

SomaticSeq Documentation

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1 Introduction

SomaticSeq is a flexible post-somatic-mutation-calling workflow for improved accuracy. We have incorporated multiple somatic mutation caller(s) to obtain a combined call set, and then it uses machine learning to distinguish true mutations from false positives from that call set. We have incorporated the following somatic mutation caller: MuTect/Indelocator, MuTect2, VarScan2, JointSNVMix, SomaticSniper, VarDict, MuSE, LoFreq, and Scalpel. You may incorporate some or all of those callers into your own pipeline with SomaticSeq.

The manuscript, An ensemble approach to accurately detect somatic mutations using SomaticSeq, is published in Genome Biology 2015, 16:197. The SomaticSeq project is located at <http://bioinform.github.io/somaticseq/>. The data described in the manuscript is also described at <http://bioinform.github.io/somaticseq/data.html>. There have been some major improvements since the publication.

SomaticSeq.Wrapper.sh is a bash script that calls a series of scripts to combine the output of the somatic mutation caller(s), after the somatic mutation callers are run. Then, depending on what R scripts are fed to SomaticSeq.Wrapper.sh, it will either 1) train the call set into a classifier, 2) predict high-confidence somatic mutations from the call set based on a pre-defined classifier, or 3) simply label the calls (i.e., PASS, LowQual, or REJECT) based on majority vote of the tools.

1.1 Dependencies

- Python 3, plus regex, pysam, numpy, and scipy libraries. All the .py scripts are written in Python 3 (Yes, Python 3. I deserve brownie points from Python developers).
- R, plus the ada package in R.
- BEDTools (if there is an inclusion and/or an exclusion region file)
- Optional: Free GATK version 3. You can use GATK CombineVariants to merge VCF files if the jar file is provided to `-gatk`. Otherwise, the sorting is done by the `vcfsort.pl` script written by German Gaston Leparé.
- Optional: dbSNP and COSMIC files in VCF format (if you want to use these features as a part of the training).
- At least one of MuTect/Indelocator, MuTect2, VarScan2, JointSNVMix, SomaticSniper, VarDict, MuSE, LoFreq, Scalpel, and Strelka2. Those are the tools we have incorporated in SomaticSeq. If there are other somatic tools that may be good addition to our list, please make the suggestion to us.

2 To use SomaticSeq.Wrapper.sh

The SomaticSeq.Wrapper.sh is a wrapper script that calls a series of programs and procedures. It can be easily run if all the dependencies are met. Some optional parameters are hard-coded as defaults, but can be easily edited by advanced users. In the next section, we also described the workflow in more detail, so you are not dependent on this wrapper script. You can either modify this wrapper script or create your own workflow.

2.1 To train data set into a classifier

To create a trained classifier, ground truth files are required for the data sets. There is also an option to include a list of regions to include and/or exclude. The exclusion or inclusion regions can be VCF or BED files. An inclusion region may be subset of the call sets where you have validated their true/false mutation status, so that only those regions will be used for training. An exclusion region can be regions where the “truth” is ambiguous.

All the output VCF files from individual callers are optional. Those VCF files can be bgzipped if they have .vcf.gz extensions. It is imperative that the parameters used for the training and prediction are identical.

```
1 # For training, truth file and the correct R script are required.
3 SomaticSeq.Wrapper.sh \
4   --mutect MuTect/variants.snp.vcf \
5   --mutect2 MuTect2/variants.vcf \
6   --indelocator Indelocator/variants.indel.vcf \
7   --varscan-snv VarScan2/variants.snp.vcf \
8   --varscan-indel VarScan2/variants.indel.vcf \
9   --jsm JointSNVMix2/variants.snp.vcf \
10  --sniper SomaticSniper/variants.snp.vcf \
11  --vardict VarDict/variants.vcf \
12  --muse MuSE/variants.snp.vcf \
13  --lofreq-snv LoFreq/variants.snp.vcf \
14  --lofreq-indel LoFreq/variants.indel.vcf \
15  --scalpel Scalpel/variants.indel.vcf \
16  --strelka-snv Strelka/variants.snv.vcf \
17  --strelka-indel Strelka/variants.indel.vcf \
18  --normal-bam matched_normal.bam \
19  --tumor-bam tumor.bam \
20  --ada-r-script ada_model_builder.R \
21  --genome-reference human_b37.fasta \
22  --cosmic cosmic.b37.v71.vcf \
23  --dbsnp dbSNP.b37.v141.vcf \
24  --gatk $PATH/TO/GenomeAnalysisTK.jar \
25  --exclusion-region ignore.bed \
26  --inclusion-region validated.bed \
27  --truth-snv truth.snp.vcf \
28  --truth-indel truth.indel.vcf \
29  --output-dir $OUTPUT_DIR
```

