

# VAR-Seq Workflow Report for Single Computer

Project ID: VARseq.PI.Name.Organism\_July2015  
Author of Report: Thomas Girke (thomas.girke@ucr.edu)

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## Contents

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<b>1</b>	<b>Introduction</b>	<b>2</b>
<b>2</b>	<b>Sample definitions and environment settings</b>	<b>2</b>
2.1	Environment settings and input data . . . . .	2
2.2	Required packages and resources . . . . .	2
2.3	Experiment definition provided by <i>targets</i> file . . . . .	2
<b>3</b>	<b>Read preprocessing</b>	<b>3</b>
3.1	Read quality filtering and trimming . . . . .	3
3.2	FASTQ quality report . . . . .	3
<b>4</b>	<b>Alignments</b>	<b>6</b>
4.1	Read mapping with BWA . . . . .	6
4.2	Read mapping with <i>gsnap</i> . . . . .	6
4.3	Read and alignment stats . . . . .	7
4.4	Create symbolic links for viewing BAM files in IGV . . . . .	7
<b>5</b>	<b>Variant calling</b>	<b>7</b>
5.1	Variant calling with GATK . . . . .	7
5.2	Variant calling with BCFtools . . . . .	8
5.3	Variant calling with <i>VariantTools</i> . . . . .	8
<b>6</b>	<b>Filter variants</b>	<b>9</b>
6.1	Filter variants called by <i>GATK</i> . . . . .	9
6.2	Filter variants called by <i>BCFtools</i> . . . . .	9
6.3	Filter variants called by <i>VariantTools</i> . . . . .	9
<b>7</b>	<b>Annotate filtered variants</b>	<b>10</b>
7.1	Annotate filtered variants called by GATK . . . . .	10
7.2	Annotate filtered variants called by BCFtools . . . . .	10
7.3	Annotate filtered variants called by <i>VariantTools</i> . . . . .	10
<b>8</b>	<b>Combine annotation results among samples</b>	<b>11</b>
8.1	Combine results from <i>GATK</i> . . . . .	11
8.2	Combine results from <i>BCFtools</i> . . . . .	11
8.3	Combine results from <i>VariantTools</i> . . . . .	11
<b>9</b>	<b>Summary statistics of variants</b>	<b>12</b>
9.1	Summary for <i>GATK</i> . . . . .	12
9.2	Summary for <i>BCFtools</i> . . . . .	12

9.3 Summary for <i>VariantTools</i> . . . . .	12
10 Venn diagram of variants	12
11 Version Information	13
12 Funding	14
13 References	14

## 1 Introduction

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This report describes the analysis of an VAR-Seq project from Dr. First Last's lab which studies the genetic differences of ... in *organism* .... The experimental design is as follows...

## 2 Sample definitions and environment settings

---

### 2.1 Environment settings and input data

Typically, the user wants to record here the sources and versions of the reference genome sequence along with the corresponding annotations. In the provided sample data set all data inputs are stored in a data subdirectory and all results will be written to a separate results directory, while the systemPipeVARseq.Rnw script and the targets file are expected to be located in the parent directory. The R session is expected to run from this parent directory.

To run this sample report, mini sample FASTQ and reference genome files can be downloaded from [here](#). The chosen data set [SRP010938](#) contains 18 paired-end (PE) read sets from *Arabidopsis thaliana* [Howard et al. \(2013\)](#). This data set comes from a different NGS application area, but it is sufficient to demonstrate the analysis steps of this workflow. To minimize processing time during testing, each FASTQ file has been subsetting to 90,000-100,000 randomly sampled PE reads that map to the first 100,000 nucleotides of each chromosome of the *A. thaliana* genome. The corresponding reference genome sequence (FASTA) and its GFF annotation files (provided in the same download) have been truncated accordingly. This way the entire test sample data set is less than 200MB in storage space. A PE read set has been chosen for this test data set for flexibility, because it can be used for testing both types of analysis routines requiring either SE (single end) reads or PE reads.

### 2.2 Required packages and resources

The *systemPipeR* package needs to be loaded to perform the analysis steps shown in this report ([Girke, 2014](#)).

```
library(systemPipeR)
```

If applicable load custom functions not provided by *systemPipeR*

```
source("systemPipeVARseq_Fct.R")
```

### 2.3 Experiment definition provided by targets file

The *targets* file defines all FASTQ files and sample comparisons of the analysis workflow.

```
targets <- read.delim("targetsPE.txt", comment.char = "#")[,1:5]
targets
```

