

SomaticSeq Documentation

Li Tai Fang / li_tai.fang@roche.com

July 21, 2018

1 Introduction

SomaticSeq is a flexible post-somatic-mutation-calling algorithm for improved accuracy. We have incorporated 10+ somatic mutation caller(s). Any combination of them can be used to obtain a combined call set, and then SomaticSeq uses machine learning (adaptive boosting) to distinguish true mutations from false positives from that call set. The mutation callers we have incorporated are 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, was published in Genome Biology 2015, 16:197. The SomaticSeq project is located at <https://github.com/bioinform/somaticseq>. There have been some major improvements in SomaticSeq since that Genome Biology publication in 2015.

SomaticSeq.Wrapper.sh is a bash script that calls a series of algorithms to combine the output of the somatic mutation caller(s). Then, depending on the input files and R scripts that 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 inclusion and/or an exclusion region files are supplied)
- Optional: dbSNP in VCF format (if you want to use dbSNP membership 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 images

SomaticSeq and most somatic mutation callers we have incorporated are dockerized.

- SomaticSeq: <https://hub.docker.com/r/lethalfang/somaticseq>
- MuTect2: <https://hub.docker.com/r/broadinstitute/gatk>
- VarScan2: <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 How to run SomaticSeq

The *somaticseq/run_somaticseq.py* calls a series of programs and procedures **after** you have run your individual somatic mutation callers, and *run_parallel.py* is a wrapper script that allows parallel processing. Section 4 will teach you how to run those mutation callers that we have been dockerized. It also includes ways to create semi-simulated training data that can be used to create SomaticSeq classifiers. In the next section, we will describe the workflow in this wrapper script in detail.

Both paired and single modes are supported, although single mode is not as well validated scientifically as the paired mode. To see the required and optional input files and parameters to *run_parallel.py*:

```
1 # See the global input parameters
  run_parallel.py --help
3
4 # Input parameters for paired-sample mode (i.e., tumor-normal)
5 run_parallel.py paired --help
6
7 # Input parameters for single-sample mode
  run_parallel.py single --help
```

2.1 SomaticSeq Training Mode

To create SomaticSeq classifiers, you need a VCF file containing true SNVs and a VCF file containing true INDELs. There is also an option to include a list of regions to include and/or exclude from this exercise. 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 variants in the truth VCF files are assumed to be true positives. Every mutation call not in the truth VCF files is assumed to be false positives (as long as the genomic coordinate is in inclusion region and not in exclusion region if those regions are provided).

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 you will use the same parameter for prediction as you do for training.

```
1 # An example command for SomaticSeq Training.
2 run_parallel.py \
3   --somaticseq-train \
4   --output-directory $OUTPUT_DIR \
5   --genome-reference GRCh38.fa \
6   --truth-snv truePositives.snv.vcf \
7   --truth-indel truePositives.indel.vcf \
8   --inclusion-region genome.bed \
9   --exclusion-region blacklist.bed \
10  --threads 12 \
11  paired \
12  --tumor-bam-file tumor.bam \
13  --normal-bam-file matched_normal.bam \
14  --mutect2-vcf MuTect2/variants.vcf \
15  --varscan-snv VarScan2/variants.snp.vcf \
16  --varscan-indel VarScan2/variants.indel.vcf \
```

```

—jsm—vcf          JointSNVMix2/variants.snp.vcf \
18 —somaticsniper—vcf SomaticSniper/variants.snp.vcf \
—vardict—vcf      VarDict/variants.vcf \
20 —muse—vcf         MuSE/variants.snp.vcf \
—lofreq—snv       LoFreq/variants.snp.vcf \
22 —lofreq—indel     LoFreq/variants.indel.vcf \
—scalpel—vcf      Scalpel/variants.indel.vcf \
24 —strelka—snv      Strelka/variants.snv.vcf \
—strelka—indel    Strelka/variants.indel.vcf

```

For the command's argument placement, caller output and bam files are input "after" *paired* or *single* option. Everything else goes before, e.g., reference, ground truths, resources such as dbSNP and COSMIC, etc.

