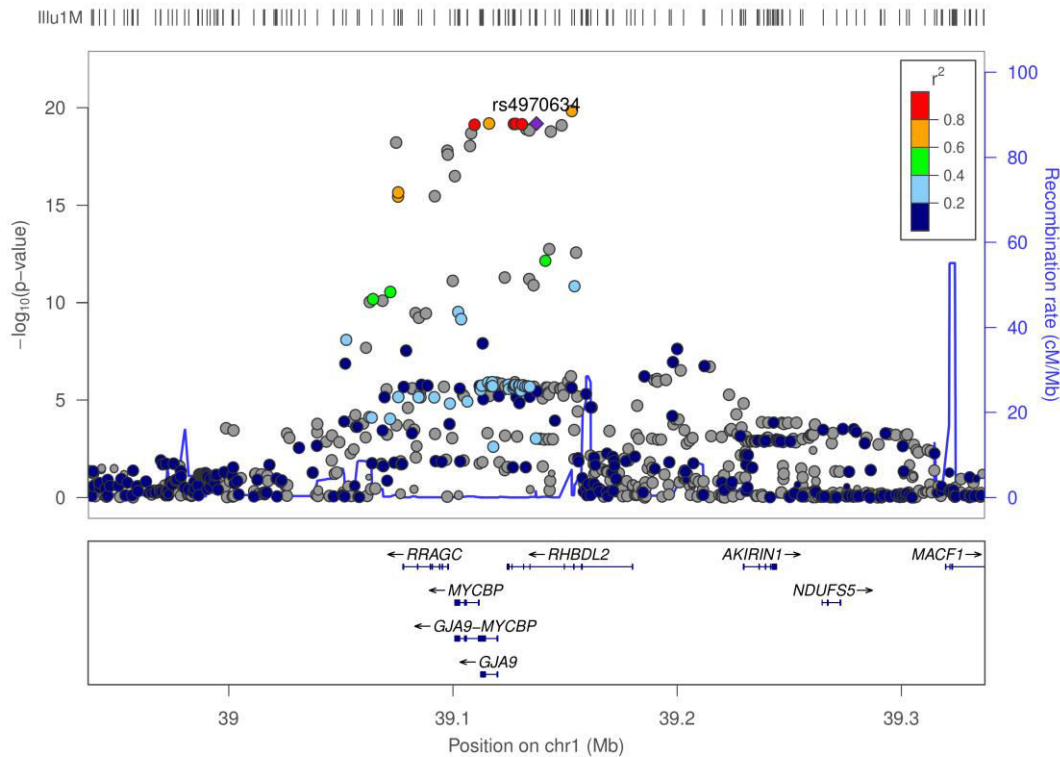


FM-pipeline

This is a pipeline for finemapping using GWAS summary statistics, implemented in Bash as a series of steps to furnish an incremental analysis. As depicted in the diagram below



where our lead SNP rs4970634 is in LD with many others, the procedure attempts to identify causal variants from region(s) showing significant SNP-trait association.

The process involves the following steps, 1. Extraction of effect (beta)/z statistics from GWAS summary statistics (.sumstats), 2. Extraction of correlation from the reference panel among overlapped SNPs from 1 and the reference panel containing individual level data. 3. Information from 1 and 2 above is then used as input for finemapping.

The measure of evidence is typically (log10) Bayes factor (BF) and associate SNP probability in the causal set.

Software included in this pipeline are listed in the table below.

Name	Function	Input	Output	Reference
CAVIAR	finemapping	z, correlation matrix	causal sets and probabilities	Hormozdiari, et al. (2014)
CAVIARBF	finemapping	z, correlation matrix	BF and probabilities for all configurations	Chen, et al. (2015)

GCTA	joint/conditional analysis	.sumstats, reference data	association results	Yang, et al. (2012)
FM-summary	finemapping	.sumstats Association results	updated results	Huang, et al. (2017)
JAM	finemapping	beta, individual reference data	Bayes Factor of being causal	Newcombe, et al. (2016)
LocusZoom	regional plot	partial .sumstats	.pdf/.png plots	Pruim, et al. (2010)
fgwas	functional GWAS			Pickrell (2014)
finemap	finemapping	z, correlation matrix	causal SNPs and configuration	Benner, et al. (2016)

so they range from regional association plots via LocusZoom, joint/conditional analysis via GCTA, functional annotation via fgwas to dedicated finemapping software including CAVIAR, CAVIARBF, an adapted version of FM-summary, R2BGLiMS/JAM and finemap. One can optionally use a subset of these for a particular analysis by specifying relevant flags from the pipeline's settings.

INSTALLATION

On many occasions, the pipeline takes advantage of the [GNU parallel](#).

Besides (sub)set of software listed in the table above, the pipeline requires [GTOOL](#), [PLINK](#) 1.9, and the companion program LDstore from finemap's website need to be installed.