SomaticSeq.Wrapper.sh supports any combination of the somatic mutation callers we have incorporated into the workflow. SomaticSeq will run based on the output VCFs you have provided. It will train for SNV and/or INDEL if you provide the truth.snp.vcf and/or truth.indel.vcf file(s) as well as the proper R script (ada_model_builder.R). Otherwise, it will fall back to the simple caller consensus mode.

2.2 To predict somatic mutation based on trained classifiers

Make sure the classifiers and the proper R script (ada_model_predictor.R) are supplied, Without either of them, it will fall back to the simple caller consensus mode.

```
1 # The *.RData files are trained classifier from the training mode.
SomaticSeq.Wrapper.sh \
3 --mutect MuTect/variants.snp.vcf \
--mutect2 MuTect2/variants.vcf \
5 --indelocator Indelocator/variants.indel.vcf \
--varscan-snv VarScan2/variants.snp.vcf \
7 --varscan-indel VarScan2/variants.indel.vcf \
--jsm JointSNVMix2/variants.snp.vcf \
9 --sniper SomaticSniper/variants.snp.vcf \
--vardict VarDict/variants.vcf \
11 --muse MuSE/variants.snp.vcf \
--lofreq-snv LoFreq/variants.snp.vcf \
13 --lofreq-indel LoFreq/variants.indel.vcf \
--scalpel Scalpel/variants.indel.vcf \
15 --strelka-snv Strelka/variants.snv.vcf \
--strelka-indel Strelka/variants.indel.vcf \
17 --normal-bam matched_normal.bam \
--tumor-bam tumor.bam \
19 --ada-r-script ada_model_predictor.R \
--genome-reference human_b37.fasta \
21 --cosmic cosmic.b37.v71.vcf \
--dbsnp dbSNP.b37.v141.vcf \
23 --snpeff-dir $PATH/TO/DIR/snpSift \
--gatk $PATH/TO/GenomeAnalysisTK.jar \
25 --exclusion-region ignore.bed \
--inclusion-region validated.bed
27 --classifier-snv sSNV.Classifier.RData \
--classifier-indel sINDEL.Classifier.RData \
29 --pass-threshold 0.5 \
--lowqual-threshold 0.1 \
31 --output-dir $OUTPUT_DIR
```

If both MuTect2 and MuTect/Indelocator VCF files are provided, the script is written such that it will use MuTect2 and ignore MuTect.

2.3 To classify based on simple majority vote

Same as the command previously, but not including the R script or the ground truth files. Without those information, SomaticSeq will fall back into a simple majority vote.

3 The step-by-step SomaticSeq Workflow

We'll describe the workflow here, so you may modify the workflow and/or create your own workflow instead of using the wrapper script described previously.

3.1 Combine the call sets

We use GATK CombineVariants to combine the VCF files fkeep-intermediates:rom different callers, although it does not matter what tools are used to merge VCF files. We GATK CombineVariants because it's quite fast. To make them compatible with GATK, the VCF files are modified.

A simple alternative method is to use GNU sort and uniq in Linux to list all the unique first-5-column (i.e., CHROM, POS, ID, REF, and ALT) from all the VCF files, and then fill the remaining required VCF columns with whatever string and sort it according to the reference. That VCF file will do the job just fine.