Parallel processing is achieved by splitting the inclusion BED file into a number of sub-BED files of equal region sizes, named 1.th.input.bed, 2.th.input.bed, ..., n.th.input.bed. Then each process will be run using each sub-BED file as the inclusion BED file. If there is no inclusion BED file in the command argument, it will split the reference.fa.fai file instead.

SomaticSeq 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 truePositives.snv.vcf and/or truePositives.indel.vcf file(s) and invoke the *--somaticseq-train* option. Otherwise, it will fall back to the simple caller consensus mode.

2.2 SomaticSeq Prediction Mode

Make sure the classifiers (.RData files) are supplied, Without either of them, or it will fall back to the simple caller consensus mode.

```

1 # The *.RData files are trained classifier from the training mode.
run_parallel.py \
3 —classifier—snv      Ensemble.sSNV.tsv.ntChange.Classifier.RData \
—classifier—indel     Ensemble.sINDEL.tsv.ntChange.Classifier.RData \
5 —output—directory   $OUTPUT_DIR \
—genome—reference     GRCh38.fa \
7 —inclusion—region    genome.bed \
—exclusion—region     blacklist.bed \
9 —threads            12 \
paired \
11 —tumor—bam—file      tumor.bam \
—normal—bam—file      matched_normal.bam \
13 —mutect2—vcf         MuTect2/variants.vcf \
—varscan—snv         VarScan2/variants.snp.vcf \
15 —varscan—indel      VarScan2/variants.indel.vcf \
—jsm—vcf             JointSNVMix2/variants.snp.vcf \
17 —somaticsniper—vcf SomaticSniper/variants.snp.vcf \
—vardict—vcf         VarDict/variants.vcf \
19 —muse—vcf           MuSE/variants.snp.vcf \
—lofreq—snv         LoFreq/variants.snp.vcf \
21 —lofreq—indel       LoFreq/variants.indel.vcf \
—scalpel—vcf        Scalpel/variants.indel.vcf \
23 —strelka—snv        Strelka/variants.snv.vcf \
—strelka—indel       Strelka/variants.indel.vcf

```

2.3 Consensus Mode

Same as the commands previously, but without including classifiers or invoking *--somaticseq-train*. Without those information, SomaticSeq will forgo machine learning, and fall back into a simple majority vote.

3 The step-by-step SomaticSeq Workflow

We'll describe the workflow here.

3.1 Apply inclusion and exclusion regions

This step may be needed for model training. BEDTools is invoked by SomaticSeq. 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. It is also a routine used to parallelize the process by splitting large regions into equal-sized (in terms of number of pairs) regions, so that they can be processed in parallel.

3.2 Combine the call sets

We use *vcfModifier/getUniqueVcfPositions.py* and *bedtools sort* to combine the VCF files from different callers. For each caller output, intermediate VCF file(s) may be created to separate the SNVs and INDELs calls, and also remove some REJECT calls to reduce file sizes.

The following scripts are used to modify original VCF outputs.

```
vcfModifier/modify_JointSNVMix2.py
vcfModifier/modify_MuTect2.py
vcfModifier/modify_MuTect.py
vcfModifier/modify_SomaticSniper.py
vcfModifier/modify_ssMuTect2.py
vcfModifier/modify_ssStrelka.py
vcfModifier/modify_Strelka.py
vcfModifier/modify_VarDict.py
vcfModifier/modify_VarScan2.py
```

modify_ssTOOL.py denotes it's for single-sample mode.

JointSNVMix2 does not output VCF files. In our own workflow, we convert its output into a basic VCF file with an 2 awk one-liners, which you may see at *utilities/dock-ered_pipelines/mutation_callers/submit_JointSNVMix2.sh*.

