RVD27 command line program (CLI) instruction

Contents

I. The overall Flowchart of RVD2 program

Figure 1 provides the overall flowchart for RVD2 algorithm. We start from bam files, and then use SAMtools mpileup to convert bam files to pileup files. Next, we use a pileup2dc program to convert pileup files(.pileup) to depth chart files (.dc). Finally, we feed depth chart files to RVD2 program to call variants.

In the RVD2 program, first you apply the function **gibbs** to the depth chart, to fit the RVD2 statistical model and generate hdf5 files. Then you feed the hdf5 files to the **test** functions and call variants. Results including hdf5 files and vcf files will be created upon finish.

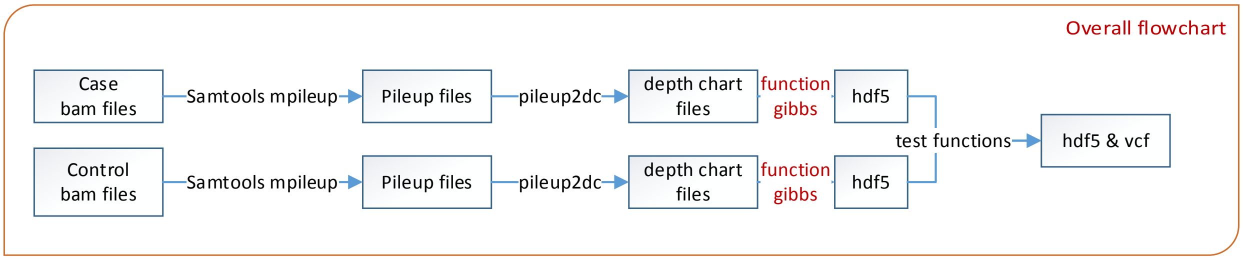

Figure 1 The overall Flowchart of RVD2 program

II. The overall Flow chart of Test functions

Figure 2 shows the four types of test functions available in RVD2 program, and Figure 3 summarizes the difference between them. **One_sample_test** is a Bayesian posterior distribution test, which reports the positions where $1-\alpha$ percent of the samples are within the interval of interest, intvl in one single sample. **Germline_test** incorporate an optional chi square test upon the one_sample_test, aiming at improving specificity. **Paired_difference_test** is a one-sided Bayesian posterior distribution test. This test requires control case paired samples. This test reports if the error rate in case sample is significantly higher than the control sample. Chi square test is optional in this test. Somatic_test is a two-sided

Bayesian posterior distribution test, which reports positions where control sample are significantly different from case sample.

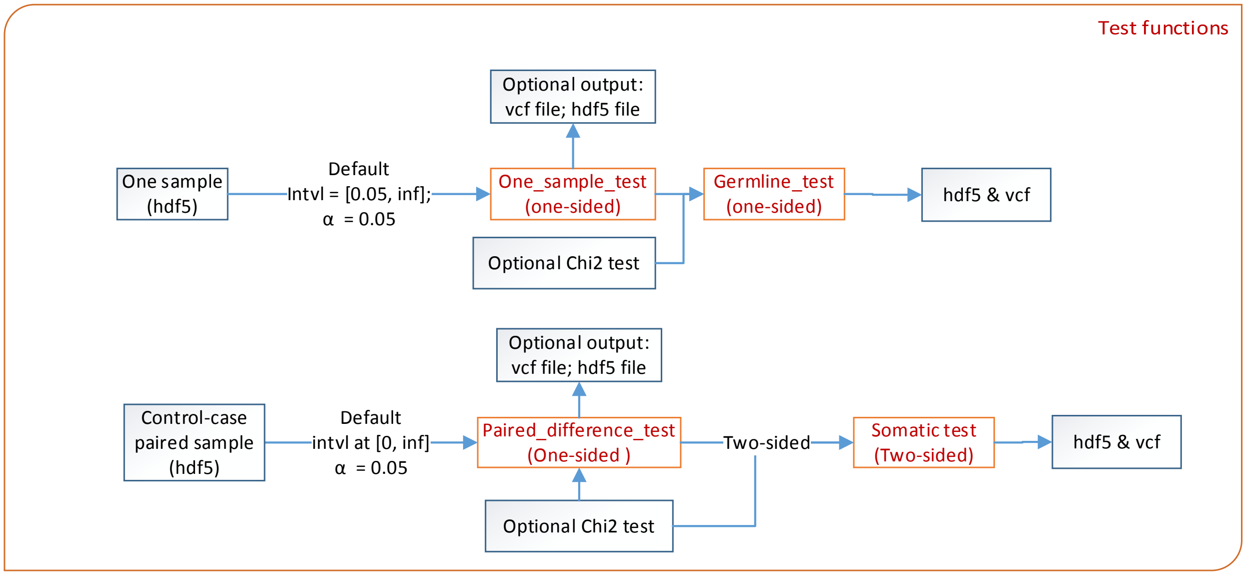
Test functions
Optional output: vcf file; hdf5 file
One sample (hdf5)
Default Intvl = [0.05, inf]; α = 0.05
One_sample_test (one-sided)
Germline_test (one-sided)
hdf5 & vcf
Optional Chi2 test
Optional output: vcf file; hdf5 file
Control-case paired sample (hdf5)
Default intvl at [0, inf] α = 0.05
Paired_difference_test (One-sided)
Two-sided
Somatic test (Two-sided)
hdf5 & vcf
Optional Chi2 test

