

VAR-Seq Workflow Template

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Package

systemPipeR 1.24.0

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1 Introduction

Users want to provide here background information about the design of their VAR-Seq project.

1.1 Background and objectives

This report describes the analysis of a VAR-Seq project studying the genetic differences among several strains ... from *organism*

1.2 Experimental design

Typically, users want to specify here all information relevant for the analysis of their NGS study. This includes detailed descriptions of FASTQ files, experimental design, reference genome, gene annotations, etc.

2 Workflow environment

2.1 Generate workflow environment

`systemPipeRdata` package is a helper package to generate a fully populated `systemPipeR` workflow environment in the current working directory with a single command. All the instruction for generating the workflow template are provide in the `systemPipeRdata` vignette [here](#).

After building and loading the workflow environment generated by `genWorkenvir` from `systemPipeRdata` all data inputs are stored in a `data/` directory and all analysis results will be written to a separate `results/` directory, while the `systemPipeVARseq.Rmd` 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. Additional parameter files are stored under `param/`.

To work with real data, users want to organize their own data similarly and substitute all test data for their own data. To rerun an established workflow on new data, the initial `targets` file along with the corresponding FASTQ files are usually the only inputs the user needs to provide.

For more details, please consult the documentation [here](#). More information about the `targets` files from `systemPipeR` can be found [here](#).

2.2 Run workflow

Now open the R markdown script `systemPipeVARseq.Rmd` in your R IDE (e.g. `vim-r` or `RStudio`) and run the workflow as outlined below.

Here pair-end workflow example is provided. Please refer to the main vignette `systemPipeR.Rmd` for running the workflow with single-end data.

The `systemPipeR` package needs to be loaded to perform the analysis steps shown in this report (H Backman and Girke 2016).

```
library(systemPipeR)
```

If you are running on a single machine, use following code as an example to check if some tools used in this workflow are in your environment **PATH**. No warning message should be shown if all tools are installed.

3 Read preprocessing

3.1 Experiment definition provided by `targets` file

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

```
targetspath <- system.file("extdata", "targetsPE.txt", package = "systemPipeR")
targets <- read.delim(targetspath, comment.char = "#")
targets[1:4, 1:4]
##           FileName1           FileName2
## 1 ./data/SRR446027_1.fastq.gz ./data/SRR446027_2.fastq.gz
## 2 ./data/SRR446028_1.fastq.gz ./data/SRR446028_2.fastq.gz
## 3 ./data/SRR446029_1.fastq.gz ./data/SRR446029_2.fastq.gz
## 4 ./data/SRR446030_1.fastq.gz ./data/SRR446030_2.fastq.gz
## SampleName Factor
## 1      M1A      M1
## 2      M1B      M1
## 3      A1A      A1
## 4      A1B      A1
```

3.2 Read quality filtering and trimming

The following removes reads with low quality base calls (here a certain pattern) from all FASTQ files.

```
targetsPE <- system.file("extdata", "targetsPE.txt", package = "systemPipeR")
dir_path <- system.file("extdata/cwl/preprocessReads/trim-pe",
  package = "systemPipeR")
trim <- loadWorkflow(targets = targetsPE, wf_file = "trim-pe.cwl",
  input_file = "trim-pe.yml", dir_path = dir_path)
trim <- renderWF(trim, inputvars = c(FileName1 = "_FASTQ_PATH1_",
  FileName2 = "_FASTQ_PATH2_", SampleName = "_SampleName_"))
trim
output(trim)[1:2]

preprocessReads(args = trim, Fct = "trimLRPatterns(Rpattern='GCCCGGTAA', subject=fq)",
  batchsize = 1e+05, overwrite = TRUE, compress = TRUE)
writeTargetsout(x = trim, file = "targets_trimPE.txt", step = 1,
  new_col = c("FileName1", "FileName2"), new_col_output_index = c(1,
  2), overwrite = TRUE)
```

3.3 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`. Use the output from previous step (fastq trimming) as the demonstration here to generate fastq report.

```
fqlist <- seeFastq(fastq = infile1(trim), batchsize = 1e+05,
  klength = 8)
pdf("./results/fastqReport.pdf", height = 18, width = 4 * length(fqlist))
seeFastqPlot(fqlist)
dev.off()
```

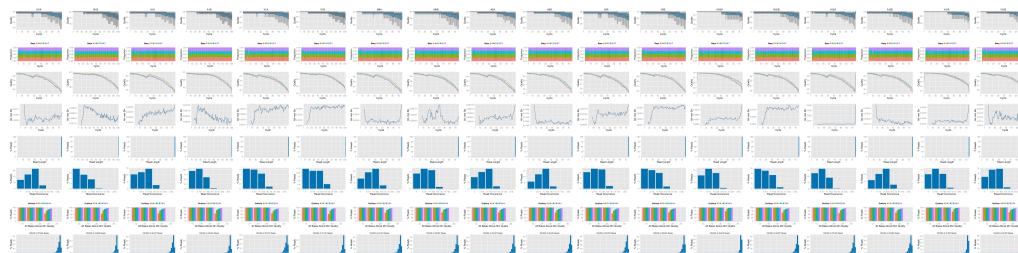


Figure 1: FASTQ quality report for 18 samples

4 Alignments

4.1 Read mapping with BWA-MEM

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

DNA sequencing nowadays are usually solid for base quality and therefore, trimming is usually not needed in most cases. Also, variant calling tools like GATK will automatically not consider low quality bases. Therefore, this test code uses untrimmed fastqs. However, it is best to test with FASTQ quality report function provided above to verify on your real data first.

