

SomaticSeq Documentation

Li Tai Fang

June 23, 2018

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, Scalpel, Strelka, and TNscope. 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.
- R, plus the ada package in R.
- BEDTools (if there is an inclusion and/or an exclusion region file)
- Optional: dbSNP and COSMIC files in VCF format (if you want to use dbSNP features as a part of the training).
- At least one of MuTect/Indelocator/MuTect2, VarScan2, JointSNVMix2, SomaticSniper, VarDict, MuSE, LoFreq, Scalpel, Strelka2 and/or TNscope. 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.

1.2 Docker repos

SomaticSeq and most somatic mutation callers we have incorporated are now dockerized. The exceptions are VarScan2 and TNscope because we do not have distribution rights.

- SomaticSeq is dockerized at <https://hub.docker.com/r/lethalfang/somaticseq/>.
- MuTect2 (tested with GATK4): <https://hub.docker.com/r/broadinstitute/gatk>
- VarScan2 (untested): <https://hub.docker.com/r/djordjeklisc/sbg-varscan2/>

- JointSNVMix2: <https://hub.docker.com/r/lethalfang/jointsnvmix2/>
- SomaticSniper: <https://hub.docker.com/r/lethalfang/somaticsniper/>
- VarDict: <https://hub.docker.com/r/lethalfang/vardictjava/>
- MuSE: <https://hub.docker.com/r/marghoob/muse/>
- LoFreq: <https://hub.docker.com/r/marghoob/lofreq/>
- Scalpel: <https://hub.docker.com/r/lethalfang/scalpel/>
- Strelka2: <https://hub.docker.com/r/lethalfang/strelka/>

2 To use SomaticSeq.Wrapper.sh

The SomaticSeq.Wrapper.sh is a wrapper script that calls a series of programs and procedures **after** you have run your individual somatic mutation callers. In the next section, we will describe the workflow in more detail, so you may not be 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  --tnscope         TNscope.vcf.gz \
19  --normal-bam      matched_normal.bam \
20  --tumor-bam       tumor.bam \
21  --ada-r-script    ada_model_builder.R \
22  --genome-reference human_b37.fasta \
23  --cosmic           cosmic.b37.v71.vcf \
24  --dbSNP           dbSNP.b37.v141.vcf \
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 --tnscope TNscope.vcf.gz \
--normal-bam matched_normal.bam \
19 --tumor-bam tumor.bam \
--ada-r-script ada_model_predictor.R \
21 --genome-reference human_b37.fasta \
--cosmic cosmic.b37.v71.vcf \
23 --dbsnp dbSNP.b37.v141.vcf \
--snpeff-dir $PATH/TO/DIR/snpSift \
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 utilities/getUniqueVcfPositions.py and vcf sorter.pl to combine the VCF files from different callers. The intermediate VCF files were modified to separate SNVs and INDELS.

VCF modifications were previously done to primarily make them compatible with GATK CombineVariants. We no longer depend on CombineVariants, so some of the steps are legacy.

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.

```

1 # 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:
5 modify_MuTect.py -infile input.vcf -outfile output.vcf -nsm NormalSampleName -tsm
6 TumorSampleName

```

2. For MuTect2, this script will split multi-allelic records into one variant per line in the VCF file. This is to make thing easier for the SSeq_merged.vcf2tsv.py script later.

```

1 # Based on the sample name you supply:
2 modify_MuTect2.py -infile MuTect2.Filtered.vcf -snv mutect.snp.vcf -indel mutect.indel.vcf

```

3. 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
2 modify_VJSD.py -method VarScan2 -infile input.vcf -outfile output.vcf

```

4. 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:

```

1 # To avoid text files in the order of terabytes, this awk one-liner keeps entries where the
2 reference is not "N", and the somatic probabilities are at least 0.95.
3 awk -F "\t" 'NR!=1 && $4!="N" && $10+$11>=0.95'
4
5 # This awk one-liner converts the text file into a basic VCF file
6 awk -F "\t" '{print $1 "\t" $2 "\t.\t" $3 "\t" $4 "\t.\t.\tAAAB=" $10 ";AABB=" $11 "\tRD:AD\
7 t" $5 ":" $6 "\t" $7 ":" $8}'
8
9 ## The actual commands we've used in our workflow:
10 echo -e '##fileformat=VCFv4.1' > unsorted.vcf
11 echo -e '##INFO<<ID=AAAB,Number=1,Type=Float,Description="Probability of Joint Genotype AA
12 in Normal and AB in Tumor">>' >> unsorted.vcf
13 echo -e '##INFO<<ID=AABB,Number=1,Type=Float,Description="Probability of Joint Genotype AA
14 in Normal and BB in Tumor">>' >> unsorted.vcf
15 echo -e '##FORMAT<<ID=RD,Number=1,Type=Integer,Description="Depth of reference-supporting
16 bases (reads1)">>' >> unsorted.vcf
17 echo -e '##FORMAT<<ID=AD,Number=1,Type=Integer,Description="Depth of variant-supporting
18 bases (reads2)">>' >> unsorted.vcf
19 echo -e '#CHROM\tPOS\tID\tREF\tALT\tQUAL\tFILTER\tINFO\tFORMAT\tNORMAL\tTUMOR' >> unsorted.
20 vcf
21
22 python $PATH/TO/jsm.py classify joint_snv_mix_two genome.GRCh37.fa normal.bam tumor.bam
23 trained.parameter.cfg /dev/stdout | \
24 awk -F "\t" 'NR!=1 && $4!="N" && $10+$11>=0.95' | \
25 awk -F "\t" '{print $1 "\t" $2 "\t.\t" $3 "\t" $4 "\t.\t.\tAAAB=" $10 ";AABB=" $11 "\tRD:AD\
26 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
```

5. Modify SomaticSniper's output:

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

6. 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.

```
# Default VarDict tagging criteria, only PASS (and Likely or Strong Somatic):
modify_VJSD.py -method VarDict -infile input.vcf -outfile output.vcf

# When running VarDict, if var2vcf_paired.pl is used to generate the VCF file, you may relax
the tagging criteria with -filter paired
modify_VJSD.py -method VarDict -infile input.vcf -outfile output.vcf -filter paired

# 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.

7. 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
```

8. LoFreq and Scalpel do not require modification. LoFreq has no sample columns anyway.
9. Add "GT" field to sample columns to make it compatible with GATK CombineVariants.

```
modify_Strelka.py -infile somatic.snvs.vcf.gz -outfile stralka.snv.vcf
```

10. 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
   jointsnvmix.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
3 intersectBed -header -a BINA_somatic.snp.vcf -b ignore.bed -v > somatic.snp.processed.vcf
4 intersectBed -header -a BINA_somatic.indel.vcf -b ignore.bed -v > somatic.indel.processed.vcf
5
6 # Alternatively (or both), this command uses BEDtools to keep only calls in the inclusion region
7 intersectBed -header -a BINA_somatic.snp.vcf -b inclusion.bed > somatic.snp.processed.vcf
8 intersectBed -header -a BINA_somatic.indel.vcf -b inclusion.bed > somatic.indel.processed.vcf

```

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
2 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.

```

1 # 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.

```

1 -myvcf      Input VCF file of the merged calls [REQUIRED]
2 -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.

```

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:

```

# Training:
r_script/ada_model_builder.R Ensemble.sSNV.tsv
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:

```

# Mutation prediction:
r_script/ada_model_predictor.R Ensemble.sSNV.tsv.Classifier.RData Ensemble.sSNV.tsv Trained.sSNV.tsv
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 To run the dockerized somatic mutation callers

For your convenience, we have created a couple of scripts that can generate run script for the dockerized somatic mutation callers.

4.1 Location

- somaticseq/utilities/dockered_pipelines/

4.2 Requirements

- Have internet connection, and able to pull and run docker images from docker.io
- Have cluster management system such as Sun Grid Engine, so that the "qsub" command is valid

4.3 Example commands

For single-threaded jobs, best suited for whole exome sequencing or less.