For our GATK CombineVariants procedure:

1. Modify MuTect and/or Indelocator output VCF files. Since MuTect's output VCF do not always put the tumor and normal samples in the same columns, the script will determine that information based on either the BAM files (the header has sample name information), or based on the sample information that you tell it, and then determine which column belongs to the normal, and which column belongs to the tumor.

```
# Modify MuTect and Indelocator's output VCF based on BAM files
2 modify_MuTect.py -infile input.vcf -outfile output.vcf -nbam normal.bam -tbam
  tumor.bam

4 # Based on the sample name you supply:
  modify_MuTect.py -infile input.vcf -outfile output.vcf -nsn NormalSampleName -
    tsn TumorSampleName
```

2. Modify VarScan's output VCF files to be rigorously concordant to VCF format standard, and to attach the tag 'VarScan2' to somatic calls.

```
1 # Do it for both the SNV and indel
  modify_VJSD.py -method VarScan2 -infile input.vcf -outfile output.vcf
```

3. JointSNVMix2 does not output VCF files. In our own workflow, we have already converted its text file into a basic VCF file with an 2 awk one-liners, which you may see in the Run_5_callers directory, which are:

```
# To avoid text files in the order of terabytes, this awk one-liner keeps
  entries where the reference is not "N", and the somatic probabilities are
  at least 0.95.
2 awk -F "\t" 'NR!=1 && $4!="N" && $10+$11>=0.95'

4 # This awk one-liner converts the text file into a basic VCF file
  awk -F "\t" '{print $1 "\t" $2 "\t.\t" $3 "\t" $4 "\t.\t.\tAAAB=" $10 " ";AABB="
    $11 "\tRD:AD\t" $5 ":" $6 "\t" $7 ":" $8}'

6

8 ## The actual commands we've used in our workflow:
  echo -e '##fileformat=VCFv4.1' > unsorted.vcf
10 echo -e '##INFO=<ID=AAAB,Number=1,Type=Float,Description="Probability of Joint
  Genotype AA in Normal and AB in Tumor">' >> unsorted.vcf
  echo -e '##INFO=<ID=AABB,Number=1,Type=Float,Description="Probability of Joint
  Genotype AA in Normal and BB in Tumor">' >> unsorted.vcf
12 echo -e '##FORMAT=<ID=RD,Number=1,Type=Integer,Description="Depth of reference
  -supporting bases (reads1)">' >> unsorted.vcf
  echo -e '##FORMAT=<ID=AD,Number=1,Type=Integer,Description="Depth of variant-
  supporting bases (reads2)">' >> unsorted.vcf
14 echo -e '#CHROM\tPOS\tID\tREF\tALT\tQUAL\tFILTER\tINFO\tFORMAT\tNORMAL\tTUMOR'
  >> unsorted.vcf

16 python $PATH/TO/jsm.py classify joint-snv-mix-two genome.GRCh37.fa normal.bam
  tumor.bam trained.parameter.cfg /dev/stdout | \
```

```

18 awk -F "\t" 'NR!=1 && $4!="N" && $10+$11>=0.95' |\
awk -F "\t" '{print $1 "\t" $2 "\t.\t" $3 "\t" $4 "\t.\t.\tAAAB=" $10 ";AABB="
    $11 "\tRD:AD\t" $5 ":" $6 "\t" $7 ":" $8}' >> unsorted.vcf

```

After that, you'll also want to sort the VCF file. Now, to modify that basic VCF into something that will be compatible with other VCF files under GATK CombineVariants:

```

modify_VJSD.py -method JointSNVMix2 -infile input.vcf -outfile output.vcf

```

4. Modify SomaticSniper's output:

```

1 modify_VJSD.py -method SomaticSniper -infile input.vcf -outfile output.vcf

```

5. VarDict has both SNV and indel, plus some other variants in the same VCF file. Our script will create two files, one for SNV and one for indel, while everything else is ignored for now. By default, LikelySomatic/StrongSomatic and PASS calls will be labeled VarDict. However, in our SomaticSeq paper, based on our experience in DREAM Challenge, we implemented two custom filters to relax the VarDict tagging criteria.

```

1 # Default VarDict tagging criteria, only PASS (and Likely or Strong Somatic):
  modify_VJSD.py -method VarDict -infile input.vcf -outfile output.vcf
3
4 # When running VarDict, if var2vcf_paired.pl is used to generate the VCF file,
  you may relax the tagging criteria with -filter paired
5 modify_VJSD.py -method VarDict -infile input.vcf -outfile output.vcf -filter
  paired
7
8 # When running VarDict, if var2vcf_somatic.pl is used to generate the VCF file
  , you may relax the tagging criteria with -filter somatic
  modify_VJSD.py -method VarDict -infile input.vcf -outfile output.vcf -filter
  somatic