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

3.3 Convert the VCF file into TSV file

This script *somaticseq/somatic_vcf2tsv.py* works for all VCF files (requires input for two BAM files). It extracts information from the BAM files, as well as some individual callers' output VCF files. 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. *somaticseq/single_sample_vcf2tsv.py* is used for single-sample mode. At the end of this, *Ensemble.sSNV.tsv* and *Ensemble.sINDEL.tsv* are created. All the options for *somaticseq/somatic_vcf2tsv.py* or *somaticseq/single_sample_vcf2tsv.py* can be found by running.

```
somaticseq/somatic_vcf2tsv.py -h
somaticseq/single_sample_vcf2tsv.py -h
```

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_scripts/ada_model_builder_ntChange.R Ensemble.sSNV.tsv Consistent_Mates Inconsistent_Mates
r_scripts/ada_model_builder_ntChange.R Ensemble.sINDEL.tsv Strelka_QSS Strelka_TQSS
Consistent_Mates Inconsistent_Mates
```

Ensemble.sSNV.tsv.ntChange.Classifier.RData and *Ensemble.sINDEL.tsv.ntChange.Classifier.RData* will be created from model training. The arguments after *Ensemble.sSNV.tsv* and *Ensemble.sINDEL.tsv* tells the builder script to ignore those features in training. These features do not improve accuracy in our data sets (mostly WGS data, but they may help other data sets)

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 MuTect2/MuTect/Indelocator, VarScan2, JointSNVMix2, SomaticSniper, VarDict, MuSE, LoFreq, Scalpel, Strelka, and/or TNscope. 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, which is probably undesirable.

```

1 # Probability above 0.7 labeled PASS (-pass 0.7), and between 0.1 and 0.7 labeled LowQual (-low
2 0.1):
3 # Use -all to include REJECT calls in the VCF file
4 # Use -phred to convert probability values (between 0 to 1) into Phred scale in the QUAL column
5   in the VCF file
6
7 somaticseq/SSeq_tsv2vcf.py -tsv Trained.sSNV.tsv -vcf Trained.sSNV.vcf -pass 0.7 -low 0.1 -
8   tools MuTect2 VarScan2 JointSNVMix2 SomaticSniper VarDict MuSE LoFreq Strelka -all -phred
9
10 somaticseq/SSeq_tsv2vcf.py -tsv Trained.sINDEL.tsv -vcf Trained.sINDEL.vcf -pass 0.7 -low 0.1 -
11   tools MuTect2 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

4.3.1 Single-threaded Jobs

This is best suited for whole exome sequencing or less.

```

1 # Example command to submit the run scripts for each of the following somatic mutation callers
2 $PATH/TO/somaticseq/utilities/dockered_pipelines/submit_callers_singleThread.sh \
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 --dbsnp /ABSOLUTE/PATH/TO/dbSNP.GRCh38.vcf \
8 --somaticseq-dir /ABSOLUTE/PATH/TO/SomaticSeq \
9 --action echo \
10 --mutect2 --somaticsniper --vardict --muse --lofreq --scalpel --strelka --somaticseq

```

The command shown above will create scripts for MuTect2, SomaticSniper, VarDict, MuSE, LoFreq, Scalpel, and Strelka. Then, it will create the SomaticSeq script that merges those 7 callers. This command defaults to majority-vote consensus.

Since it's `--action echo`, it will echo the mutation caller scripts locations, but these scripts will not be run. If you do `--action qsub` instead, then those mutation caller scripts will be qsub'ed. You'll still need to manually run/submit the SomaticSeq script after all the caller jobs are done.

4.3.2 Multi-threaded Jobs

This is best suited for whole genome sequencing. This is same as above, except it will create 36 equal-size regions in 36 bed files, and parallelize the jobs into 36 regions.

```

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

```

4.3.3 SomaticSeq Training

Two classifiers will be created (*.RData files), one for SNV and one for INDEL.

```

# Submitting mutation caller jobs by splitting each job into 36 even regions.
2 $PATH/TO/somaticseq/utilities/dockered_pipelines/submit_callers_singleThread.sh \
—normal-bam /ABSOLUTE/PATH/TO/normal_sample.bam \
4 —tumor-bam /ABSOLUTE/PATH/TO/tumor_sample.bam \
—truth-snv /ABSOLUTE/PATH/TO/snvTruth.vcf \
6 —truth-indel /ABSOLUTE/PATH/TO/indelTruth.vcf \
—human-reference /ABSOLUTE/PATH/TO/GRCh38.fa \
8 —output-dir /ABSOLUTE/PATH/TO/RESULTS \
—dbsnp /ABSOLUTE/PATH/TO/dbSNP.GRCh38.vcf \
10 —somaticseq-dir /ABSOLUTE/PATH/TO/SomaticSeq \
—action echo \
12 —mutect2 —somaticsniper —vardict —muse —lofreq —scalpel —strelka —somaticseq —somaticseq
—train

```

Notice the command includes `—truth-snv` and `—truth-indel`, and invokes `somaticseq-train`.