```

1 # Example command to submit the run scripts for each of the following somatic mutation callers
  utilities/dockered_pipelines/singleThread/submit_callers_singleThread.sh \
2
3 --normal-bam /ABSOLUTE/PATH/TO/normal_sample.bam \
4 --tumor-bam /ABSOLUTE/PATH/TO/tumor_sample.bam \
5 --human-reference /ABSOLUTE/PATH/TO/GRCh38.fa \
6 --output-dir /ABSOLUTE/PATH/TO/RESULTS \
7 --selector /ABSOLUTE/PATH/TO/Exome_Capture.GRCh38.bed \
8 --dbsnp /ABSOLUTE/PATH/TO/dbsnp.GRCh38.vcf \
9 --action qsub \
10 --mutect2 --jointsvmix2 --somaticsniper --vardict --muse --lofreq --scalpel --strelka --
  somaticseq

```

For multi-threaded jobs, best suited for whole genome sequencing.

```

1 # Submitting mutation caller jobs by splitting each job into 36 even regions.
2 utilities/dockered_pipelines/multiThreads/submit_callers_multiThreads.sh \
3
4 --normal-bam /ABSOLUTE/PATH/TO/normal_sample.bam \
5 --tumor-bam /ABSOLUTE/PATH/TO/tumor_sample.bam \
6 --human-reference /ABSOLUTE/PATH/TO/GRCh38.fa \
7 --output-dir /ABSOLUTE/PATH/TO/RESULTS \
8 --dbsnp /ABSOLUTE/PATH/TO/dbsnp.GRCh38.vcf \
9 --threads 36 \
10 --action qsub \
11 --mutect2 --somaticsniper --vardict --muse --lofreq --scalpel --strelka --somaticseq

```


4.3.1 Parameters