4.1.1 Build index and dictionary files for BWA and GATK

The following object `dir_path` is the folder where all BWA and GATK param files are located.

```
dir_path <- system.file("extdata/cwl/gatk", package = "systemPipeR")
```

Build the index and dictionary files for BWA and GATK to run.

```
## Index for BWA
args <- loadWorkflow(targets = NULL, wf_file = "bwa-index.cwl",
  input_file = "gatk.yaml", dir_path = dir_path)
args <- renderWF(args)
cmdlist(args) # shows the command
output(args) # shows the expected output files
# Run single Machine
runCommandLine(args, make_bam = FALSE)

## Index needed for gatk tools
```

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```
args <- loadWorkflow(wf_file = "fasta_dict.cwl", input_file = "gatk.yaml",
  dir_path = dir_path)
args <- renderWF(args)
args <- runCommandLine(args, make_bam = FALSE)

## Index
args <- loadWorkflow(wf_file = "fasta_faidx.cwl", input_file = "gatk.yaml",
  dir_path = dir_path)
args <- renderWF(args)
args <- runCommandLine(args, make_bam = FALSE)
```

4.1.2 Run the read mapping

```
targetsPE <- system.file("extdata", "targetsPE.txt", package = "systemPipeR")
args <- loadWorkflow(targets = targetsPE, wf_file = "bwa-pe.cwl",
  input_file = "gatk.yaml", dir_path = dir_path)
args <- renderWF(args, inputvars = c(FileName1 = "_FASTQ_PATH1_",
  FileName2 = "_FASTQ_PATH2_", SampleName = "_SampleName_"))
cmdlist(args)[1:2]
output(args)[1:2]
```

Runs the alignments sequentially (e.g. on a single machine) by `runCommandLine` function.

```
args <- runCommandLine(args = args, make_bam = FALSE)
writeTargetsout(x = args[1:2], file = "./results/targetsPE.txt",
  step = 1, new_col = "BWA_SAM", new_col_output_index = 1,
  overwrite = TRUE)
```

Alternatively, the alignment jobs can be submitted to a compute cluster. Here is the example to run cluster jobs by `clusterRun` on a `slurm` based system. 4 cpus for each task for 18 samples, totally 72 cpus.

```
library(batchtools)
resources <- list(walltime = 120, ntasks = 1, ncpus = 4, memory = 1024)
reg <- clusterRun(args, FUN = runCommandLine, more.args = list(args = args,
  dir = FALSE, make_bam = FALSE), conffile = ".batchtools.conf.R",
  template = "batchtools.slurm.tmpl", Njobs = 18, runid = "01",
  resourceList = resources)
getStatus(reg = reg)
writeTargetsout(x = args, file = "./results/targetsPE.txt", step = 1,
  new_col = "BWA_SAM", new_col_output_index = 1, overwrite = TRUE)
```

Check whether all BAM files have been created.

```
outpaths <- subsetWF(args, slot = "output", subset = 1, index = 1)
file.exists(outpaths)
```

4.2 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.

```
read_statsDF <- alignStats(args = args)
write.table(read_statsDF, "results/alignStats.xls", row.names = FALSE,
            quote = FALSE, sep = "\t")
```

4.3 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, htmlDir = c("~/html/", "somedir/"),
            urlbase = "http://cluster.hpcc.ucr.edu/~tgirke/", urlfile = "IGVurl.txt")
```

5 Variant calling

The following performs variant calling with `GATK` and `BCFtools` on a single machine by `runCommandLine` function can be used to run the variant calling with `GATK` and `BCFtools` for each sample sequentially. If a cluster is available, running in parallel mode on a compute cluster can be performed by `clusterRun` (McKenna et al. 2010; Li 2011). Typically, the user would choose here only one variant caller rather than running several ones.

Not all users have a cluster system, so here to demonstrate an example variant calling workflow, only single-machine commands are shown. For cluster jobs, please refer to previous steps like code for `BWA` as a template to run on the cluster.

5.1 Variant calling with GATK

The following steps are based on `GATK 4.1.1.0 Best Practice`. A `targets` file is needed to load samples to a `SYSargs2` instance. There are 10 individual steps where the user can choose where to jump in and where to skip. All scripts are located at `param/cwl/gatk`. `BQSR` (Base Quality Score Recalibration) and `VQSR` (Variant Quality Score Recalibration) are very specific to a limited species like human, so this workflow does not support these steps.