For multi-threaded job, you should not invoke `somaticseq-train`. Instead, you should combine all the *Ensemble.sSNV.tsv* and *Ensemble.sINDEL.tsv* files (separately), and then train on the combined files.

4.3.4 SomaticSeq Prediction

```

# Submitting mutation caller jobs by splitting each job into 36 even regions.
2 $PATH/TO/somaticseq/utilities/dockered_pipelines/submit_callers_singleThread.sh \
—normal-bam /ABSOLUTE/PATH/TO/normal_sample.bam \
4 —tumor-bam /ABSOLUTE/PATH/TO/tumor_sample.bam \
—classifier-snv /ABSOLUTE/PATH/TO/Ensemble.sSNV.tsv.ntChange.Classifier.RData \
6 —classifier-indel /ABSOLUTE/PATH/TO/Ensemble.sINDEL.tsv.ntChange.Classifier.RData \
—human-reference /ABSOLUTE/PATH/TO/GRCh38.fa \
8 —output-dir /ABSOLUTE/PATH/TO/RESULTS \
—dbsnp /ABSOLUTE/PATH/TO/dbSNP.GRCh38.vcf \
10 —somaticseq-dir /ABSOLUTE/PATH/TO/SomaticSeq \
—action echo \
12 —mutect2 —somaticsniper —vardict —muse —lofreq —scalpel —strelka —somaticseq

```

Notice the command includes `—classifier-snv` and `—classifier-indel`.

4.3.5 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)

```

6  --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)
8  --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)
10 --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)
12 --varscan2 (Optional flag to invoke VarScan2)
--jointsnvmix2 (Optional flag to invoke JointSNVMix2)
14 --somaticsniper (Optional flag to invoke SomaticSniper)
--vardict (Optional flag to invoke VarDict)
16 --muse (Optional flag to invoke MuSE)
--lofreq (Optional flag to invoke LoFreq)
18 --scalpel (Optional flag to invoke Scalpel)
--strelka (Optional flag to invoke Strelka)
20 --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)
22 --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.)
24 --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)
26 --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)
28 --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)
30 --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')
32 --mutect2-filter-arguments (Extra parameters to pass onto FilterMutectCalls)
--varscan-arguments (Extra parameters to pass onto VarScan2)
34 --varscan-pileup-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)
36 --jsm-classify-arguments (Extra parameters to pass onto JointSNVMix2's classify command)
--somaticsniper-arguments (Extra parameters to pass onto SomaticSniper)
38 --vardict-arguments (Extra parameters to pass onto VarDict)
--muse-arguments (Extra parameters to pass onto MuSE)
40 --lofreq-arguments (Extra parameters to pass onto LoFreq)
--scalpel-discovery-arguments (Extra parameters to pass onto Scalpel's discovery command)
42 --scalpel-export-arguments (Extra parameters to pass onto Scalpel's export command)
--strelka-config-arguments (Extra parameters to pass onto Strelka's config command)
44 --strelka-run-arguments (Extra parameters to pass onto Strelka's run command)
--somaticseq-arguments (Extra parameters to pass onto SomaticSeq.Wrapper.sh)

```

4.3.6 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/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.

4.3.7 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 data

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.

This pipeline is used to spike in in silico somatic mutations into existing BAM files in order to create a training set for somatic mutations.

After the in silico data are generated, you can use the somatic mutation pipeline on the training data to generate the SomaticSeq classifiers.