```

—normal-bam /ABSOLUTE/PATH/TO/normal_sample.bam (Required)
—tumor-bam /ABSOLUTE/PATH/TO/tumor_sample.bam (Required)
—human-reference /ABSOLUTE/PATH/TO/human_reference.fa (Required)
—dbsnp /ABSOLUTE/PATH/TO/dbsnp.vcf (Required for MuSE and LoFreq)
—cosmic /ABSOLUTE/PATH/TO/cosmic.vcf (Optional)
—selector /ABSOLUTE/PATH/TO/Capture_region.bed (Optional. Will assume whole
genome from the .fai file without it.)
—exclude /ABSOLUTE/PATH/TO/Blacklist_region.bed (Optional)
—min-af (Optional. The minimum VAF cutoff for VarDict and VarScan2.
Defaults are 0.10 for VarScan2 and 0.05 for VarDict).
—action qsub (Optional: the command preceding the .cmd scripts. Default is
echo)
—threads 36 (Optional for multiThreads and invalid for singleThread: evenly
split the genome into 36 BED files. Default = 12).
—mutect2 (Optional flag to invoke MuTect2)
—varscan2 (Optional flag to invoke VarScan2)
—jointsvnmix2 (Optional flag to invoke JointSNVMix2)
—somaticsniper (Optional flag to invoke SomaticSniper)
—vardict (Optional flag to invoke VarDict)
—muse (Optional flag to invoke MuSE)
—lofreq (Optional flag to invoke LoFreq)
—scalpel (Optional flag to invoke Scalpel)
—strelka (Optional flag to invoke Strelka)
—somaticseq (Optional flag to invoke SomaticSeq. This script always be echo'ed,
as it should not be submitted until all the callers above complete).
—output-dir /ABSOLUTE/PATH/TO/OUTPUT_DIRECTORY (Required)
—somaticseq-dir SomaticSeq_Output_Directory (Optional. The directory name of the
SomaticSeq output. Default = SomaticSeq).
—somaticseq-train (Optional flag to invoke SomaticSeq to produce classifiers if
ground truth VCF files are provided. Only recommended in singleThread mode, because otherwise
it's better to combine the output TSV files first, and then train classifiers.)
—somaticseq-action (Optional. What to do with the somaticseq.cmd. Default is echo.
Only do "qsub" if you have already completed all the mutation callers, but want to run
SomaticSeq at a different setting.)
—classifier-snv Trained_sSNV_Classifier.RData (Optional if there is a classifier you
want to use)
—classifier-indel Trained_sINDEL_Classifier.RData (Optional if there is a classifier
you want to use)
—truth-snv sSNV_ground_truth.vcf (Optional if there is a ground truth, and
everything else will be labeled false positive)
—truth-indel sINDEL_ground_truth.vcf (Optional if there is a ground truth, and
everything else will be labeled false positive)
—exome (Optional flag for Strelka)
—scalpel-two-pass (Optional parameter for Scalpel. Default = false.)
—mutect2-arguments (Extra parameters to pass onto Mutect2, e.g., —mutect2-arguments
'--initial_tumor_lod 3.0 —log_somatic_prior -5.0 —min_base_quality_score 20')
—mutect2-filter-arguments (Extra parameters to pass onto FilterMutectCalls)
—varscan-arguments (Extra parameters to pass onto VarScan2)
—varscan-coverage-arguments (Extra parameters to pass onto samtools mpileup that creates pileup
files for VarScan)
—jsm-train-arguments (Extra parameters to pass onto JointSNVMix2's train command)
—jsm-classify-arguments (Extra parameters to pass onto JointSNVMix2's classify command)
—somaticsniper-arguments (Extra parameters to pass onto SomaticSniper)
—vardict-arguments (Extra parameters to pass onto VarDict)
—muse-arguments (Extra parameters to pass onto MuSE)
—lofreq-arguments (Extra parameters to pass onto LoFreq)
—scalpel-discovery-arguments (Extra parameters to pass onto Scalpel's discovery command)
—scalpel-export-arguments (Extra parameters to pass onto Scalpel's export command)
—strelka-config-arguments (Extra parameters to pass onto Strelka's config command)
—strelka-run-arguments (Extra parameters to pass onto Strelka's run command)
—somaticseq-arguments (Extra parameters to pass onto SomaticSeq.Wrapper.sh)

```

4.3.2 What does the single-threaded command do