```

In the SomaticSeq paper, -filter somatic was used because var2vcf_somatic.pl was used to generate VarDict's VCF files. In the SomaticSeq.Wrapper.sh script, however, -filter paired is used because VarDict authors have since recommended var2vcf_paired.pl script to create the VCF files. While there are some differences (different stringencies in some filters) in what VarDict labels as PASS between the somatic.pl and paired.pl scripts, the difference is miniscule after applying our custom filter (which relaxes the filter, resulting in a difference about 5 calls out of 15,000).

The output files will be snp.output.vcf and indel.output.vcf.

6. MuSE was not a part of our analysis in the SomaticSeq paper. We have implemented it later.

```

modify_VJSD.py -method MuSE -infile input.vcf -outfile output.vcf

```

7. LoFreq and Scalpel do not require modification. LoFreq has no sample columns anyway.

8. Strelka's INDEL VCF clashes with Scalpel's VCF during GATK CombineVariants, for reasons we haven't bothered to figure out. We just removed the sample columns for Strelka's INDEL to solve the problem during variant merging.

```
1 gunzip -c somatic.indel.vcf.gz | awk -F "\t" '{ if ($0 !~ /^##/) print $1 "\t"
    $2 "\t" $3 "\t" $4 "\t" $5 "\t" $6 "\t" $7 "\t" $8; else print $0}' OFS
    ="\t" > strelka.indel.truncated.vcf
```

9. Finally, with the VCF files modified, you may combine them with GATK CombineVariants: one for SNV and one for indel separately. There is no particular reason to use GATK CombineVariants. Other combiners should also work. The only useful thing here is to combine the calls and GATK CombineVariants does it well and pretty fast.

```
1 # Combine the VCF files for SNV. Any or all of the VCF files may be present.
2 # -nt 6 means to use 6 threads in parallel
3 java -jar $PATH/TO/GenomeAnalysisTK.jar -T CombineVariants -R genome.GRCh37.fa
    -nt 6 --setKey null --genotypemergeoption UNSORTED -V mutect.vcf -V
    varscan.snp.vcf -V jointsvnmix.vcf -V snp vardict.vcf -V muse.vcf --out
    CombineVariants.snp.vcf
4 java -jar $PATH/TO/GenomeAnalysisTK.jar -T CombineVariants -R genome.GRCh37.fa
    -nt 6 --setKey null --genotypemergeoption UNSORTED -V indelocator.vcf -V
    varscan.snp.vcf -V indel vardict.vcf --out CombineVariants.indel.vcf
```

3.2 For model training: process and annotate the VCF files (union of call sets)

This step may be needed for model training. The workflow in SomaticSeq.Wrapper.sh allows for inclusion and exclusion region. An inclusion region means we will only use calls inside these regions. An exclusion region means we do not care about calls inside this region. DREAM Challenge had exclusion regions, e.g., blacklisted regions, etc.

```
1 # In the DREAM_Stage_3 directory, we have included an exclusion region BED file as
    an example
2 # This command uses BEDtools to rid of all calls in the exclusion region
    intersectBed -header -a BINA_somatic.snp.vcf -b ignore.bed -v > somatic.snp.
    processed.vcf
3 intersectBed -header -a BINA_somatic.indel.vcf -b ignore.bed -v > somatic.indel.
    processed.vcf
4
5 # Alternatively (or both), this command uses BEDtools to keep only calls in the
    inclusion region
6 intersectBed -header -a BINA_somatic.snp.vcf -b inclusion.bed > somatic.snp.
    processed.vcf
7 intersectBed -header -a BINA_somatic.indel.vcf -b inclusion.bed > somatic.indel.
    processed.vcf
8
```