	FileName1	FileName2	SampleName	Factor	SampleLong
1	./data/SRR446027_1.fastq.gz	./data/SRR446027_2.fastq.gz	M1A	M1	Mock.1h.A
2	./data/SRR446028_1.fastq.gz	./data/SRR446028_2.fastq.gz	M1B	M1	Mock.1h.B
3	./data/SRR446029_1.fastq.gz	./data/SRR446029_2.fastq.gz	A1A	A1	Avr.1h.A
4	./data/SRR446030_1.fastq.gz	./data/SRR446030_2.fastq.gz	A1B	A1	Avr.1h.B
5	./data/SRR446031_1.fastq.gz	./data/SRR446031_2.fastq.gz	V1A	V1	Vir.1h.A
6	./data/SRR446032_1.fastq.gz	./data/SRR446032_2.fastq.gz	V1B	V1	Vir.1h.B
7	./data/SRR446033_1.fastq.gz	./data/SRR446033_2.fastq.gz	M6A	M6	Mock.6h.A
8	./data/SRR446034_1.fastq.gz	./data/SRR446034_2.fastq.gz	M6B	M6	Mock.6h.B
9	./data/SRR446035_1.fastq.gz	./data/SRR446035_2.fastq.gz	A6A	A6	Avr.6h.A
10	./data/SRR446036_1.fastq.gz	./data/SRR446036_2.fastq.gz	A6B	A6	Avr.6h.B
11	./data/SRR446037_1.fastq.gz	./data/SRR446037_2.fastq.gz	V6A	V6	Vir.6h.A
12	./data/SRR446038_1.fastq.gz	./data/SRR446038_2.fastq.gz	V6B	V6	Vir.6h.B
13	./data/SRR446039_1.fastq.gz	./data/SRR446039_2.fastq.gz	M12A	M12	Mock.12h.A
14	./data/SRR446040_1.fastq.gz	./data/SRR446040_2.fastq.gz	M12B	M12	Mock.12h.B
15	./data/SRR446041_1.fastq.gz	./data/SRR446041_2.fastq.gz	A12A	A12	Avr.12h.A
16	./data/SRR446042_1.fastq.gz	./data/SRR446042_2.fastq.gz	A12B	A12	Avr.12h.B
17	./data/SRR446043_1.fastq.gz	./data/SRR446043_2.fastq.gz	V12A	V12	Vir.12h.A
18	./data/SRR446044_1.fastq.gz	./data/SRR446044_2.fastq.gz	V12B	V12	Vir.12h.B

## 3 Read preprocessing

### 3.1 Read quality filtering and trimming

```
source("systemPipeVARseq_Fct.R")
args <- systemArgs(sysma="param/trimPE.param", mytargets="targetsPE.txt")[1:4] # Note: subsetting!
preprocessReads(args=args, Fct="filterFct(fq, cutoff=20, Nexceptions=0)", batchsize=100000)

37646 processed reads written to file: /home/tgirke/Dropbox/Bioc2015/systemPipeRdata_tests/varseq/results/
37646 processed reads written to file: /home/tgirke/Dropbox/Bioc2015/systemPipeRdata_tests/varseq/results/
24906 processed reads written to file: /home/tgirke/Dropbox/Bioc2015/systemPipeRdata_tests/varseq/results/
24906 processed reads written to file: /home/tgirke/Dropbox/Bioc2015/systemPipeRdata_tests/varseq/results/
39247 processed reads written to file: /home/tgirke/Dropbox/Bioc2015/systemPipeRdata_tests/varseq/results/
39247 processed reads written to file: /home/tgirke/Dropbox/Bioc2015/systemPipeRdata_tests/varseq/results/
26254 processed reads written to file: /home/tgirke/Dropbox/Bioc2015/systemPipeRdata_tests/varseq/results/
26254 processed reads written to file: /home/tgirke/Dropbox/Bioc2015/systemPipeRdata_tests/varseq/results/

writeTargetsout(x=args, file="targets_PEtrim.txt", overwrite=TRUE)

Written content of 'targetsout(x)' to file: targets_PEtrim.txt
```

### 3.2 FASTQ quality report

The following `seeFastq` and `seeFastqPlot` functions generate and plot a series of useful quality statistics for a set of FASTQ files including per cycle quality box plots, base proportions, base-level quality trends, relative k-mer diversity, length and occurrence distribution of reads, number of reads above quality cutoffs and mean quality distribution. The results are written to a PDF file named `fastqReport.pdf`.

```
args <- systemArgs(sysma="param/bwa.param", mytargets="targets_PEtrim.txt")
fqlist <- seeFastq(fastq=infile1(args), batchsize=100000, klength=8)
pdf("./results/fastqReport.pdf", height=18, width=4*length(fqlist))
seeFastqPlot(fqlist)
```

```
dev.off()
```

```
pdf
```

```
  2
```