Figure 2 The structure of hypothesis testing functions in RVD2

	one-sided	two-sided
one sample	Germline test (HCC1187 data)	NA
two samples (control-case paired)	Paired difference test (Synthetic data)	Somatic test (HCC1187 data)

Figure 3 Overview of three test functions. Chi square test, which can improve specificity, is optional in all the tests. In the paper we performed paired difference test on the synthetic dataset, germline test and somatic test on the clinical dataset.

III. RVD2 CLI syntax

We provide a python module containing the core functionality of RVD2. This module depends on the following modules: numpy, scipy, itertools, h5py tempfile, logging, datetime, os, subprocess, re, pdb and time. To run in multithreaded mode, you also need the multiprocessing module.

RVD2 can be run as a command line program or imported into an existing python script as a module.

CLI Syntax:

```
usage: rvd [-h] [--version] [-v]
       {gen,gibbs,one_sample_test,germline_test,paired_difference_test,somatic_test}
```

RVD is a hierarchical bayesian model for identifying rare variants from short-read sequence data.

```
Positional arguments:
 {gen,gibbs,one_sample_test,germline_test,paired_difference_test,somatic_test}
                         sub-command help
gen                      Demo: generate simulation sample data from the RVD model
       -h, --help        show this help message and exit
       -N                Number of replicates in computer simulation data
       -J                Number of positions in computer simulation data
       -s  SEEDINT       random process seed.
gibbs                    fit the RVD model using Gibbs sampling
      positional arguments:
       dcfile           depth chart file name

      optional arguments:
       -h, --help        show this help message and exit
       -o                OUTPUTFILE output HDF5 file name, default (output)
       -p ,--pool        POOL  number of workers in multithread pool, default None
       -g, --ngibbs      NGIBBS sampling size, default 4000
       -m, --nmh         NMH     Metropolis-Hastings sampling size, default 10
       -b, --burnin      BURNIN , default 0.2
       -t, --thin        THIN  thin, default 2
       -s  SEEDINT       random process seed.
one_sample_test          One side Bayesian posterior density test of one single sample
      positional arguments:
      HDF5Name           HDF5 sample file
      optional arguments:
       -h, --help         show this help message and exit
       -i, --intvl       INTVL interval of interest in in posterior distribution.
       -a, --alpha       ALPHA hypothesis test credible level
       -o                OUTPUTFILE output HDF5 file name, default (output)
germline_test            Germline test on a single sample, which includes a one side Bayesian density
                         test and an optional chi square test.
      positional arguments:
      HDF5Name           HDF5 sample file
```

```
          optional arguments:
          -h, --help          show this help message and exit
           -i, --intvl        INTVL interval of interest in in posterior distribution.
           -a, --alpha        ALPHA hypothesis test credible level
           -o                 OUTPUTFILE output HDF5 file name, default (output)
           -c, --chi2          Whether to include chi square test in the germline test, default True (Include)
paired_difference_test One sided posterior density difference test on control-case paired sample, with
                       an optional chi square test.
          positional arguments:
           controlHDF5Name      HDF5 control sample file
           caseHDF5Name         HDF5 case sample file

          optional arguments:
           -h, --help         show this help message and exit
           -i, --intvl        INTVL interval of interest in in posterior distribution.
           -a, --alpha        ALPHA hypothesis test credible level
           -o                 OUTPUTFILE output HDF5 file name, default (variants_paired_difference)
           -c, --chi2          Whether to include chi square test in the paired difference test, default True
           -s                 SEEDINT  random process seed.
           -n                 N Posterior difference distribution sampling size.
somatic_test           Somatic test, which includes a two sided posterior density difference test and
                       chi square test on the control-case paired sample.
          positional arguments:
           controlHDF5Name      HDF5 control sample file
           caseHDF5Name         HDF5 case sample file

          optional arguments:
           -h, --help         show this help message and exit
           -i, --intvl        INTVL interval of interest in in posterior distribution.
           -a, --alpha        ALPHA hypothesis test credible level
           -o                 OUTPUTFILE output HDF5 file name, default (variants_paired_difference)
           -c, --chi2          Whether to include chi square test in the paired difference test, default True
           -s                 SEEDINT  random process seed.
           -n                 N Posterior difference distribution sampling size.

Optional arguments:
 -h, --help            show this help message and exit
--version              show program's version number and exit
-v, --verbose          increase verbosity (specify multiple times for more)
```