Classifiers built on training data work if the training data is similar to the data you want to predict. Ideally, the training data are sequenced on the same platform, same sample prep, and similar depth of coverage as the data of interest.

This method is based on BAMSurgeon, slightly modified into our own fork for some speedups.

The proper citation for BAMSurgeon is Ewing AD, Houlihan KE, Hu Y, et al. Combining tumor genome simulation with crowdsourcing to benchmark somatic single-nucleotide-variant detection. *Nat Methods*. 2015;12(7):623-30.

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

5.2 Three scenario to simulate somatic mutations

Which scenario to use depend on the data sets available to you.

5.2.1 When you have sequencing replicates of normal samples

This is our approach to define high-confidence somatic mutations in SEQC2 consortium's cancer reference samples, presented here.

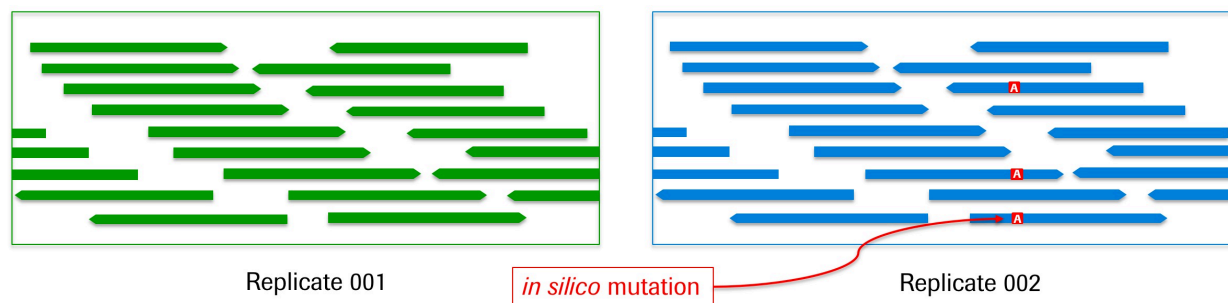
In this case, in silico mutations will be spiked into `Replicate_002.bam`. Since `Replicate_002.bam` and `Replicate_001.bam` are otherwise the same sample, any mutations detected that you did not spike in are false positives. The following command is a single-thread example.

```
1 $PATH/TO/somaticseq/utilities/dockered_pipelines/bamSimulator/BamSimulator_singleThread.sh \  
2 --genome-reference /ABSOLUTE/PATH/TO/GRCh38.fa \  
3 --tumor-bam-in /ABSOLUTE/PATH/TO/Replicate_001.bam \  
4 --normal-bam-in /ABSOLUTE/PATH/TO/Replicate_002.bam \  
5 --tumor-bam-out syntheticTumor.bam \  
6 --normal-bam-out syntheticNormal.bam \  
7 --split-proportion 0.5 \  
8 --num-snvs 20000 \  
9 --num-indels 8000 \  
10 --min-vaf 0.0 \  
11 --max-vaf 1.0 \  
12 --left-beta 2 \  
13 --right-beta 5 \  
14 --min-variant-reads 2 \  
15 --output-dir /ABSOLUTE/PATH/TO/trainingSet \  
--action qsub
```

BamSimulator_*.sh creates semi-simulated tumor-normal pairs out of your input tumor-normal pairs. The "ground truth" of the somatic mutations will be synthetic_snvs.vcf, synthetic_indels.vcf in the output directory.

For multi-thread job (WGS), use BamSimulator_multiThreads.sh instead. See below for additional options and parameters.