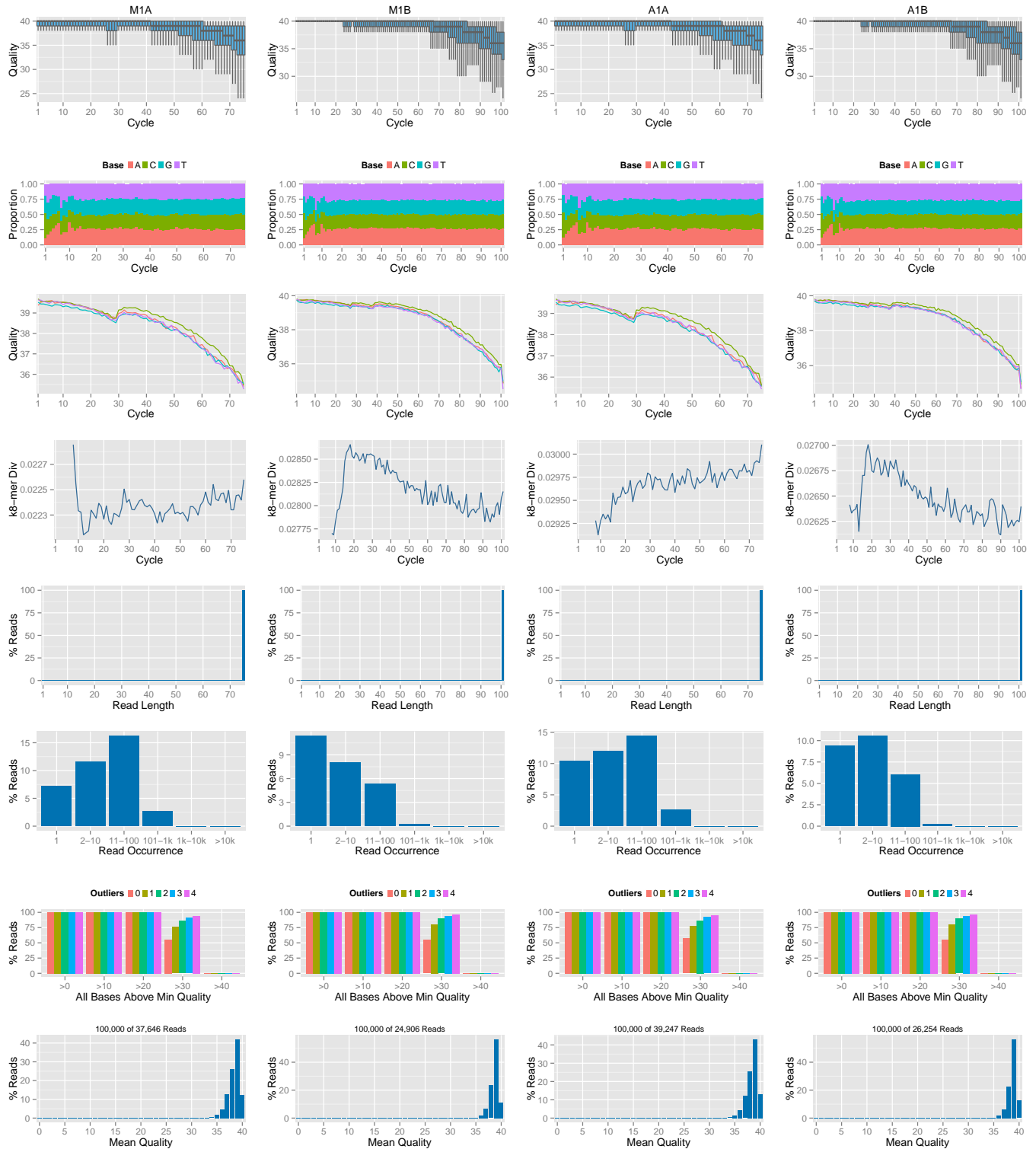


Figure 1: QC report for 18 FASTQ files.

## 4 Alignments

### 4.1 Read mapping with BWA

The NGS reads of this project are aligned against the reference genome sequence using the highly variant tolerant short read aligner BWA (Li, 2013; Li and Durbin, 2009). The parameter settings of the aligner are defined in the `bwa.param` file.

```
args <- systemArgs(sysma="param/bwa.param", mytargets="targets_PETrim.txt")
sysargs(args)[1] # Command-line parameters for first FASTQ file
```

```
"bwa mem -t 4 -M -R '@RG\tID:group1\tSM:sample1\tPL:illumina\tLB:lib1\tPU:unit1' /home/tgirke/Dropbox/
```

Runs the alignments sequentially (e.g. on a single machine)

```
moduleload(modules(args))
system("bwa index -a bwtsv ./data/tair10.fasta")
bampaths <- runCommandline(args=args)
writeTargetsout(x=args, file="targets_bam.txt", overwrite=TRUE)
```

Alternatively, the alignment jobs can be submitted to a compute cluster, here using 72 CPU cores (18 qsub processes each with 4 CPU cores).

```
resources <- list(walltime="20:00:00", nodes=paste0("1:ppn=", cores(args)), memory="4gb")
reg <- clusterRun(args, conffile=".BatchJobs.R", template="torque.tmpl", Njobs=18, runid="01",
  resourceList=resources)
waitForJobs(reg)
writeTargetsout(x=args, file="targets_bam.txt", overwrite=TRUE)
```

