences*, 95(8):4441–4446.
- Fang, Z., Pyhäjärvi, T., Weber, A. L., Dawe, R. K., Glaubitz, J. C., González, J. d. J. S., Ross-Ibarra, C., Doebley, J., Morrell, P. L., and Ross-Ibarra, J. (2012). Megabase-scale inversion polymorphism in the wild ancestor of maize. *Genetics*, 191(3):883–894.
- Felsenstein, J. (2006). Accuracy of coalescent likelihood estimates: do we need more sites, more sequences, or more loci? *Molecular biology and evolution*, 23(3):691–700.
- Fumagalli, M., Vieira, F. G., Korneliussen, T. S., Linderöth, T., Huerta-Sánchez, E., Albrechtsen, A., and Nielsen, R. (2013). Quantifying population genetic differentiation from next-generation sequencing data. *Genetics*, 195(3):979–992.
- Fumagalli, M., Vieira, F. G., Linderöth, T., and Nielsen, R. (2014). ngstools: methods for population genetics analyses from next-generation sequencing data. *Bioinformatics*, 30(10):1486–1487.
- Gagneur, J., Toedling, J., Bourgon, R., and Delhomme, N. (2015). *genomeIntervals: Operations on genomic intervals*. R package version 1.22.1.
- Garrigan, D. (2013). Popbam: tools for evolutionary analysis of short read sequence alignments. *Evolutionary Bioinformatics Online*, 9:343.
- Gentzsch, W. (2001). Sun grid engine: Towards creating a compute power grid. In *Proceedings of the 1st International Symposium on Cluster Computing and the Grid*, CCGRID '01, pages 35–, Washington, DC, USA. IEEE Computer Society.



- Huber, W., Carey, J., V., Gentleman, R., Anders, S., Carlson, M., Carvalho, S., B., Bravo, C., H., Davis, S., Gatto, L., Girke, T., Gottardo, R., Hahne, F., Hansen, D., K., Irizarry, A., R., Lawrence, M., Love, I., M., MacDonald, J., Obenchain, V., Ole's, K., A., Pag'es, H., Reyes, A., Shannon, P., Smyth, K., G., Tenenbaum, D., Waldron, L., Morgan, and M. (2015). Orchestrating high-throughput genomic analysis with Bioconductor. *Nature Methods*, 12(2):115–121.
- Hufford, M. B., Lubinsky, P., Pyhäjärvi, T., Devengenzo, M. T., Ellstrand, N. C., and Ross-Ibarra, J. (2013). The genomic signature of crop-wild introgression in maize. *PLoS Genetics*.
- Hufford, M. B., Xu, X., Van Heerwaarden, J., Pyhäjärvi, T., Chia, J.-M., Cartwright, R. A., Elshire, R. J., Glaubitz, J. C., Guill, K. E., Kaeppler, S. M., et al. (2012). Comparative population genomics of maize domestication and improvement. *Nature Genetics*, 44(7):808–811.
- Hutter, S., Vilella, A. J., and Rozas, J. (2006). Genome-wide dna polymorphism analyses using variscan. *BMC Bioinformatics*, 7(1):409.
- Jette, M. A., Yoo, A. B., and Grondona, M. (2002). Slurm: Simple linux utility for resource management. In *In Lecture Notes in Computer Science: Proceedings of Job Scheduling Strategies for Parallel Processing (JSSPP) 2003*, pages 44–60. Springer-Verlag.
- Jr, F. E. H., with contributions from Charles Dupont, and many others. (2015). *Hmisc: Harrell Miscellaneous*. R package version 3.17-1.
- Korneliussen, T., Moltke, I., Albrechtsen, A., and Nielsen, R. (2013). Calculation of tajima's d and other neutrality test statistics from low depth next-generation sequencing data. *BMC Bioinformatics*, 14(1):289.
- Korneliussen, T. S., Albrechtsen, A., and Nielsen, R. (2014). Angsd: analysis of next generation sequencing data. *BMC Bioinformatics*, 15(1):356.
- Meyer, W. K., Venkat, A., Kermany, A. R., de Geijn, B., Zhang, S., and Przeworski, M. (2015). Evolutionary history inferred from the de novo assembly of a nonmodel organism, the blue-eyed black lemur. *Molecular ecology*, 24(17):4392–4405.
- Nielsen, R., Korneliussen, T., Albrechtsen, A., Li, Y., and Wang, J. (2012). SNP calling, genotype calling, and sample allele frequency estimation from New-Generation Sequencing data. *PLoS ONE*, 7(7):e37558.
- Paradis, E., Claude, J., and Strimmer, K. (2004). APE: analyses of phylogenetics and evolution in R language. *Bioinformatics*, 20:289–290.
- Pluzhnikov, A. and Donnelly, P. (1996). Optimal sequencing strategies for surveying molecular genetic diversity. *Genetics*, 144(3):1247–1262.
- Purcell, S., Neale, B., Todd-Brown, K., Thomas, L., Ferreira, M. A., Bender, D., Maller, J., Sklar, P., De Bakker, P. I., Daly, M. J., et al. (2007). Plink: a tool set for whole-genome association and population-based linkage analyses. *The American Journal of Human Genetics*, 81(3):559–575.
- R Core Team (2014). *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna, Austria.
- Sarkar, D. (2008). *Lattice: Multivariate Data Visualization with R*. Springer, New York. ISBN 978-0-387-75968-5.
- Skotte, L., Korneliussen, T. S., and Albrechtsen, A. (2013). Estimating Individual Admixture Proportions from Next Generation Sequencing Data. *Genetics*.
- Staples, G. (2006). Torque resource manager. In *Proceedings of the 2006 ACM/IEEE Conference on Supercomputing*, SC '06, New York, NY, USA. ACM.
- van Rossum, G. (2016). Python. <https://www.python.org>. Accessed: 2016-01-27.