- For each flag such as `--mutect2`, `--jointsnvmix2`, ..., `--strelka`, a run script ending with `.cmd` will be created in `/ABSOLUTE/PATH/TO/RESULTS/logs`. By default, these `.cmd` scripts will only be created, and their file path will be printed on screen. However, if you do `--action qsub`, then these scripts will be submitted via the `qsub` command. The default action is “echo.”
 - Each of these `.cmd` script correspond to a mutation caller you specified. They all use docker images.
 - We may improve their functionalities in the future to allow more tunable parameters. For the initial releases, POC and reproducibility take precedence.
- If you do `--somaticseq`, the `somaticseq` script will be created in `/ABSOLUTE/PATH/TO/RESULTS/S/SomaticSeq/logs`. However, it will not be submitted until you manually do so after each of these mutation callers is finished running.
 - In the future, we may create more sophisticated solution that will automatically solves these dependencies. For the initial release, we'll focus on stability and reproducibility.
- Due to the way those run scripts are written, the Sun Grid Engine's standard error log will record the time the task completes (i.e., Done at 2017/10/30 29:03:02), and it will only do so when the task is completed with an exit code of 0. It can be a quick way to check if a task is done, by looking at the final line of the standard error log file.

4.3.3 What does the multi-threaded command do

It's very similar to the single-threaded WES solution, except the job will be split evenly based on genomic lengths.

- If you specified `--threads 36`, then 36 BED files will be created. Each BED file represents 1/36 of the total base pairs in the human genome (obtained from the `.fa.fai` file, but only including 1, 2, 3, ..., MT, or `chr1`, `chr2`, ..., `chrM` contigs). They are named `1.bed`, `2.bed`, ..., `36.bed`, and will be created into `/ABSOLUTE/PATH/TO/RESULTS/1`, `/ABSOLUTE/PATH/TO/RESULTS/2`, ..., `/ABSOLUTE/PATH/TO/RESULTS/36`. You may, of course, specify any number. The default is 12.
- For each mutation callers you specify (with the exception of `SomaticSniper`), a script will be created into `/ABSOLUTE/PATH/TO/RESULTS/1/logs`, `/ABSOLUTE/PATH/TO/RESULTS/2/logs`, etc., with partial BAM input. Again, they will be automatically submitted if you do `--action qsub`.
- Because `SomaticSniper` does not support partial BAM input (one would have to manually split the BAMs in order to parallelize `SomaticSniper` this way), the above mentioned procedure is not applied to `SomaticSniper`. Instead, a single-threaded script will be created (and potentially `qsub`'ed) into `/ABSOLUTE/PATH/TO/RESULTS/logs`.
 - However, because `SomaticSniper` is by far the fastest tool there, single-thread is doable even for WGS. Even single-threaded `SomaticSniper` will likely finish before parallelized `Scalpel`. When I benchmarked the DREAM Challenge Stage 3 by splitting it into 120 regions, `Scalpel` took 10 hours and 10 minutes to complete 1/120 of the data. `SomaticSniper` took a little under 5 hours for the whole thing.
 - After `SomaticSniper` finishes, the result VCF files will be split into each of the `/ABSOLUTE/PATH/TO/RESULTS/1`, `/ABSOLUTE/PATH/TO/RESULTS/2`, etc.
- `JointSNVMix2` also does not support partial BAM input. Unlike `SomaticSniper`, it's slow and takes massive amount of memory. It's not a good idea to run `JointSNVMix2` on a WGS data. The only way to do so is to manually split the BAM files and run each separately. We may do so in the future, but `JointSNVMix2` is a 5-year old that's no longer being supported, so we probably won't bother.

- Like the single-threaded case, a SomaticSeq run script will also be created for each partition like /ABSOLUTE/PATH/TO/RESULTS/1/SomaticSeq/logs, but will not be submitted until you do so manually.
- For simplicity, you may wait until all the mutation calling is done, then run a command like