Check whether all BAM files have been created

```
file.exists(outpaths(args))
```

### 4.2 Read mapping with gsnap

```
library(gmapR); library(BiocParallel); library(BatchJobs)
gmapGenome <- GmapGenome(reference(args), directory="data", name="gmap_tair10chr", create=TRUE)
args <- systemArgs(sysma="param/gsnap.param", mytargets="targets_PETrim.txt")
p <- GsnapParam(genome=gmapGenome, unique_only=TRUE, molecule="DNA", max_mismatches=3)
for(i in seq(along=args)) {
  o <- gsnap(input_a=infile1(args)[i], input_b=infile2(args)[i], params=p, output=outfile1(args)[i])
  print(c(infile1(args)[i], infile2(args)[i]))
}
```

```

M1A
"/home/tgirke/Dropbox/Bioc2015/systemPipeRdata_tests/varseq/results/SRR446027_1.fastq.trim.gz"
M1A
"/home/tgirke/Dropbox/Bioc2015/systemPipeRdata_tests/varseq/results/SRR446027_2.fastq.trim.gz"
M1B
"/home/tgirke/Dropbox/Bioc2015/systemPipeRdata_tests/varseq/results/SRR446028_1.fastq.trim.gz"
M1B
"/home/tgirke/Dropbox/Bioc2015/systemPipeRdata_tests/varseq/results/SRR446028_2.fastq.trim.gz"
A1A
"/home/tgirke/Dropbox/Bioc2015/systemPipeRdata_tests/varseq/results/SRR446029_1.fastq.trim.gz"
A1A
```

```

"/home/tgirke/Dropbox/Bioc2015/systemPipeRdata_tests/varseq/results/SRR446029_2.fastq_trim.gz"
A1B
"/home/tgirke/Dropbox/Bioc2015/systemPipeRdata_tests/varseq/results/SRR446030_1.fastq_trim.gz"
A1B
"/home/tgirke/Dropbox/Bioc2015/systemPipeRdata_tests/varseq/results/SRR446030_2.fastq_trim.gz"
writeTargetsout(x=args, file="targets_gsnap_bam.txt", overwrite=TRUE)
Written content of 'targetsout(x)' to file: targets_gsnap_bam.txt
file.exists(outpaths(args))
[1] TRUE TRUE TRUE TRUE

```

### 4.3 Read and alignment stats

The following generates a summary table of the number of reads in each sample and how many of them aligned to the reference.

```

args <- systemArgs(sysma="param/gsnap.param", mytargets="targets_PETrim.txt")
read_statsDF <- alignStats(args=args)
write.table(read_statsDF, "results/alignStats.xls", row.names=FALSE, quote=FALSE, sep="\t")
read_statsDF[1:4,]

```

	FileName	Nreads2x	Nalign	Perc_Aligned	Nalign_Primary	Perc_Aligned_Primary
M1A	M1A	75292	72727	96.59326	72727	96.59326
M1B	M1B	49812	40755	81.81763	40755	81.81763
A1A	A1A	78494	73466	93.59441	73466	93.59441
A1B	A1B	52508	41932	79.85831	41932	79.85831

### 4.4 Create symbolic links for viewing BAM files in IGV

The `symLink2bam` function creates symbolic links to view the BAM alignment files in a genome browser such as IGV. The corresponding URLs are written to a file with a path specified under `urlfile`, here [IGVurl.txt](#).

```

symLink2bam(sysargs=args, htmlidir=c("public_html/", "projects/"),
            urlbase="http://biocluster.ucr.edu/~tgirke/",
            urlfile="./results/IGVurl.txt")

```

## 5 Variant calling

The following performs variant calling with GATK, BCFtools and *VariantTools* in parallel mode on a compute cluster (McKenna et al., 2010; Li, 2011). If a cluster is not available, the `runCommandline()` function can be used to run the variant calling with GATK and BCFtools for each sample sequentially on a single machine, or `callVariants` in case of *VariantTools*. Typically, the user would choose here only one variant caller rather than running several ones.

### 5.1 Variant calling with GATK

The following creates in the initial step a new targets file (`targets_bam.txt`). The first column of this file gives the paths to the BAM files created in the alignment step. The new targets file and the parameter file `gatk.param` are used to create a new `SYSargs` instance for running GATK. Since GATK involves many processing steps, it is executed by a bash script `gatk_run.sh` where the user can specify the detailed run parameters. All three files are expected to be

located in the current working directory. Samples files for `gatk.param` and `gatk.run.sh` are available in the subdirectory `./inst/extdata/` of the source file of the *systemPipeR* package. Alternatively, they can be downloaded directly from [here](#).

```
system("java -jar /opt/picard/1.81/CreateSequenceDictionary.jar R=./data/tair10.fasta O=./data/tair10.dict")
args <- systemArgs(sysma="param/gatk.param", mytargets="targets_bam.txt")
gatkpaths <- runCommandline(args=args)
unlink(outfile1(args), recursive = TRUE, force = TRUE)
writeTargetsout(x=args, file="targets_gatk.txt", overwrite=TRUE)
```