Table S1: Table of samples used in analysis with mean depth over the region 15000000-25000000 on chromosome 10.

Sample	Mean Depth	Species
BKN009	7.00194	<i>Zea mays</i> spp. <i>mays</i>
BKN011	6.9777	<i>Zea mays</i> spp. <i>mays</i>
BKN014	6.78829	<i>Zea mays</i> spp. <i>mays</i>
BKN015	3.739	<i>Zea mays</i> spp. <i>mays</i>
BKN019	3.71944	<i>Zea mays</i> spp. <i>mays</i>
BKN022	3.71268	<i>Zea mays</i> spp. <i>mays</i>
BKN025	3.53799	<i>Zea mays</i> spp. <i>mays</i>
BKN026	3.91798	<i>Zea mays</i> spp. <i>mays</i>
BKN027	7.05576	<i>Zea mays</i> spp. <i>mays</i>
BKN033	3.85336	<i>Zea mays</i> spp. <i>mays</i>
BKN035	3.74839	<i>Zea mays</i> spp. <i>mays</i>
TIL01	3.60133	<i>Zea mays</i> spp. <i>parviglumis</i>
TIL03	4.07518	<i>Zea mays</i> spp. <i>parviglumis</i>
TIL04	6.09163	<i>Zea mays</i> spp. <i>parviglumis</i>
TIL07	5.11419	<i>Zea mays</i> spp. <i>parviglumis</i>
TIL09	5.29004	<i>Zea mays</i> spp. <i>parviglumis</i>
TIL11	3.15477	<i>Zea mays</i> spp. <i>parviglumis</i>
TIL15	6.87873	<i>Zea mays</i> spp. <i>parviglumis</i>
TIL16	2.67186	<i>Zea mays</i> spp. <i>parviglumis</i>
TIL17	2.61892	<i>Zea mays</i> spp. <i>parviglumis</i>
TIL08	6.09453	<i>Zea mays</i> ssp. <i>mexicana</i>
TIL25	13.1566	<i>Zea mays</i> ssp. <i>mexicana</i>
TDD39103	8.62	<i>Tripsacum dactyloides</i>

237 Vieira, F. G., Fumagalli, M., Albrechtsen, A., and Nielsen, R. (2013). Estimating inbreeding coeffi-  
238 cients from ngs data: Impact on genotype calling and allele frequency estimation. *Genome Research*,  
239 23(11):1852–1861.

