Cygwin cheat sheet

<http://www.voxforge.org/home/docs/cygwin-cheat-sheet>

install git on cygwin

<http://www.celinio.net/techblog/?p=818>

Download vcftools

<https://github.com/vcftools/vcftools>

install/ get started with vcftools

<http://vcftools.sourceforge.net/examples.html>

manuals

C++

<https://vcftools.github.io/documentation.html>

full man

<https://vcftools.github.io/man_latest.html>

PERL man

<https://vcftools.github.io/perl_module.html>

PERL examples

<https://vcftools.github.io/perl_examples.html>

Quirks of GWAS

<http://massgenomics.org/2014/03/gwas-sequencing-realities.html>

BigRR input:

<https://cran.r-project.org/web/packages/bigRR/bigRR.pdf>

y = a binary vector of phenotype for each of (96) lines = response variable

Z is a (96) x N matrix of genotypes (N is SNPs) for each line = shrinkage parameters (i.e. random effects in the mixed model framework); not required if model formula is used.

Practice data set is from Suzi’s 2010 Nature paper

X = optional design matrix related to the parameters not to be shrunk (i.e. fixed effects in the mixed model framework); not required if formula is already used.

<http://www.genetics.org/content/genetics/193/4/1255.full.pdf>

bigRR paper