5.1.1 Step1: fastq to bam

Convert `fastq` files to `bam` files to prepare for the following step. It is very important to specify your sequencing platform, default is `illumina`. User need to change `gatk_fastq2ubam.cwl` if the platform is different. Platform information is needed for the variant caller in later steps to correct calling parameters.

```
dir_path <- system.file("extdata/cwl/gatk", package = "systemPipeR")
targets.gatk <- "./results/targetsPE.txt" ## targets generated from BWA
args <- loadWorkflow(targets = targets.gatk, wf_file = "gatk_fastq2ubam.cwl",
                    input_file = "gatk.yaml", dir_path = dir_path)
args <- renderWF(args, inputvars = c(FileName1 = "_FASTQ_PATH1_",
```

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```
    FileName2 = "_FASTQ_PATH2_", SampleName = "_SampleName_"))
cmdlist(args)[1:2]
output(args)[1:2]
args <- runCommandLine(args = args[1:2], make_bam = FALSE)
writeTargetsout(x = args, file = "./results/targets_gatk.txt",
    step = 1, new_col = "GATK_UBAM", new_col_output_index = 1,
    overwrite = TRUE)
```

5.1.2 Step2: Merge bam and ubam

This step merges a bam and ubam and creates a third bam file that contains alignment information and remaining information that was removed by the aligner like BWA. The removed information is essential for variant statistics calculation. Previous steps are recommended, but variant calling can still be performed without these steps.

```
targets.gatk <- "./results/targets_gatk.txt"
args <- loadWorkflow(targets = targets.gatk, wf_file = "gatk_mergebams.cwl",
    input_file = "gatk.yaml", dir_path = dir_path)
args <- renderWF(args, inputvars = c(BWA_SAM = "_bwasam_", GATK_UBAM = "_ubam_",
    SampleName = "_SampleName_"))
cmdlist(args)[1:2]
output(args)[1:2]
args <- runCommandLine(args = args, make_bam = FALSE)
writeTargetsout(x = args, file = "./results/targets_gatk.txt",
    step = 1, new_col = "GATK_MERGE", new_col_output_index = 1,
    overwrite = TRUE)
```

5.1.3 Step3: Sort bam files by genomic coordinates

Sort bam files by genomic coordinates.

```
targets.gatk <- "./results/targets_gatk.txt"
args <- loadWorkflow(targets = targets.gatk, wf_file = "gatk_sort.cwl",
    input_file = "gatk.yaml", dir_path = dir_path)
args <- renderWF(args, inputvars = c(SampleName = "_SampleName_",
    GATK_MERGE = "_mergebam_"))
cmdlist(args)[1:2]
output(args)[1:2]
args <- runCommandLine(args = args, make_bam = FALSE)
writeTargetsout(x = args, file = "./results/targets_gatk.txt",
    step = 1, new_col = "GATK_SORT", new_col_output_index = 1,
    overwrite = TRUE)
```

5.1.4 Step4: Mark duplicates

Mark PCR artifacts in sequencing. A duplicate_metrics file will also be produced by this step, but will not be used for the next step. This file is just for the user to check duplicates status summary.

```
targets.gatk <- "./results/targets_gatk.txt"
args <- loadWorkflow(targets = targets.gatk, wf_file = "gatk_markduplicates.cwl",
```


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```
input_file = "gatk.yaml", dir_path = dir_path)
args <- renderWF(args, inputvars = c(SampleName = "_SampleName_",
  GATK_SORT = "_sort_"))
cmdlist(args)[1:2]
output(args)[1:2]
args <- runCommandLine(args = args, make_bam = FALSE)
writeTargetsout(x = args, file = "./results/targets_gatk.txt",
  step = 1, new_col = c("GATK_MARK", "GATK_MARK_METRICS"),
  new_col_output_index = c(1, 2), overwrite = TRUE)
```

5.1.5 Step5: Fixing tags

Takes the `bam` from the last step and calculates the NM, MD, and UQ tags. These tags are important for variant calling and filtering. This step is recommended but can be skipped.

```
targets.gatk <- "./results/targets_gatk.txt"
args <- loadWorkflow(targets = targets.gatk, wf_file = "gatk_fixtag.cwl",
  input_file = "gatk.yaml", dir_path = dir_path)
args <- renderWF(args, inputvars = c(SampleName = "_SampleName_",
  GATK_MARK = "_mark_"))
cmdlist(args)[1:2]
output(args)[1:2]
args <- runCommandLine(args = args, make_bam = FALSE)
writeTargetsout(x = args, file = "./results/targets_gatk.txt",
  step = 1, new_col = "GATK_FIXED", new_col_output_index = 1,
  overwrite = TRUE)
```

Up till this step, sample preprocess is done. All analysis ready BAM files and their index `.bai` files are created. Individual and cohort calling by `HaplotypeCaller` is performed from the next step.