A schematic of the BAMSurgeon simulation procedure



5.2.2 This example mimicks DREAM Challenge

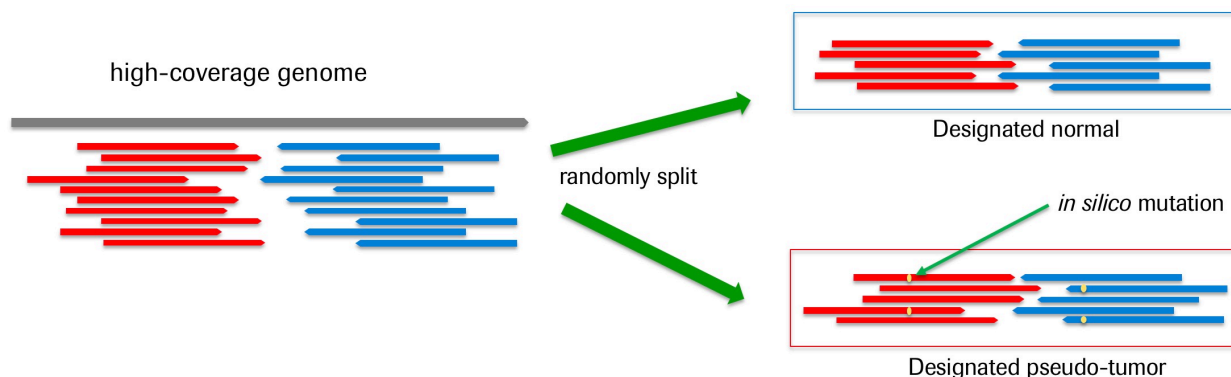
DREAM Somatic Mutation Calling Challenge was an international competition to find algorithms that gave the most accurate performances.

In that case, a high-coverage BAM file is randomly split into two. One of which is designated normal, and the other one is designated tumor where mutations will be spiked in. Like the previous example, any mutations found between the designated tumor and designated normal are false positive, since not only are they from the same sample, but also from the same sequencing run. This example will not capture false positives as a result of run-to-run biases if they exist in your sequencing data. It will, however, still capture artefacts related to sequencing errors, sampling errors, mapping errors, etc.

```
$PATH/TO/somaticseq/utilities/dockered_pipelines/bamSimulator/BamSimulator_multiThreads.sh \
—genome-reference /ABSOLUTE/PATH/TO/GRCh38.fa —tumor-bam-in /ABSOLUTE/PATH/TO/
highCoverageGenome.bam —tumor-bam-out syntheticTumor.bam —normal-bam-out syntheticNormal.
bam —split-proportion 0.5 —num-snvs 10000 —num-indels 8000 —num-svs 1500 —min-vaf 0.0
—max-vaf 1.0 —left-beta 2 —right-beta 5 —min-variant-reads 2 —output-dir /ABSOLUTE/PATH/
TO/trainingSet —threads 24 —action qsub —split-bam —indel-realign —merge-output-bams
```

The `—split-bem` will randomly split the high coverage BAM file into two BAM files, one of which is designated normal and the other one designated tumor for mutation spike in. The `—indel-realign` is an option that will perform GATK Joint Indel Realignment on the two BAM files. You may or may not invoke it depending on your real data sets. The `—merge-output-bams` creates another script that will merge the BAM and VCF files region-by-region. It will need to be run manually after all the spike in is done.