3.3 Convert the VCF file, annotated or otherwise, into a tab separated file

This script works for all VCF files. It extracts information from BAM files as well as some VCF files created by the individual callers. If the ground truth VCF file is included, a called variant will be annotated as a true positive, and everything will be annotated as a false positive.

```

1 # SNV
  SSeq-merged.vcf2tsv.py -ref genome.GRCh37.fa -myvcf somatic.snp.processed.vcf -
    truth Ground.truth.snp.vcf -mutect MuTect/variants.snp.vcf.gz -varscan VarScan2
    /variants.snp.vcf -jsm JSM2/variants.vcf -sniper SomaticSniper/variants.vcf -
    vardict VarDict/snp.variants.vcf -muse MuSE/variants.vcf -lofreq LoFreq/
    variants.snp.vcf -strelka Strelka/variants.snp.vcf -dedup -tbam tumor.bam -nbam
    normal.bam -outfile Ensemble.sSNV.tsv

```

That was for SNV, and indel is almost the same thing. After version 2.1, we have replaced all information from SAMtools and HaplotypeCaller with information directly from the BAM files. The accuracy differences are negligible with significant improvement in usability and resource requirement.

```

# INDEL:
2 SSeq-merged.vcf2tsv.py -ref genome.GRCh37.fa -myvcf somatic.indel.processed.vcf -
  truth Ground.truth.indel.vcf -varscan VarScan2/variants.snp.vcf -vardict
  VarDict/indel.variants.vcf -lofreq LoFreq/variants.indel.vcf -scalpel Scalpel/
  variants.indel.vcf -strelka Strelka/variants.indel.vcf -tbam tumor.bam -nbam
  normal.bam -dedup -outfile Ensemble.sINDEL.tsv

```

At the end of this, Ensemble.sSNV.tsv and Ensemble.sINDEL.tsv are created.

All the options for SSeq-merged.vcf2tsv.py are listed here. They can also be displayed by running SSeq-merged.vcf2tsv.py -help.

```

2 -myvcf      Input VCF file of the merged calls [REQUIRED]
3 -ref       Genome reference fa/fastq file [REQUIRED]
4 -nbam      BAM file of the matched normal sample [REQUIRED]
5 -tbam      BAM file of the tumor sample [REQUIRED]
6 -ref       Genome reference fa/fastq file [REQUIRED]
7 -truth     Ground truth VCF file. Every other position is a False Positive.
8 -dbsnp     dbSNP VCF file
9 -cosmic    COSMIC VCF file
10 -mutect    VCF file from either MuTect2, MuTect, or Indelocator
11 -sniper    VCF file from SomaticSniper
12 -varscan   VCF file from VarScan2
13 -jsm       VCF file from Bina's workflow that contains JointSNVMix2
14 -vardict   VCF file that contains only SNV or only INDEL from VarDict
15 -muse      VCF file from MuSE
16 -lofreq    VCF file from LoFreq
17 -scalpel   VCF file from Scalpel
18 -strelka   VCF file from Strelka
19 -dedup     A flag to consider only primary reads
20 -minMQ     Minimum mapping quality for reads to be considered (Default = 1)
21 -minBQ     Minimum base quality for reads to be considered (Default = 5)
22 -mincaller Minimum number of caller classification for a call to be considered
    (Use 0.5 to consider some LowQual calls. Default = 0).
23 -scale     The options are phred, fraction, or None, to convert numbers to
    Phred scale or fractional scale. (default = None, i.e., no conversion)
24 -outfile   Output TSV file name

```

Note: Do not worry if Python throws a warning like this.

```

1 RuntimeWarning: invalid value encountered in double_scalars
  z = (s - expected) / np.sqrt(n1*n2*(n1+n2+1)/12.0)

```

This is to tell you that scipy was attempting some statistical test with empty data. That's usually due to the fact that normal BAM file has no variant reads at that given position. That is why lots of values are NaN for the normal.

3.4 Model Training or Mutation Prediction

You can use Ensemble.sSNV.tsv and Ensemble.sINDEL.tsv files either for model training (provided that their mutation status is annotated with 0 or 1) or mutation prediction. This is done with stochastic boosting algorithm we have implemented in R.