5.1.6 Step6: HaplotypeCaller gvcf

The `HaplotypeCaller` is running a `gvcf` mode in this step. G stands for 'genomic'. The file not only contains variant sites information but also non-variant sites information; thus, at the following step, the cohort caller can use this information to validate the true variants.

```
targets.gatk <- "./results/targets_gatk.txt"
args <- loadWorkflow(targets = targets.gatk, wf_file = "gatk_haplotypecaller.cwl",
  input_file = "gatk.yaml", dir_path = dir_path)
args <- renderWF(args, inputvars = c(SampleName = "_SampleName_",
  GATK_FIXED = "_fixed_"))
cmdlist(args)[1:2]
output(args)[1:2]
args <- runCommandLine(args = args, make_bam = FALSE)
writeTargetsout(x = args, file = "./results/targets_gatk.txt",
  step = 1, new_col = "GVCF", new_col_output_index = 1, overwrite = TRUE)
```

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5.1.7 Step7: Import all gvcfs

It is recommended to import all **gvcfs** to a **TileDB** database for fast cohort variant calling at the following step. Note: if you are working with non-diploid data, use **CombineGVCFs** function from **GATK** and change the **gvcf_db_folder** parameter in **param/cwl/gatk/gatk.yaml** to be your combined **gvcf** file.

```
# drop all *.g.vcf.gz files into results folder, make sure
# the tbi index is also there.
args <- loadWorkflow(targets = NULL, wf_file = "gatk_genomicsDBImport.cwl",
  input_file = "gatk.yaml", dir_path = dir_path)
args <- renderWF(args)
cmdlist(args)
output(args)
args <- runCommandLine(args = args, make_bam = FALSE)
```

5.1.8 Step8: Cohort calling of gvcf

Assess variants by information from all gvcfs. A collective vcf called **samples.vcf.gz** is created by default naming.

```
args <- loadWorkflow(targets = NULL, wf_file = "gatk_genotypeGVCFs.cwl",
  input_file = "gatk.yaml", dir_path = dir_path)
args <- renderWF(args)
cmdlist(args)
output(args)
args <- runCommandLine(args = args, make_bam = FALSE)
```

5.1.9 Step9: Cohort hard filter variants

VQSR is not included in this workflow. Variants are hard filtered together. See this [Post](#) for parameters for hard filtering. Change these settings in **param/cwl/gatk/gatk_variantFiltration.sh** if needed.

```
args <- loadWorkflow(wf_file = "gatk_variantFiltration.cwl",
  input_file = "gatk.yaml", dir_path = dir_path)
args <- renderWF(args)
cmdlist(args)
output(args)
args <- runCommandLine(args = args, make_bam = FALSE)
```

5.1.10 Step10: Extract variant

After cohort calling, filtering, all variants for all samples are stored in one big file. Extract variants for each sample and save them separately (only variants that have passed the filters are stored).

```
targets.gatk <- "./results/targets_gatk.txt"
args <- loadWorkflow(targets = targets.gatk, wf_file = "gatk_select_variant.cwl",
  input_file = "gatk.yaml", dir_path = dir_path)
args <- renderWF(args, inputvars = c(SampleName = "_SampleName_"))
cmdlist(args)[1:2]
```

```
output(args)[1:2]
args <- runCommandLine(args = args, make_bam = FALSE)
writeTargetsout(x = args, file = "./results/targets_gatk.txt",
  step = 1, new_col = "FileName1", new_col_output_index = 1,
  overwrite = TRUE)
```

5.2 Variant calling with BCFtools

The following runs the variant calling with BCFtools. This tool takes BWA aligned BAM files, sort, mark duplicates by samtools and finally call variants by BCFtools.

```
dir_path <- system.file("extdata/cwl/workflow-bcftools", package = "systemPipeR")
targetsPE <- "./results/targetsPE.txt"
args <- loadWorkflow(targets = targetsPE, wf_file = "workflow_bcftools.cwl",
  input_file = "bcftools.yml", dir_path = dir_path)
args <- renderWF(args, inputvars = c(SampleName = "_SampleName_",
  BWA_SAM = "_SAM_"))
cmdlist(args[1])
output(args[1])
args <- runCommandLine(args = args, make_bam = FALSE)
writeTargetsout(x = args, file = "./results/targets_bcf.txt",
  step = 5, new_col = "FileName1", new_col_output_index = 1,
  overwrite = TRUE)
```

Variant calling ends here. Downstream analysis starts from the next section.

5.3 Inspect VCF file

Scripts of downstream analysis are stored in param/cwl/varseq_downstream

```
dir_path <- system.file("extdata/cwl/varseq", package="systemPipeR")
```

VCF files can be imported into R with the readVcf function. Both VCF and VRanges objects provide convenient data structure for working with variant data (e.g. SNP quality filtering).

```
library(VariantAnnotation)
args <- loadWorkflow(targets = "./results/targets_gatk.txt",
  wf_file = "filter.cwl", input_file = "varseq.yml", dir_path = dir_path)
args <- renderWF(args, inputvars = c(FileName1 = "_FILE1_"))
vcf <- readVcf(infile1(args)[1], "A. thaliana")
vcf
vr <- as(vcf, "VRanges")
vr
```

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

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this filter to the internally generated `VRanges` object using the standard subsetting syntax for two dimensional objects such as: `vr[filter,]`. The parameter files are stored under `param/cwl/varseq_downstream` as dummy cwl files. Please do not run them in `cwltool`. These files are used in the filtering steps, which helps to define the paths to the input and output VCF files that are stored in `SYSargs2` 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).