A schematic of the DREAM Challenge simulation procedure

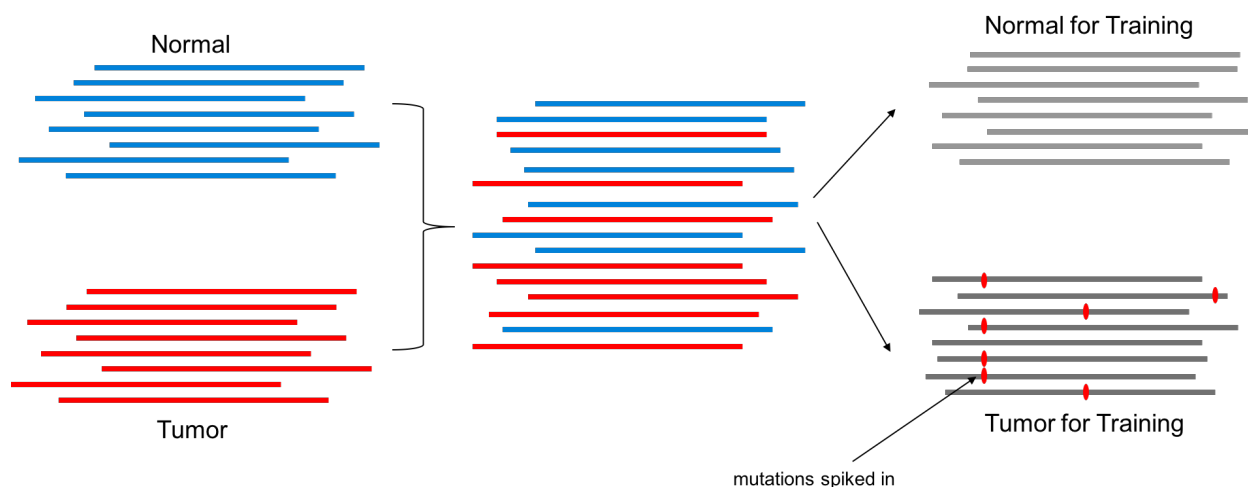


5.2.3 Merge and then split the input tumor and normal BAM files

```
$PATH/TO/somaticseq/utilities/dockered_pipelines/bamSimulator/BamSimulator_multiThreads.sh \
--genome-reference /ABSOLUTE/PATH/TO/GRCh38.fa --tumor-bam-in /ABSOLUTE/PATH/TO/Tumor_Sample.bam
--normal-bam-in /ABSOLUTE/PATH/TO/Normal_Sample.bam --tumor-bam-out syntheticTumor.bam --
normal-bam-out syntheticNormal.bam --split-proportion 0.5 --num-snvs 30000 --num-indels
10000 --num-svs 1500 --min-vaf 0.0 --max-vaf 1.0 --left-beta 2 --right-beta 5 --min-variant-
reads 2 --output-dir /ABSOLUTE/PATH/TO/trainingSet --threads 24 --action qsub --merge-bam --
split-bam --indel-realign --merge-output-bams
```

The `--merge-bam` will merge the normal and tumor BAM files into a single BAM file. Then, `--split-bam` will randomly split the merged BAM file into two BAM files. One of which is designated normal, and one of which is designated tumor. Synthetic mutations will then be spiked into the designated tumor to create "real" mutations. This is the approach described in our 2017 AACR Abstract.

A schematic of the simulation procedure



5.3 Parameters and Options

```
--genome-reference /ABSOLUTE/PATH/TO/human_reference.fa (Required)
--selector /ABSOLUTE/PATH/TO/capture_region.bed (BED file to limit where mutation spike
in will be attempted)
--tumor-bam-in Input BAM file (Required)
--normal-bam-in Input BAM file (Optional, but required if you want to merge it with the tumor
input)
--tumor-bam-out Output BAM file for the designated tumor after BAMSurgeon mutation spike in
--normal-bam-out Output BAM file for the designated normal if --split-bam is chosen
--split-proportion The faction of total reads designated to the normal. (Default = 0.5)
--num-snvs Number of SNVs to spike into the designated tumor
--num-indels Number of INDELs to spike into the designated tumor
--num-svs Number of SVs to spike into the designated tumor (Default = 0)
--min-depth Minimum depth where spike in can take place
--max-depth Maximum depth where spike in can take place
--min-vaf Minimum VAF to simulate
--max-vaf Maximum VAF to simulate
--left-beta Left beta of beta distribution for VAF
--right-beta Right beta of beta distribution for VAF
--min-variant-reads Minimum number of variant-supporting reads for a successful spike in
--output-dir Output directory
--merge-bam Flag to merge the tumor and normal bam file input
--split-bam Flag to split BAM file for tumor and normal
```

```

—clean-bam      Flag to go through the BAM file and remove reads where more than 2 identical
                read names are present, or reads where its read length and CIGAR string do not match. This
                was necessary for some BAM files downloaded from TCGA. However, a proper pair-end BAM file
                should not have the same read name appearing more than twice. Use this only when necessary as
                it first sorts BAM file by qname, goes through the cleaning procedure, then re-sort by
                coordinates.
22 —indel-realign  Conduct GATK Joint Indel Realignment on the two output BAM files. Instead of
                syntheticNormal.bam and syntheticTumor.bam, the final BAM files will be syntheticNormal.
                JointRealigned.bam and syntheticTumor.JointRealigned.bam.
—seed          Random seed. Pick any integer for reproducibility purposes.
24 —threads      Split the BAM files evenly in N regions, then process each (pair) of sub-BAM
                files in parallel.
—action        The command preceding the run script created into /ABSOLUTE/PATH/TO/
                BamSurgeoned_SAMPLES/logs. "qsub" is to submit the script in SGE system. Default = echo