## 5.2 Variant calling with BCFtools

The following runs the variant calling with BCFtools. This step requires in the current working directory the parameter file `sambcf.param` and the bash script `sambcf_run.sh`.

```
args <- systemArgs(sysma="param/sambcf.param", mytargets="targets_bam.txt")
sambcfpaths <- runCommandline(args=args)
unlink(outfile1(args), recursive = TRUE, force = TRUE)
writeTargetsout(x=args, file="targets_sambcf.txt", overwrite=TRUE)
```

## 5.3 Variant calling with VariantTools

```
library(gmapR); library(VariantTools)
args <- systemArgs(sysma="param/vartools.param", mytargets="targets_gsnap_bam.txt")
gmapGenome <- GmapGenome(systemPipeR::reference(args), directory="data", name="gmap_tair10chr", create=FALSE)
tally.param <- TallyVariantsParam(gmapGenome, high_base_quality = 23L, indels = TRUE)
for(x in seq(along=args)) {
  bfl <- BamFileList(infile1(args)[x], index=character())
  var <- callVariants(bfl[[1]], tally.param)
  sampleNames(var) <- names(bfl)
  writeVcf(asVCF(var), outfile1(args)[x], index = TRUE)
  print(outfile1(args)[x])
}
```

```
"/home/tgirke/Dropbox/Bioc2015/systemPipeRdata_tests/varseq/results/SRR446027_1.fastq_trim.gz.gsnap.sam.bam"
```

```
"/home/tgirke/Dropbox/Bioc2015/systemPipeRdata_tests/varseq/results/SRR446028_1.fastq_trim.gz.gsnap.sam.bam"
```

```
"/home/tgirke/Dropbox/Bioc2015/systemPipeRdata_tests/varseq/results/SRR446029_1.fastq_trim.gz.gsnap.sam.bam"
```

```
"/home/tgirke/Dropbox/Bioc2015/systemPipeRdata_tests/varseq/results/SRR446030_1.fastq_trim.gz.gsnap.sam.bam"
```

```
file.exists(outpaths(args))
```

```
[1] TRUE TRUE TRUE TRUE
```



```
writeTargetsout(x=args, file="targets_vartools.txt", overwrite=TRUE)
Written content of 'targetsout(x)' to file: targets_vartools.txt
```

## 6 Filter variants

The function `filterVars` filters VCF files based on user definable quality parameters. It sequentially imports each VCF file into R, applies the filtering on an internally generated `VRanges` object and then writes the results to a new subsetted VCF file. The filter parameters are passed on to the corresponding argument as a character string. The function applies this filter to the internally generated `VRanges` object using the standard subsetting syntax for two dimensional objects such as: `vr[filter, ]`. The parameter files (`filter_gatk.param`, `filter_sambcf.param` and `filter_vartools.param`), used in the filtering steps, define the paths to the input and output VCF files which are stored in new `SYSargs` instances.

### 6.1 Filter variants called by GATK

The below example filters for variants that are supported by  $\geq x$  reads and  $\geq 80\%$  of them support the called variants. In addition, all variants need to pass  $\geq x$  of the soft filters recorded in the VCF files generated by GATK. Since the toy data used for this workflow is very small, the chosen settings are unreasonably relaxed. A more reasonable filter setting is given in the line below (here commented out).

```
library(VariantAnnotation)
library(BBmisc) # Defines suppressAll()
args <- systemArgs(sysma="param/filter_gatk.param", mytargets="targets_gatk.txt")[1:4]
filter <- "totalDepth(vr) >= 2 & (altDepth(vr) / totalDepth(vr) >= 0.8) & rowSums(softFilterMatrix(vr))>=1
# filter <- "totalDepth(vr) >= 20 & (altDepth(vr) / totalDepth(vr) >= 0.8) & rowSums(softFilterMatrix(vr))>=1
suppressAll(filterVars(args, filter, varcaller="gatk", organism="A. thaliana"))
writeTargetsout(x=args, file="targets_gatk_filtered.txt", overwrite=TRUE)
Written content of 'targetsout(x)' to file: targets_gatk_filtered.txt
```

### 6.2 Filter variants called by BCFtools

The following shows how to filter the VCF files generated by *BCFtools* using similar parameter settings as in the previous filtering of the GATK results.

```
args <- systemArgs(sysma="param/filter_sambcf.param", mytargets="targets_sambcf.txt")[1:4]
filter <- "rowSums(vr) >= 2 & (rowSums(vr[,3:4])/rowSums(vr[,1:4]) >= 0.8)"
# filter <- "rowSums(vr) >= 20 & (rowSums(vr[,3:4])/rowSums(vr[,1:4]) >= 0.8)"
suppressAll(filterVars(args, filter, varcaller="bcftools", organism="A. thaliana"))
writeTargetsout(x=args, file="targets_sambcf_filtered.txt", overwrite=TRUE)
Written content of 'targetsout(x)' to file: targets_sambcf_filtered.txt
```