Model training:

```
1 # Training:
2 r_script/ada_model_builder.R Ensemble.sSNV.tsv
3 r_script/ada_model_builder.R Ensemble.sINDEL.tsv
```

Ensemble.sSNV.tsv.Classifier.RData and Ensemble.sINDEL.tsv.Classifier.RData will be created from model training.

Mutation prediction:

```
1 # Mutation prediction:
2 r_script/ada_model_predictor.R Ensemble.sSNV.tsv.Classifier.RData Ensemble.sSNV.
   tsv Trained.sSNV.tsv
3 r_script/ada_model_predictor.R Ensemble.sINDEL.tsv.Classifier.RData Ensemble.sINDEL
   .tsv Trained.sINDEL.tsv
```

After mutation prediction, if you feel like it, you may convert Trained.sSNV.tsv and Trained.sINDEL.tsv into VCF files. Use -tools to list ONLY the individual tools used to have appropriately annotated VCF files. Accepted tools are CGA (for MuTect/Indelocator), VarScan2, JointSNVMix2, SomaticSniper, VarDict, MuSE, LoFreq, and/or Scalpel. To list a tool without having run it, the VCF will be annotated as if the tool was run but did not identify that position as a somatic variant.

```
1 # Probability above 0.7 labeled PASS (-pass 0.7), and between 0.1 and 0.7 labeled
   LowQual (-low 0.1):
2 # Use -all to include REJECT calls in the VCF file
3 # Use -phred to convert probability values (between 0 to 1) into Phred scale in the
   QUAL column in the VCF file
4
5 SSeq_tsv2vcf.py -tsv Trained.sSNV.tsv -vcf Trained.sSNV.vcf -pass 0.7 -low 0.1
   -tools CGA VarScan2 JointSNVMix2 SomaticSniper VarDict MuSE LoFreq Strelka -all
   -phred
6
7 SSeq_tsv2vcf.py -tsv Trained.sINDEL.tsv -vcf Trained.sINDEL.vcf -pass 0.7 -low 0.1
   -tools CGA VarScan2 VarDict LoFreq Scalpel Strelka -all -phred
```

4 Release Notes

Make sure training and prediction use the same version. Otherwise the prediction is not valid.

4.1 Version 1.0

Version used to generate data in the manuscript and Stage 5 of the ICGC-TCGA DREAM Somatic Mutation Challenge, where SomaticSeq’s results were #1 for INDEL and #2 for SNV.

In the original manuscript, VarDict’s `var2vcf_somatic.pl` script was used to generate VarDict VCFs, and subsequently “-filter somatic” was used for `SSeq_merged.vcf2tsv.py`. Since then (including DREAM Challenge Stage 5), VarDict recommends `var2vcf_paired.pl` over `var2vcf_somatic.pl`, and subsequently “-filter paired” was used for `SSeq_merged.vcf2tsv.py`. The difference in SomaticSeq results, however, is pretty much negligible.

4.2 Version 1.1

Automated the `SomaticSeq.Wrapper.sh` script for both training and prediction mode. No change to any algorithm.

4.3 Version 1.2

Have implemented the following improvement, mostly for indels:

- `SSeq_merged.vcf2tsv.py` can now accept pileup files to extract read depth and DP4 (reference forward, reference reverse, alternate forward, and alternate reverse) information (mainly for indels). Previously, that information can only be extracted from SAMtools VCF. Since the SAMtools or HaplotypeCaller generated VCFs hardly contain any indel information, this option improves the indel model. The `SomaticSeq.Wrapper.sh` script is modified accordingly.
- Extract mapping quality (MQ) from VarDict output if this information cannot be found in SAMtools VCF (also mostly benefits the indel model).
- Indel length now positive for insertions and negative for deletions, instead of using the absolute value previously.