The pipeline itself can be installed in the usual way,

```
git clone https://github.com/jinghuazhao/FM-pipeline
```

The setup is in line with summary statistics from consortia where only RSid are given for the fact that their chromosomal position may be changed over different builds. To remedy this, we use information from UCSC, i.e.,

```
wget http://hgdownload.soe.ucsc.edu/goldenPath/hg19/database/snp150.txt.gz
gunzip -c snp150.txt.gz | \
awk '{split($2,a,"_");sub(/chr/, "",a[1]);print a[1],$4,$5}' | \
sort -k3,3 > snp150.txt
```

Note that JAM requires Java 1.8 so call to Java -jar inside the function needs to reflect this, not straightforward with `install_github()` from `devtools` but one needs to clone the package, modify the R source code and then use

```
git clone https://github.com/pjnewcombe/R2BGLiMS
### change java to java-1.8 in R2BGLiMS/R/R2BGLiMS.R
R CMD INSTALL R2BGLiMS
```

Implementations have been done for the finemapping software along with LocusZoom and GCTA; support for fgwas is still alpha tested. To facilitate handling of graphics, e.g., importing them into Excel, pdftopng from [xpdf](#) is used.

USAGE

Before start, settings at the beginning of the script need to be changed and only minor change is expected after this. The syntax of pipeline is then simply

```
bash fm-pipeline.sh <input>
```

Inputs

--- GWAS summary statistics and lead SNPs ---

The **first input file** will be GWAS summary statistics with the following columns,

Column	Name	Description
1	SNP	RSid
2	A1	Effect allele
3	A2	Other allele
4	freqA1	A1 frequency
5	beta	effect estimate
6	se	standard error of effect
7	P	P-value
8	N	sample size
9*	chr	chromosome
10*	pos	position

This format is in line with joint/conditional analysis by GCTA. Note the last two columns are not normally required as they are obtained from UCSC (use_UCSC=1). However, for one of our analyses UCSC does not have all the coordinates as in the GWAS summary statistics, so we set use_ucsc==0 and provide st.bed containing the (chr, start, end, pos, rsid, r) sextuplets.

The **second input file** is a list of SNPs for which finemapping will be conducted.

A header is required for neither file.

--- Reference panel ---

The pipeline uses a reference panel in a .GEN format, taking into account directions of effect in both the GWAS summary statistics and the reference panel. Its development will facilitate

summary statistics from a variety of consortia as with reference panels such as the HRC and 1000Genomes.

A .GEN file is required for each region, named such that chr{chr}_{start}_{end}.gen, together with a sample file. For our own data, a [utility program in Stata](#) is written to generate such files from their whole chromosome counterpart using SNPinfo.dta.gz which has the following information,

chr	rsid	RSnum	pos	FreqA2	info	type	A1	A2
1	1:54591_A_G	rs561234294	54591	.0000783	.33544	0	A	G
1	1:55351_T_A	rs531766459	55351	.0003424	.5033	0	T	A
...

Given these, one can do away with Stata and work on a text version for instance SNPinfo.txt. When option stbed=1 in the settings, it only generates st.bed which contains chr, start, end, RSid, pos corresponding to the lead SNPs specified.

Optionally, a file is specified which contains sample to be excluded from the reference panel; one leaves it unspecified when not needed

Outputs

The output will involve counterpart(s) from individual software, i.e., .set/post, caviarbf, .snp/.config, .jam/.top

Software	Output	Description
CAVIAR	.set/.post	causal set and probabilities in the causal set/posterior probabilities
CAVIARBF	.caviarbf	causal configurations and their BF's
FM-summary	.txt	additional information to the GWAS summary statistics
JAM	.jam/.top	the posterior summary table and top models containing selected SNPs
finemap	.snp/.config	top SNPs with largest log10(BF) and top configurations as with their log10(BF)

It is helpful to examine directions of effects together with the correlation of them, e.g., for use with finemap, the code [here](#) is now embedded in the pipeline.

EXAMPLES

1. We use GWAS on 2-hr glucose level as reported by the MAGIC consortium, Saxena, et al. (2010). The GWAS summary data is obtained as follows,

```
wget ftp://ftp.sanger.ac.uk/pub/magic/MAGIC_2hrGlucose_AdjustedForBMI.txt
awk -vOFS="\t" -vN=15234 '(NR>1){print $0, N}'
MAGIC_2hrGlucose_AdjustedForBMI.txt > 2hrglucose.txt
```

For two SNPs contained in [2.snps](#), the Stata program [p0.do](#) generates [Extract.sh](#) excluding SNPs in [exc3_122844451_123344451.txt](#) and [exc3_122881254_123381254.txt](#). The command to call is

```
bash fm-pipeline.sh 2hrglucose.txt
```

2. Next we show how to set up for BMI GWAS summary data as reported by the GIANT consortium, Locke, et al. (2015),

```
# GWAS summary statistics
wget
http://portals.broadinstitute.org/collaboration/giant/images/1/15/SNP_gwa
s_mc_merge_nogc.tbl.uniq.gz
gunzip -c SNP_gwas_mc_merge_nogc.tbl.uniq.gz |
awk 'NR>1' > bmi.txt
# A list of 97 SNPs
R --no-save <<END
library(openxlsx)
xlsx <-
"https://www.nature.com/nature/journal/v518/n7538/extref/nature14177-
s2.xlsx"
snps <- read.xlsx(xlsx, sheet = 4, colNames=FALSE, skipEmptyRows = FALSE,
cols = 1, rows = 5:101)
snplist <- sort(as.vector(snps[,1]))
write.table(snplist, file="97.snps", row.names=FALSE, col.names=FALSE,
quote=FALSE)
END
```

so the GWAS summary statistics from GIANT is almost ready (we only drop the header) as with the list of 97 SNPs. The positions of these SNPs were in build 36 while we used build 37.

In both cases, the GWAS summary data are used together with the reference panel in .GEN format to furnish the finemapping analysis.

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