There is already some cohort filtering in GATK step 10. Some additional hard filtering is provided here. Apply if you need or skip this step.

```
dir_path <- system.file("extdata/cwl/varseq", package = "systemPipeR")
library(VariantAnnotation)
library(BBmisc) # Defines suppressAll()
args <- loadWorkflow(targets = "./results/targets_gatk.txt",
  wf_file = "filter.cwl", input_file = "varseq.yml", dir_path = dir_path)
args <- renderWF(args, inputvars = c(FileName1 = "_FILE1_", SampleName = "_SampleName_"))
filter <- "totalDepth(vr) >= 2 & (altDepth(vr) / totalDepth(vr) >= 0.8)"
# filter <- 'totalDepth(vr) >= 20 & (altDepth(vr) /
# totalDepth(vr) >= 0.8)'
suppressAll(filterVars(args, filter, varcaller = "gatk", organism = "A. thaliana"))
writeTargetsout(x = args, file = "./results/targets_filter_gatk.txt",
  step = 1, new_col = "FileName1", new_col_output_index = 1,
  overwrite = TRUE)
```

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 <- loadWorkflow(targets = "./results/targets_bcf.txt", wf_file = "filter.cwl",
  input_file = "varseq.yml", dir_path = dir_path)
args <- renderWF(args, inputvars = c(FileName1 = "_FILE1_", SampleName = "_SampleName_"))
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 = "./results/targets_filter_bcf.txt",
  step = 1, new_col = "FileName1", new_col_output_index = 1,
  overwrite = TRUE)
```

Check filtering outcome for one sample

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

```
length(as(readVcf(subsetWF(args, slot = "output", subset = 1,
  index = 1)[1], genome = "Ath"), "VRanges"))[, 1])
```

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 CWL file `param/cwl/varseq_downstream/annotate.cwl` defines the paths to the input and output files which are stored in a `SYSargs2` instance.

7.1 Basics of annotating variants

Variants overlapping with common annotation features can be identified with `locateVariants`.

```
dir_path <- system.file("extdata/cwl/varseq", package = "systemPipeR")
library("GenomicFeatures")
args <- loadWorkflow(targets = "./results/targets_filter_gatk.txt",
  wf_file = "annotate.cwl", input_file = "varseq.yml", dir_path = dir_path)
args <- renderWF(args, inputvars = c(FileName1 = "_FILE1_", SampleName = "_SampleName_"))
txdb <- loadDb("./data/tair10.sqlite")
vcf <- readVcf(infile1(args)[1], "A. thaliana")
locateVariants(vcf, txdb, CodingVariants())
```

Synonymous/non-synonymous variants of coding sequences are computed by the `predictCoding` function for variants overlapping with coding regions.

```
fa <- FaFile(normalizePath(file.path(args$yamlinput$data_path$path,
  args$yamlinput$ref_name)))
predictCoding(vcf, txdb, seqSource = fa)
```

7.2 Annotate filtered variants GATK

```
library("GenomicFeatures")
args <- loadWorkflow(targets = "./results/targets_filter_gatk.txt",
  wf_file = "annotate.cwl", input_file = "varseq.yml", dir_path = dir_path)
args <- renderWF(args, inputvars = c(FileName1 = "_FILE1_", SampleName = "_SampleName_"))
txdb <- loadDb("./data/tair10.sqlite")
fa <- FaFile(normalizePath(file.path(args$yamlinput$data_path$path,
  args$yamlinput$ref_name)))
suppressAll(variantReport(args = args, txdb = txdb, fa = fa,
  organism = "A. thaliana"))
writeTargetsout(x = args, file = "./results/targets_report_gatk.txt",
  step = 1, new_col = "FileName1", new_col_output_index = 1,
  overwrite = TRUE)
```

7.3 Annotate filtered variants `bcftools`

```
library("GenomicFeatures")
args <- loadWorkflow(targets = "./results/targets_filter_bcf.txt",
  wf_file = "annotate.cwl", input_file = "varseq.yml", dir_path = dir_path)
args <- renderWF(args, inputvars = c(FileName1 = "_FILE1_", SampleName = "_SampleName_"))
txdb <- loadDb("./data/tair10.sqlite")
fa <- FaFile(normalizePath(file.path(args$yamlinput$data_path$path,
  args$yamlinput$ref_name)))
suppressAll(variantReport(args = args, txdb = txdb, fa = fa,
  organism = "A. thaliana"))
writeTargetsout(x = args, file = "./results/targets_report_bcf.txt",
  step = 1, new_col = "FileName1", new_col_output_index = 1,
  overwrite = TRUE)
```

View annotation result for single sample

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

8 Combine annotation results among samples

To simplify comparisons among samples, the `combineVarReports` function combines all variant annotation reports referenced in a `SYSargs2` 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 `GATK`