### 6.3 Filter variants called by VariantTools

The following shows how to filter the VCF files generated by *VariantTools* using similar parameter settings as in the previous filtering of the GATK results.

```
library(VariantAnnotation)
library(BBmisc) # Defines suppressAll()
args <- systemArgs(sysma="param/filter_vartools.param", mytargets="targets_vartools.txt")
```

```

filter <- "(values(vr)$n.read.pos.ref + values(vr)$n.read.pos) >= 2 & (values(vr)$n.read.pos / (values(vr)$n.read.pos.ref + values(vr)$n.read.pos) >= 20 & (values(vr)$n.read.pos / (values(vr)$n.read.pos.ref + values(vr)$n.read.pos) >= 20)"
filterVars(args, filter, varcaller="vartools", organism="A. thaliana")

[1] "Generated file 1 SRR446027_1.fastq_trim.gz.gsnap.sam.bam.vartools.bgz.filtered.vcf.bgz"
[1] "Generated file 2 SRR446028_1.fastq_trim.gz.gsnap.sam.bam.vartools.bgz.filtered.vcf.bgz"
[1] "Generated file 3 SRR446029_1.fastq_trim.gz.gsnap.sam.bam.vartools.bgz.filtered.vcf.bgz"
[1] "Generated file 4 SRR446030_1.fastq_trim.gz.gsnap.sam.bam.vartools.bgz.filtered.vcf.bgz"

writeTargetsout(x=args, file="targets_vartools_filtered.txt", overwrite=TRUE)

Written content of 'targetsout(x)' to file: targets_vartools_filtered.txt

```

Check filtering outcome for one sample

```

length(as(readVcf(infile1(args)[1], genome="Ath"), "VRanges")[,1])

[1] 53

length(as(readVcf(outpaths(args)[1], genome="Ath"), "VRanges")[,1])

[1] 42

```

## 7 Annotate filtered variants

The function `variantReport` generates a variant report using utilities provided by the *VariantAnnotation* package. The report for each sample is written to a tabular file containing genomic context annotations (e.g. coding or non-coding SNPs, amino acid changes, IDs of affected genes, etc.) along with confidence statistics for each variant. The parameter `file annotate_vars.param` defines the paths to the input and output files which are stored in a new `SYSargs` instance.

### 7.1 Annotate filtered variants called by GATK

```

library("GenomicFeatures")
args <- systemArgs(sysma="param/annotate_vars.param", mytargets="targets_gatk_filtered.txt")
txdb <- loadDb("./data/tair10.sqlite")
fa <- FaFile(systemPipeR::reference(args))
suppressAll(variantReport(args=args, txdb=txdb, fa=fa, organism="A. thaliana"))

```

### 7.2 Annotate filtered variants called by BCFtools

```

args <- systemArgs(sysma="param/annotate_vars.param", mytargets="targets_sambcf_filtered.txt")
txdb <- loadDb("./data/tair10.sqlite")
fa <- FaFile(systemPipeR::reference(args))
suppressAll(variantReport(args=args, txdb=txdb, fa=fa, organism="A. thaliana"))

```

### 7.3 Annotate filtered variants called by VariantTools

```

args <- systemArgs(sysma="param/annotate_vars.param", mytargets="targets_vartools_filtered.txt")
txdb <- loadDb("./data/tair10.sqlite")
fa <- FaFile(systemPipeR::reference(args))
suppressAll(variantReport(args=args, txdb=txdb, fa=fa, organism="A. thaliana"))

```

View annotation result for single sample

```
read.delim(outpaths(args)[1])[38:40,]
```

	VARID	totalDepth	refDepth	altDepth	REF	ALT	QUAL	LOCATION
38	ChrM:16916_T/C	2	0	2	T	C	0	coding promoter coding
39	ChrM:16983_T/G	3	0	3	T	G	0	coding promoter coding
40	ChrM:17003_G/T	3	0	3	G	T	0	coding promoter coding

	GENEID	Strand	Consequence	Codon	AA
38	ATMG00050	ATMG00040	c(+, -) nonsynonymous	synonymous	61_TCT/CCT 876_AGA/AGG 21_S/P 292_R/R
39	ATMG00050	ATMG00040	c(+, -) nonsynonymous	nonsynonymous	128_ATC/AGC 809_GAT/GCT 43_I/S 270_D/A
40	ATMG00050	ATMG00040	c(+, -) nonsense	synonymous	148_GAG/TAG 789_CTC/CTA 50_E/* 263_L/L