240 Xie, Y. (2015). *DT: A Wrapper of the JavaScript Library 'DataTables'*. R package version 0.1.

Figure S1: Workflow diagram for all methods available in ANGSD-wrapper.

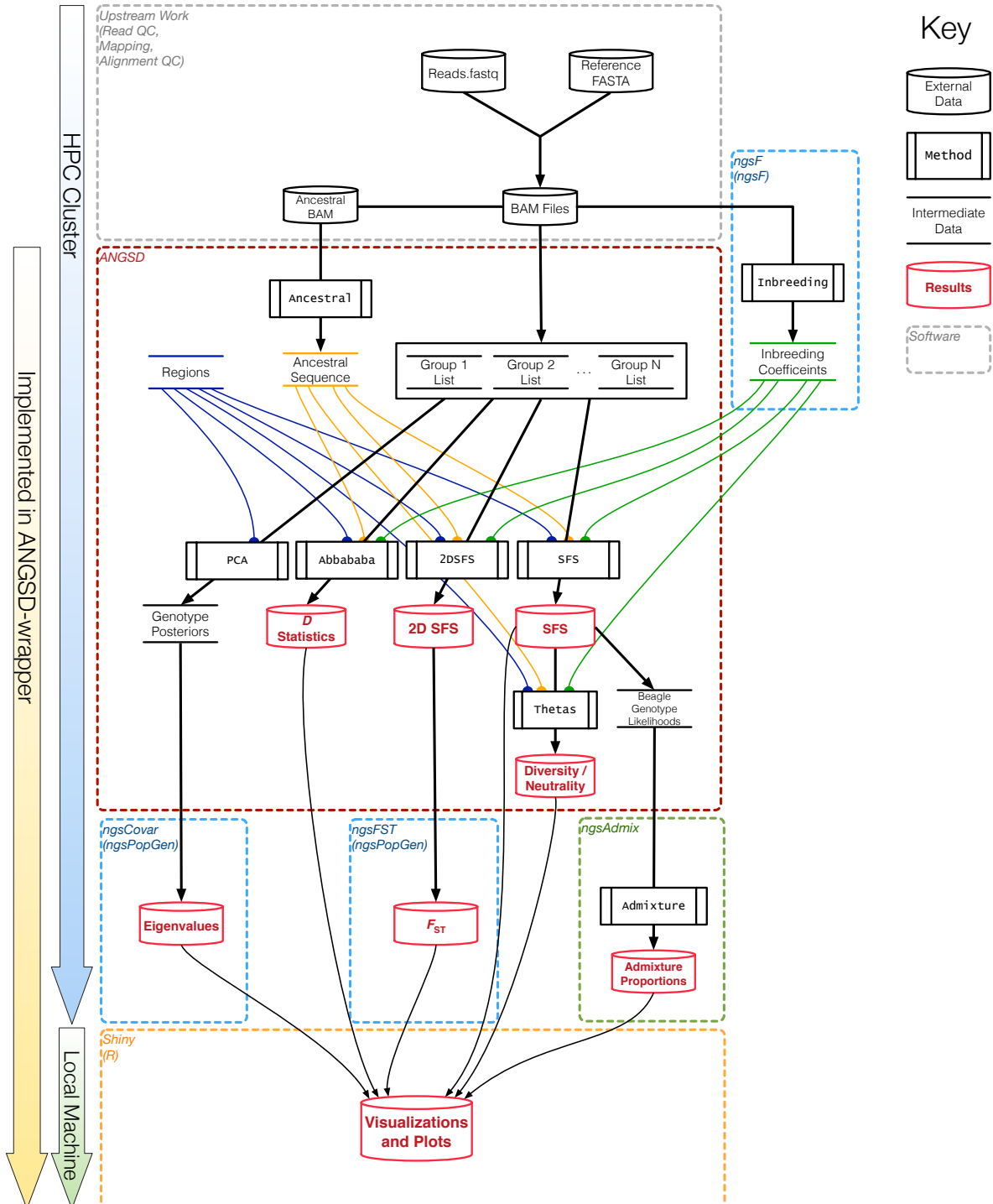


Figure S2: Admixture analysis for K=2 (top), K=3 (middle), and K=4 (bottom).