```
dir_path <- system.file("extdata/cwl/varseq", package = "systemPipeR")
args <- loadWorkflow(targets = "results/targets_report_gatk.txt",
  wf_file = "combine.cwl", input_file = "varseq.yml", dir_path = dir_path)
args <- renderWF(args, inputvars = c(FileName1 = "_FILE1_", SampleName = "_SampleName_"))
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 `bcftools`

```
args <- loadWorkflow(targets = "results/targets_report_bcf.txt",
  wf_file = "combine.cwl", input_file = "varseq.yml", dir_path = dir_path)
args <- renderWF(args, inputvars = c(FileName1 = "_FILE1_", SampleName = "_SampleName_"))
combinedDF <- combineVarReports(args, filtercol = c(Consequence = "nonsynonymous"))
write.table(combinedDF, "./results/combinedDF_nonsyn_bcf.xls",
  quote = FALSE, row.names = FALSE, sep = "\t")
```

9 Summary statistics of variants

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

9.1 Summary of variants GATK

```
args <- loadWorkflow(targets = "./results/targets_report_gatk.txt",
  wf_file = "combine.cwl", input_file = "varseq.yml", dir_path = dir_path)
args <- renderWF(args, inputvars = c(FileName1 = "_FILE1_", SampleName = "_SampleName_"))
varSummary(args)
write.table(varSummary(args), "./results/variantStats_gatk.xls",
  quote = FALSE, col.names = NA, sep = "\t")
```

9.2 Summary of variants bcf

```
args <- loadWorkflow(targets = "./results/targets_report_bcf.txt",
  wf_file = "combine.cwl", input_file = "varseq.yml", dir_path = dir_path)
args <- renderWF(args, inputvars = c(FileName1 = "_FILE1_", SampleName = "_SampleName_"))
varSummary(args)
write.table(varSummary(args), "./results/variantStats_bcf.xls",
  quote = FALSE, col.names = NA, sep = "\t")
```

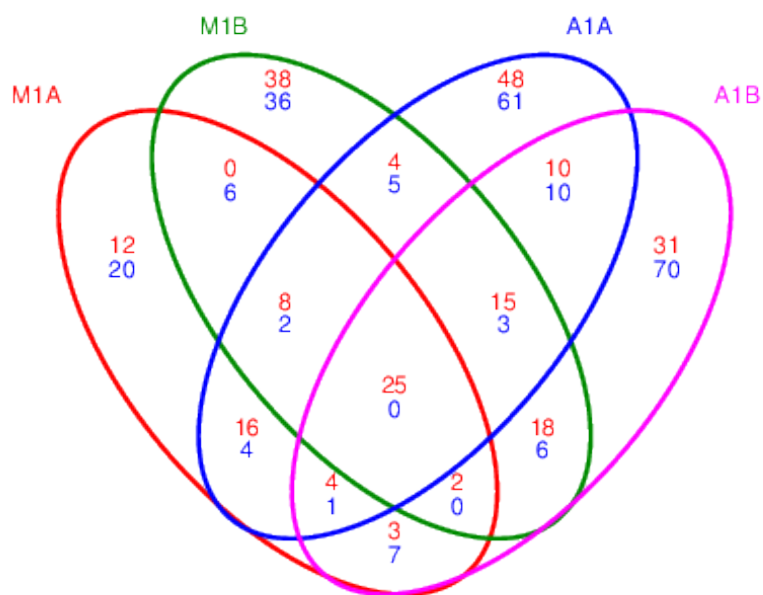
10 Venn diagram of variants

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.

```
dir_path <- system.file("extdata/cwl/varseq", package = "systemPipeR")
## gatk
args <- loadWorkflow(targets = "results/targets_report_gatk.txt",
  wf_file = "combine.cwl", input_file = "varseq.yml", dir_path = dir_path)
args <- renderWF(args, inputvars = c(FileName1 = "_FILE1_", SampleName = "_SampleName_"))
varlist <- sapply(names(subsetWF(args[1:2], slot = "output",
  subset = 1, index = 1)), function(x) as.character(read.delim(subsetWF(args[1:2],
  slot = "output", subset = 1, index = 1)[x])$VARID))
vennset_gatk <- overLapper(varlist, type = "vennsets")

## bcf
args <- loadWorkflow(targets = "./results/targets_report_bcf.txt",
  wf_file = "combine.cwl", input_file = "varseq.yml", dir_path = dir_path)
args <- renderWF(args, inputvars = c(FileName1 = "_FILE1_", SampleName = "_SampleName_"))
varlist <- sapply(names(subsetWF(args[1:2], slot = "output",
  subset = 1, index = 1)), function(x) as.character(read.delim(subsetWF(args[1:2],
  slot = "output", subset = 1, index = 1)[x])$VARID))
vennset_bcf <- overLapper(varlist, type = "vennsets")
```

```
pdf("./results/vennplot_var.pdf")
vennPlot(list(vennset_gatk, vennset_bcf), mymain = "", mysub = "GATK: red; BCFtools: blue",
          colmode = 2, ccol = c("red", "blue"))
dev.off()
```



GATK: red; BCFtools: blue

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

11 Plot variants programmatically

The following plots a selected variant with `ggbio`.