4.4 Version 2.0

- Removed dependencies for SAMtools and HaplotypeCaller during feature extraction. `SSeq_merged.vcf2tsv.py` extracts those information (plus more) directly from BAM files.
- Allow not only VCF file, but also BED file or a list of chromosome coordinate as input format for `SSeq_merged.vcf2tsv.py`, i.e., use `-mybed` or `-mypos` instead of `-myvcf`.
- Instead of a separate step to annotate ground truth, that can be done directly by `SSeq_merged.vcf2tsv.py` by supplying the ground truth VCF via `-truth`.
- `SSeq_merged.vcf2tsv.py` can annotate dbSNP and COSMIC information directly if BED file or a list of chromosome coordinates are used as input in lieu of an annotated VCF file.
- Consolidated feature sets, e.g., removed some redundant. Fixed a bug: if `JointSNVMix2` is not included, the values should be “NaN” instead of 0’s. This is to keep consistency with how we handle all other callers’ feature sets coming from different resources.

4.5 Version 2.0.2

- Incorporated `LoFreq`.
- Used `getopt` to replace `getopts` in the `SomaticSeq.Wrapper.sh` script to allow long options.

4.6 Version 2.1.2

- Properly handle cases when multiple ALT's are calls in the same position. The VCF files can either contain multiple calls in the ALT column (i.e., A,G), or have multiple lines corresponding to the same position (one line for each variant call). Some functions were significantly re-written to allow this.
- Incorporated Scalpel.
- Deprecated HaplotypeCaller and SAMTools dependencies completely as far as feature generation is concerned.
- The Wrapper script removed SnpSift/SnpEff dependencies. Those information can be directly obtained during the SSeq_merged.vcf2tsv.py step. Also removed some additional legacy steps that has become useless since v2 (i.e., score_Somatic.Variants.py). Added a step to check the correctness of the input. The v2.1 and 2.1.1 had some typos in the wrapper script, so only describing v2.1.2 here.

4.7 Version 2.2

- Added MuTect2 support.

4.8 Version 2.2.1

- InDel_3bp now stands for indel counts within 3 bps of the variant site, instead of exactly 3 bps from the variant site as it was previously (likewise for InDel_2bp).
- Collapse MQ0 (mapping quality of 0) reads supporting reference/variant reads into a single metric of MQ0 reads (i.e., tBAM_MQ0 and nBAM_MQ0). From experience, the number of MQ0 reads is at least equally predictive of false positive calls, rather than distinguishing if those MQ0 reads support reference or variant.
- Obtain SOR (Somatic Odds Ratio) from BAM files instead of VarDict's VCF file.
- Fixed a typo in the SomaticSeq.Wrapper.sh script that did not handle inclusion region correctly.

4.9 Version 2.2.2

- Got around an occasional unexplained issue in then ada package were the SOR is sometimes categorized as type, by forcing it to be numeric.
- Defaults PASS score from 0.7 to 0.5, and make them tunable in the SomaticSeq.Wrapper.sh script (`-pass-threshold` and `-lowqual-threshold`).

4.10 Version 2.2.3

- Incorporated Strelka2 since it's now GPLv3.
- Added another R script (`ada_model_builder_ntChange.R`) that uses nucleotide substitution pattern as a feature. Limited experiences have shown us that it improves the accuracy, but it's not heavily tested yet.

- If a COSMIC site is labeled SNP in the COSMIC VCF file, `if_cosmic` and `CNT` will be labeled as 0. The COSMIC ID will still appear in the ID column. This will not change any results because both of those features are turned off in the training R script.
- Fixed a bug: if `JointSNVMix2` is not included, the values should be “NaN” instead of 0’s. This is to keep consistency with how we handle all other callers.

4.11 Version 2.2.4

- Resolved a bug in v2.2.3 where the VCF files of Strelka INDEL and Scalpel clash on GATK `CombineVariants`, by outputting a temporary VCF file for Strelka INDEL without the sample columns.
- Caller classification: consider `if_Scalpel = 1` only if there is a `SOMATIC` flag in its INFO.

4.12 Version 2.2.5

- Added a dockerfile. Docker repo at <https://hub.docker.com/r/lethalfang/somaticseq/>.
- Ability to use `vcfsort.pl` instead of GATK `CombineVariants` to merge VCF files.

5 Future development

- Develop a version for deep sequencing cfDNA/ctDNA.

6 Contact Us

For suggestions, bug reports, or technical support, please post in <https://github.com/bioinform/somaticseq/issues>. The developers are alerted when issues are created there. Alternatively, you may also email li_tai.fang@roche.com.