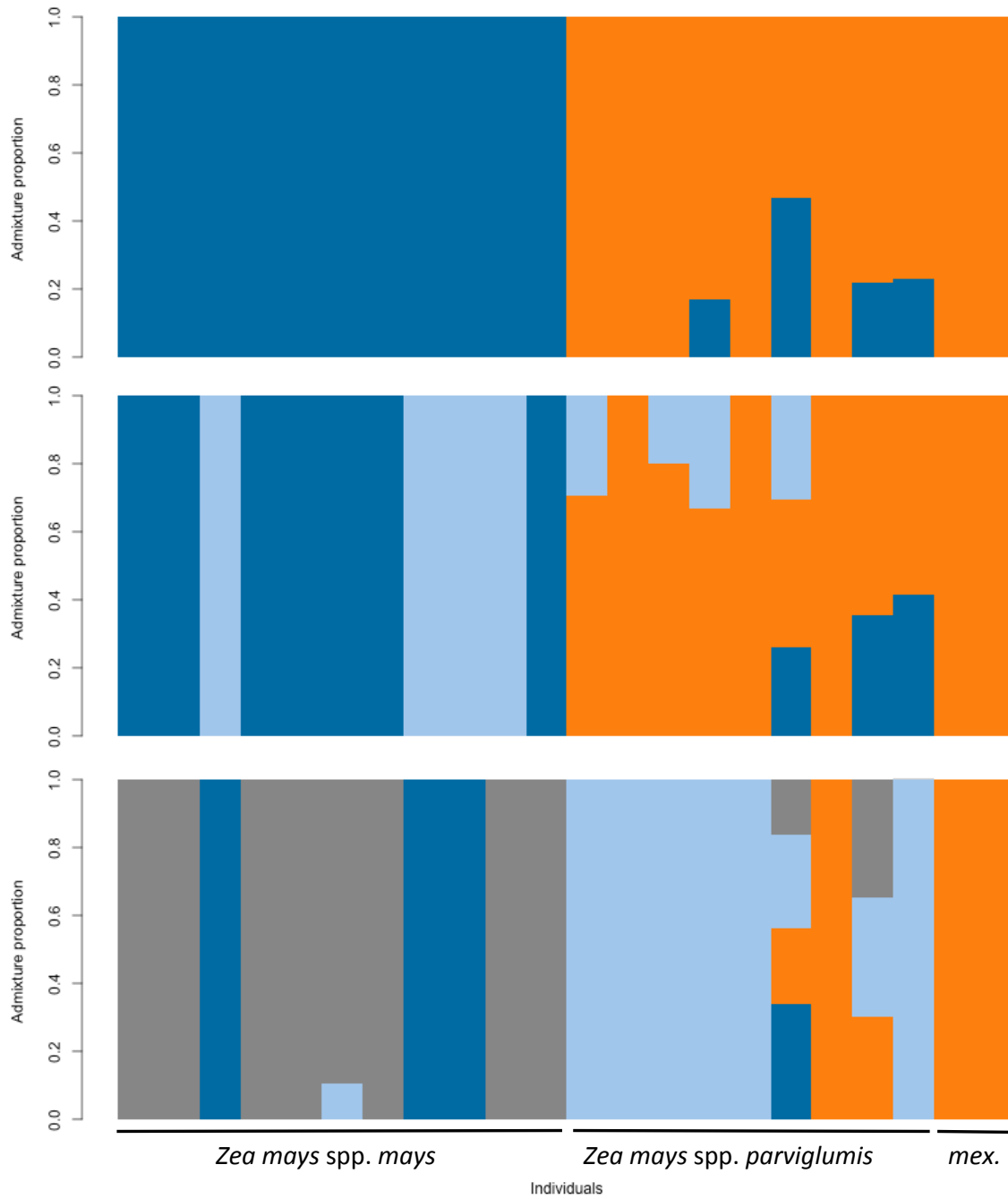


Figure S3:  $F_{ST}$  values plotted against base pair position on chromosome 10 of maize.  $F_{ST}$  is calculated between the maize and teosinte samples.