In this example, the input BAM file is from the GATK step 5, analysis ready bam. You can use other aligned BAMs as well, but make sure they are indexed. The VCF file is taken from Inspect VCF file section or you can load your own vcf.

```
library(ggbio)
mychr <- "ChrC"
mystart <- 11000
```


VAR-Seq Workflow Template

```
myend <- 13000
args <- loadWorkflow(targets = "results/targets_gatk.txt", wf_file = "combine.cwl",
  input_file = "varseq.yml", dir_path = "param/cwl/varseq_downstream/")
args <- renderWF(args, inputvars = c(GATK_FIXED = "_FILE1_",
  SampleName = "_SampleName_"))
ga <- readGAlignments(subsetWF(args, slot = "input", subset = 1)[1],
  use.names = TRUE, param = ScanBamParam(which = GRanges(mychr,
    IRanges(mystart, myend))))
p1 <- autoplot(ga, geom = "rect")
p2 <- autoplot(ga, geom = "line", stat = "coverage")
p3 <- autoplot(vcf[seqnames(vcf) == mychr], type = "fixed") +
  xlim(mystart, myend) + theme(legend.position = "none", axis.text.y = element_blank(),
    axis.ticks.y = element_blank())
p4 <- autoplot(loadDb("./data/tair10.sqlite"), which = GRanges(mychr,
  IRanges(mystart, myend)), names.expr = "gene_id")
png("./results/plot_variant.png")
tracks(Reads = p1, Coverage = p2, Variant = p3, Transcripts = p4,
  heights = c(0.3, 0.2, 0.1, 0.35)) + ylab("")
dev.off()
```

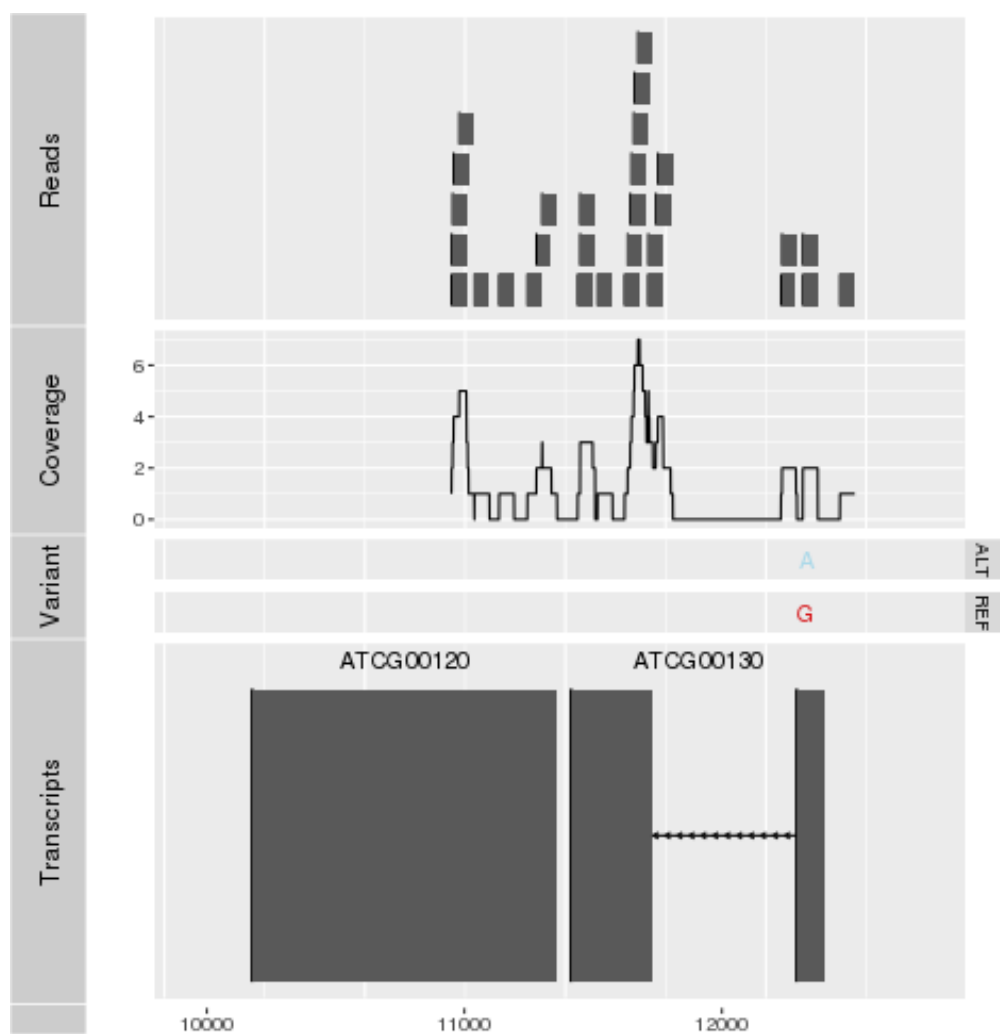


Figure 3: Plot variants with programmatically.