	TXIDs	GENEIDcode
38	ATMG00050.1	ATMG00040.1
39	ATMG00050.1	ATMG00040.1
40	ATMG00050.1	ATMG00040.1

## 8 Combine annotation results among samples

To simplify comparisons among samples, the `combineVarReports` function combines all variant annotation reports referenced in a `SYSargs` instance (here `args`). At the same time the function allows to consider only certain feature types of interest. For instance, the below setting `filtercol=c(Consequence="nonsynonymous")` will include only nonsynonymous variances listed in the `Consequence` column of the annotation reports. To omit filtering, one can use the setting `filtercol="All"`

### 8.1 Combine results from GATK

```
args <- systemArgs(sysma="param/annotate_vars.param", mytargets="targets_gatk_filtered.txt")
combinedDF <- combineVarReports(args, filtercol=c(Consequence="nonsynonymous"))
write.table(combinedDF, "./results/combinedDF_nonsyn_gatk.xls", quote=FALSE, row.names=FALSE, sep="\t")
```

### 8.2 Combine results from BCFtools

```
args <- systemArgs(sysma="param/annotate_vars.param", mytargets="targets_sambcf_filtered.txt")
combinedDF <- combineVarReports(args, filtercol=c(Consequence="nonsynonymous"))
write.table(combinedDF, "./results/combinedDF_nonsyn_sambcf.xls", quote=FALSE, row.names=FALSE, sep="\t")
```

### 8.3 Combine results from VariantTools

```
args <- systemArgs(sysma="param/annotate_vars.param", mytargets="targets_vartools_filtered.txt")
combinedDF <- combineVarReports(args, filtercol=c(Consequence="nonsynonymous"))
write.table(combinedDF, "./results/combinedDF_nonsyn_vartools.xls", quote=FALSE, row.names=FALSE, sep="\t")
combinedDF[2:4,]
```

	Sample	VARID	totalDepth	refDepth	altDepth	REF	ALT	QUAL	LOCATION	GENEID	Strand
2	M1B	Chr2:1259_G/A	2	0	2	G	A	0	coding	AT2G01008	+
21	A1B	Chr2:1259_G/A	2	0	2	G	A	0	coding	AT2G01008	+
3	M1B	Chr2:1263_C/G	2	0	2	C	G	0	coding	AT2G01008	+

	Consequence	Codon	AA	TXIDs	GENEIDcode
2	nonsynonymous	235_GAA/AAA	79_E/K	AT2G01008.1	AT2G01008

```
21 nonsynonymous 235_GAA/AAA 79_E/K AT2G01008.1 AT2G01008
3 nonsynonymous 239_TCG/TGG 80_S/W AT2G01008.1 AT2G01008
```

## 9 Summary statistics of variants

The function `varSummary` counts the number of variants for each feature type included in the annotation reports.

### 9.1 Summary for GATK

```
args <- systemArgs(sysma="param/annotate_vars.param", mytargets="targets_gatk_filtered.txt")
write.table(varSummary(args), "./results/variantStats_gatk.xls", quote=FALSE, col.names = NA, sep="\t")
```

### 9.2 Summary for BCFtools

```
args <- systemArgs(sysma="param/annotate_vars.param", mytargets="targets_sambcf_filtered.txt")
write.table(varSummary(args), "./results/variantStats_sambcf.xls", quote=FALSE, col.names = NA, sep="\t")
```

### 9.3 Summary for VariantTools

```
args <- systemArgs(sysma="param/annotate_vars.param", mytargets="targets_vartools_filtered.txt")
write.table(varSummary(args), "./results/variantStats_vartools.xls", quote=FALSE, col.names = NA, sep="\t")
read.delim("results/variantStats_vartools.xls", row.names=1)
```

	M1A	M1B	A1A	A1B
all	42	69	76	72
coding	13	16	27	23
intergenic	32	49	50	45
promoter	16	33	28	37
nonsense	1	0	1	0
nonsynonymous	6	13	15	21
synonymous	5	1	6	0

## 10 Venn diagram of variants

The venn diagram utilities defined by the *systemPipeR* package can be used to identify common and unique variants reported for different samples and/or variant callers. The below generates a 4-way venn diagram comparing four samples for each of the two variant callers.

```
args <- systemArgs(sysma="param/annotate_vars.param", mytargets="targets_gatk_filtered.txt")
varlist <- sapply(names(outpaths(args))[1:4], function(x) as.character(read.delim(outpaths(args)[x])$VARID))
vennset_gatk <- overLapper(varlist, type="vennsets")
args <- systemArgs(sysma="param/annotate_vars.param", mytargets="targets_sambcf_filtered.txt")
varlist <- sapply(names(outpaths(args))[1:4], function(x) as.character(read.delim(outpaths(args)[x])$VARID))
vennset_bcf <- overLapper(varlist, type="vennsets")
args <- systemArgs(sysma="param/annotate_vars.param", mytargets="targets_vartools_filtered.txt")
varlist <- sapply(names(outpaths(args))[1:4], function(x) as.character(read.delim(outpaths(args)[x])$VARID))
vennset_vartools <- overLapper(varlist, type="vennsets")
```

```
pdf("./results/vennplot_var.pdf")
vennPlot(list(vennset_gatk, vennset_bcf, vennset_vartools), mymain="", mysub="GATK: red; BCFtools: blue; V",
dev.off())

pdf
2
```