```
find /ABSOLUTE/PATH/TO/RESULTS -name 'somaticseq*.cmd' -exec qsub {} \;
```

5 Use BAMSurgeon to create training set

For your convenience, we have created a couple of wrapper scripts that can generate the run script to create training data using BAMSurgeon at somaticseq/utilities/dockered_pipelines/bamSimulator. Descriptions and example commands can be found in the README there.

5.1 Requirements

- Have internet connection, and able to pull and run docker images from docker.io
- Have cluster management system such as Sun Grid Engine, so that the "qsub" command is valid

6 Release Notes

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

6.1 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.

6.2 Version 1.1

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

6.3 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.

6.4 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 callersnt feature sets coming from different resources.

6.5 Version 2.0.2

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

6.6 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.

6.7 Version 2.2

- Added MuTect2 support.

6.8 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.

6.9 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`).

6.10 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.

6.11 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.

6.12 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.

6.13 Version 2.3.0

- Moved some scripts to the utilities directory to clean up the clutter.
- Added the `split_Bed_into_equal_regions.py` to utilities, which will split a input BED file into multiple BED files of equal size. This is to be used to parallelize large WGS jobs.
- Made compatible with MuTect2 from GATK4.
- Removed long options for the SomaticSeq.Wrapper.sh script because it's more readable this way.
- Added a script to add "GT" field to Strelka's VCF output before merging it with other VCF files. That was what caused GATK CombineVariants errors mentioned in v2.2.4's release notes.
- Added a bunch of scripts at `utilities/dockerized_pipelines` that can be used to submit (requiring Sun Grid Engine or equivalent) dockerized pipeline to a computing cluster.

6.14 Version 2.3.1

- Improve the automated run script generator at `utilities/dockerized_pipelines`.
- No change to SomaticSeq algorithm

6.15 Version 2.3.2

- Added run script generators for dockerized BAMSurgeon pipelines at `utilities/dockered_pipelines/bamSurgeon`
- Added an error message to `r_scripts/ada_model_builder_ntChange.R` when `TrueVariants_or_False` don't have both 0's and 1's. Other than this warning message change, no other change to SomaticSeq algorithm.

6.16 Version 2.4.0

- Restructured the utilities scripts.
- Added the `utilities/filter_SomaticSeq_VCF.py` script that “demotes” PASS calls to LowQual based on a set of tunable hard filters.
- BamSurgeon scripts invokes modified BamSurgeon script that splits a BAM file without the need to sort by read name. This works if the BAM files have proper read names, i.e., 2 and only 2 identical read names for each paired-end reads.
- No change to SomaticSeq algorithm

6.17 Version 2.4.1

- Updated some docker job scripts.
- Added a script that converts some items in the VCF's INFO field into the sample field, to precipitate the need to merge multiple VCF files into a single multi-sample VCF, i.e., `utilities/reformat_VCF2SEQC2.py`.
- No change to SomaticSeq algorithm

6.18 Version 2.5.0

- In `modify_VJSD.py`, get rid of VarDict's END tag (in single sample mode) because it causes problem with GATK CombineVariants.
- Added limited single-sample support, i.e., `ssSomaticSeq.Wrapper.sh` is the wrapper script. `singleSample_callers_singleThread.sh` is the wrapper script to submit single-sample mutation caller scripts.
- Added run scripts for read alignments and post-alignment processing, i.e., FASTQ → BAM, at `utilities/dockered_pipelines/alignments`.
- Fixed a bug where the last two CD4 numbers were both alternate concordant reads in the output VCF file, when the last number should've been alternate discordant reads.
- Changed the output file names from `Trained.s(SNV|INDEL).vcf` and `Untrained.s(SNV|INDEL).vcf` to `SSeq.Classified.s(SNV|INDE).vcf` and `Consensus.s(SNV|INDEL).vcf`. No change to the actual tumor-normal SomaticSeq algorithm.
- Added `utilities/modify_VarDict.py` to VarDict's “complex” variant calls (e.g., GCA>TAC) into SNVs when possible.
- Modified `r_scripts/ada_model_builder_ntChange.R` to allow you to ignore certain features, e.g., `r_scripts/ada_model_builder_ntChange.R Training_Data.tsv nBAM_REF_BQ tBAM_REF_BQ SiteHomopolymer_Length ...`

Everything after the input file are features to be ignored during training.

Also added `r_scripts/ada_cross_validation.R`.

6.19 Version 2.5.1

- Additional passable parameters options to pass extra parameters to somatic mutation callers. Fixed a bug where the “two-pass” parameter is not passed onto Scalpel in multiThreads scripts.
- Ignore Strelka_QSS and Strelka_TQSS for indel training in the SomaticSeq.Wrapper.sh script.

6.20 Version 2.5.2

- Ported some pipeline scripts to singularities at utilities/singularities.

6.21 Version 2.6.0

- VarScan2_Score is no longer extracted from VarScan’s output. Rather, it’s now calculated directly using Fisher’s Exact Test, which reproduces VarScan’s output, but will have a real value when VarScan2 does not output a particular variant.
- Incorporate TNscope’s output VCF into SomaticSeq, but did not incorporate TNscope caller into the dockerized workflow because we don’t have distribution license.

6.22 Version 2.6.1

- Optimized memory for singularity scripts.
- Updated utilities/bamQC.py and added utilities/trimSoftClippedReads.py (removed soft-clipped bases on soft-clipped reads)
- Added some docker scripts at utilities/dockered_pipelines/QC

6.23 Version 2.7.0

- Added another feature: consistent/inconsistent calls for paired reads if the position is covered by both forward and reverse reads. However, they’re excluded as training features in SomaticSeq.Wrapper.sh script for the time being.
- Change non-GCTA characters to N in VarDict.vcf file to make it conform to VCF file specifications.

6.24 Version 2.7.1

- Without `-gatk $PATH/TO/GenomeAnalysisTK.jar` in the SomaticSeq.Wrapper.sh script, it will use utilities/getUniqueVcfPositions.py and utilities/vcf sorter.pl to (in lieu of GATK3 CombineVariants) to combine all the VCF files.
- Fixed bugs in the docker/singularities scripts where extra arguments for the callers are not correctly passed onto the callers.

6.25 Version 2.7.2

- Make compatible with .cram format
- Fixed a bug where Strelka-only calls are not considered by SomaticSeq.

6.26 Version 2.8.0

- The program will now throw an exception and crash if the VCF file(s) are not sorted according to the .fasta reference file.

7 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.