12 Version Information

```
sessionInfo()
## R version 4.0.3 (2020-10-10)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 20.04.1 LTS
##
## Matrix products: default
## BLAS:   /usr/lib/x86_64-linux-gnu/blas/libblas.so.3.9.0
## LAPACK: /home/dcassol/src/R-4.0.3/lib/libRlapack.so
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8      LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
```

VAR-Seq Workflow Template

```
## [7] LC_PAPER=en_US.UTF-8      LC_NAME=C
## [9] LC_ADDRESS=C                 LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8  LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats4      parallel  stats      graphics  grDevices
## [6] utils       datasets  methods    base
##
## other attached packages:
## [1] systemPipeR_1.24.0      ShortRead_1.48.0
## [3] GenomicAlignments_1.26.0 SummarizedExperiment_1.20.0
## [5] Biobase_2.50.0          MatrixGenerics_1.2.0
## [7] matrixStats_0.57.0      BiocParallel_1.24.0
## [9] Rsamtools_2.6.0         Biostrings_2.58.0
## [11] XVector_0.30.0          GenomicRanges_1.42.0
## [13] GenomeInfoDb_1.26.0     IRanges_2.24.0
## [15] S4Vectors_0.28.0        BiocGenerics_0.36.0
## [17] BiocStyle_2.18.0
##
## loaded via a namespace (and not attached):
## [1] colorspace_1.4-1      rjson_0.2.20
## [3] hwriter_1.3.2         ellipsis_0.3.1
## [5] bit64_4.0.5           AnnotationDbi_1.52.0
## [7] xml2_1.3.2            codetools_0.2-16
## [9] splines_4.0.3         knitr_1.30
## [11] jsonlite_1.7.1        annotate_1.68.0
## [13] GO.db_3.12.0          dbplyr_1.4.4
## [15] png_0.1-7             pheatmap_1.0.12
## [17] graph_1.68.0          BiocManager_1.30.10
## [19] compiler_4.0.3        httr_1.4.2
## [21] GOstats_2.56.0         backports_1.1.10
## [23] assertthat_0.2.1      Matrix_1.2-18
## [25] limma_3.46.0          formatR_1.7
## [27] htmltools_0.5.0       prettyunits_1.1.1
## [29] tools_4.0.3           gtable_0.3.0
## [31] glue_1.4.2            GenomeInfoDbData_1.2.4
## [33] Category_2.56.0       dplyr_1.0.2
## [35] rsvg_2.1              batchtools_0.9.14
## [37] rappdirs_0.3.1        V8_3.3.1
## [39] Rcpp_1.0.5            vctrs_0.3.4
## [41] rtracklayer_1.50.0    xfun_0.18
## [43] stringr_1.4.0         lifecycle_0.2.0
## [45] XML_3.99-0.5          edgeR_3.32.0
## [47] zlibbioc_1.36.0       scales_1.1.1
## [49] BSgenome_1.58.0       VariantAnnotation_1.36.0
## [51] hms_0.5.3             RBGL_1.66.0
## [53] RColorBrewer_1.1-2    yaml_2.2.1
## [55] curl_4.3              memoise_1.1.0
## [57] ggplot2_3.3.2         biomaRt_2.46.0
## [59] latticeExtra_0.6-29   stringi_1.5.3
## [61] RSQLite_2.2.1         genefilter_1.72.0
```

```
## [63] checkmate_2.0.0      GenomicFeatures_1.42.0
## [65] DDT_0.1               rlang_0.4.8
## [67] pkgconfig_2.0.3       bitops_1.0-6
## [69] evaluate_0.14         lattice_0.20-41
## [71] purrr_0.3.4           bit_4.0.4
## [73] tidyselect_1.1.0      GSEABase_1.52.0
## [75] AnnotationForge_1.32.0 magrittr_1.5
## [77] bookdown_0.21         R6_2.5.0
## [79] generics_0.0.2        base64url_1.4
## [81] DelayedArray_0.16.0   DBI_1.1.0
## [83] pillar_1.4.6          withr_2.3.0
## [85] survival_3.2-7        RCurl_1.98-1.2
## [87] tibble_3.0.4          crayon_1.3.4
## [89] BiocFileCache_1.14.0  rmarkdown_2.5
## [91] jpeg_0.1-8.1          progress_1.2.2
## [93] locfit_1.5-9.4        grid_4.0.3
## [95] data.table_1.13.2     blob_1.2.1
## [97] Rgraphviz_2.34.0      digest_0.6.27
## [99] xtable_1.8-4          brew_1.0-6
## [101] openssl_1.4.3         munsell_0.5.0
## [103] askpass_1.1
```

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