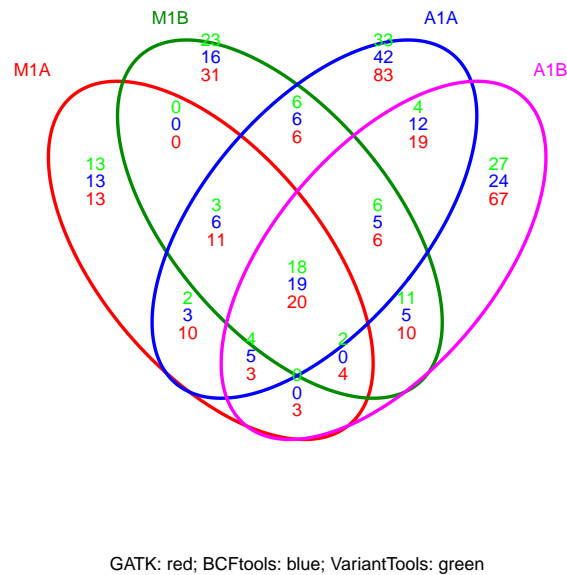


Figure 2: Venn Diagram for 4 samples from GATK, BCFtools and VariantTools.

## 11 Version Information

```
toLatex(sessionInfo())
```

- R version 3.2.1 (2015-06-18), x86\_64-pc-linux-gnu
- Locale: LC\_CTYPE=en\_US.UTF-8, LC\_NUMERIC=C, LC\_TIME=en\_US.UTF-8, LC\_COLLATE=en\_US.UTF-8, LC\_MONETARY=en\_US.UTF-8, LC\_MESSAGES=en\_US.UTF-8, LC\_PAPER=en\_US.UTF-8, LC\_NAME=C, LC\_ADDRESS=C, LC\_TELEPHONE=C, LC\_MEASUREMENT=en\_US.UTF-8, LC\_IDENTIFICATION=C
- Base packages: base, datasets, graphics, grDevices, methods, parallel, stats, stats4, utils
- Other packages: AnnotationDbi 1.31.17, BatchJobs 1.6, BBmisc 1.9, Biobase 2.29.1, BiocGenerics 0.15.3, BiocParallel 1.3.34, Biostrings 2.37.2, DBI 0.3.1, GenomInfoDb 1.5.8, GenomicAlignments 1.5.11, GenomicFeatures 1.21.13, GenomicRanges 1.21.16, gmapR 1.11.0, IRanges 2.3.14, knitr 1.10.5, Rsamtools 1.21.14, RSQLite 1.0.0, S4Vectors 0.7.10, ShortRead 1.27.5, SummarizedExperiment 0.3.2, systemPipeR 1.3.16, VariantAnnotation 1.15.21, VariantTools 1.11.0, XVector 0.9.1
- Loaded via a namespace (and not attached): annotate 1.47.1, AnnotationForge 1.11.12, base64enc 0.1-2, BiocStyle 1.7.4, biomaRt 2.25.1, bitops 1.0-6, brew 1.0-6, BSgenome 1.37.3, Category 2.35.1, checkmate 1.6.1, codetools 0.2-14, colorspace 1.2-6, crayon 1.3.1, digest 0.6.8, edgeR 3.11.2, evaluate 0.7, fail 1.2, formatR 1.2, futile.logger 1.4.1, futile.options 1.0.0, genefilter 1.51.0, ggplot2 1.0.1, GO.db 3.1.2, GOstats 2.35.1, graph 1.47.2, grid 3.2.1, GSEABase 1.31.3, gtable 0.1.2, highr 0.5, hwriter 1.3.2, labeling 0.3, lambda.r 1.1.7,

lattice 0.20-33, latticeExtra 0.6-26, limma 3.25.13, magrittr 1.5, MASS 7.3-43, Matrix 1.2-2, memoise 0.2.1, munsell 0.4.2, pheatmap 1.0.7, plyr 1.8.3, proto 0.3-10, RBGL 1.45.1, RColorBrewer 1.1-2, Rcpp 0.11.6, RCurl 1.95-4.7, reshape2 1.4.1, rjson 0.2.15, rtracklayer 1.29.12, scales 0.2.5, sendmailR 1.2-1, splines 3.2.1, stringi 0.5-5, stringr 1.0.0, survival 2.38-3, testthat 0.10.0, tools 3.2.1, XML 3.98-1.3, xtable 1.7-4, zlibbioc 1.15.0

## 12 Funding

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## 13 References

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