```

5.3.1 -merge-bam / -split-bam / -indel-realign

If you have sequenced replicate normal, that's the best data set for training. You can use one of the normal as normal, and designate the other normal (of the same sample) as tumor. Use *--indel-realign* to invoke GATK IndelRealign.

When you have a normal that's roughly 2X the coverage as your data of choice, you can split that into two halves. One designated as normal, and the other one designated as tumor. That DREAM Challenge's approach. Use *--split-bam --indel-realign* options.

Another approach is to merge the tumor and normal data, and then randomly split them as described above. When you merge the tumor and normal, the real tumor mutations are relegated as germline or noise, so they are considered false positives, because they are supposed to be evenly split into the designated normal. To take this approach, use *--merge-bam --split-bam --indel-realign* options.

Don't use *--indel-realign* if you do not use indel realignment in your alignment pipeline.

In some BAM files, there are reads where read lengths and CIGAR strings don't match. Spike in will fail in these cases, and you'll need to invoke *--clean-bam* to get rid of these problematic reads.

You can control and visualize the shape of target VAF distribution with python command:

```

1  import scipy.stats as stats
2  import numpy as np
3  import matplotlib.pyplot as plt
4
5  leftBeta, righthBeta = 2,5
6  minAF, maxAF = 0,1
7  x = np.linspace(0,1,101)
8  y = stats.beta.pdf(x, leftBeta, righthBeta, loc = minAF, scale = minAF + maxAF)
9  _ = plt.plot(x, y)

```

5.4 To create SomaticSeq classifiers

After the mutation simulation jobs are completed, you may create classifiers with the training data with the following command:

See our somatic mutation pipeline for more details.

```

1 $PATH/TO/somaticseq/utilities/dockered_pipelines/submit_callers_multiThreads.sh \
—output-dir    /ABSOLUTE/PATH/TO/trainingSet/somaticMutationPipeline \
3 —normal-bam   /ABSOLUTE/PATH/TO/trainingSet/syntheticNormal.bam \
—tumor-bam     /ABSOLUTE/PATH/TO/trainingSet/syntheticTumor.bam \
5 —human-reference /ABSOLUTE/PATH/TO/GRCh38.fa \
—dbsnp         /ABSOLUTE/PATH/TO/dbSNP.GRCh38.vcf \
7 —thread      24 \
—truth-snv     /ABSOLUTE/PATH/TO/trainingSet/synthetic_snvs.vcf \
9 —truth-indel  /ABSOLUTE/PATH/TO/trainingSet/synthetic_indels.leftAlign.vcf \
—action        echo \

```

6 Release Notes

Make sure training and prediction use the same SomaticSeq version, or at least make sure the different minor version changes do not change the results significantly.

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 callers’ feature sets coming from different resources.

6.5 Version 2.0.2

- Incorporated LoFreq.
- Used getopt to replace getopts 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/dockerized_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|INDEL).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 is now designed to crash if the VCF file(s) are not sorted according to the .fasta reference file.

6.27 Version 2.8.1

- Fixed a bug in the ssSomaticSeq.Wrapper.sh script (single-sample mode), where the SNV algorithm weren't looking for SNV VCF files during merging when using utilities/getUniqueVcfPositions.py, causing empty SNV files. For previous commands (invoking `-gatk` for CombineVariants), the results have never changed.

6.28 Version 3.0.0

- Refactored the codes.
 1. The wrapper scripts written in bash script (i.e., SomaticSeq.Wrapper.sh and ssSomaticSeq.Wrapper.sh) are replaced by somaticseq/run_somaticseq.py.
 2. Allow parallel processing using run_parallel.py

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.