IV. RVD2 CLI demo

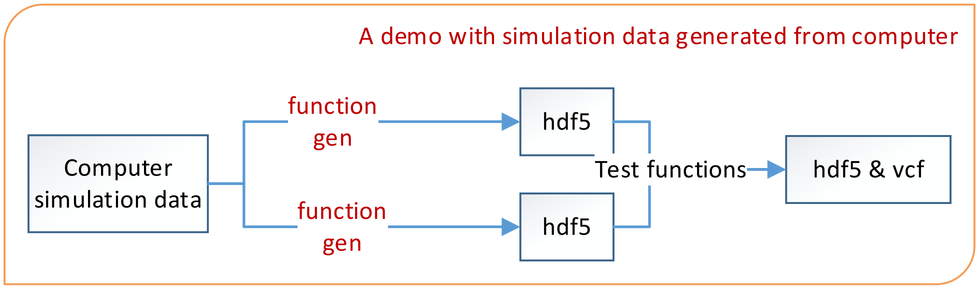

Figure 4 The flowchart of a demo using computer generated simulation data

A demo written in bash is provided to test if RVD2 can be successfully run in the computer. In the demo, simulation data will be generated by the computer and variants will be called in the simulation data. A success message will be displayed upon finish. Three hdf5 files and a vcf file will be created in the directory provided.

The content inside of the vcf file is provided in below. The positions in the vcf file are variants called by RVD2.

```
##fileformat=VCFv4.1
##fileDate=20140514
##source=rvd2
##Posterior test in cancer-normal-paired sample.
##contig=<ID=0,length=10>
##INFO=<ID=COAF,Number=1,Type=Float,Description="Control Allele Frequency">
##INFO=<ID=CAAF,Number=1,Type=Float,Description="Case Allele Frequency">
##FORMAT=<ID=AU,Number=1,Type=Integer,Description="Number of 'A' alleles">
##FORMAT=<ID=CU,Number=1,Type=Integer,Description="Number of 'C' alleles">
##FORMAT=<ID=GU,Number=1,Type=Integer,Description="Number of 'G' alleles">
##FORMAT=<ID=TU,Number=1,Type=Integer,Description="Number of 'T' alleles">
#CHROM   POS  ID  REF  ALT  QUAL  FILTER  INFO                    FORMAT       Normal      Case
chr0       1  .   A    C    .     PASS    COAF=1.211;CAAF=11.834  AU:CU:GU:TU  1979:7:7:7  1747:253:0:0
chr0       4  .   A    C    .     PASS    COAF=0.916;CAAF=9.604   AU:CU:GU:TU  1979:7:7:7  1811:189:0:0
chr0       5  .   A    C    .     PASS    COAF=0.921;CAAF=13.120  AU:CU:GU:TU  1988:4:4:4  1711:289:0:0
chr0       6  .   A    C    .     PASS    COAF=0.797;CAAF=9.280   AU:CU:GU:TU  1988:4:4:4  1819:181:0:0
chr0       7  .   A    C    .     PASS    COAF=0.825;CAAF=10.421  AU:CU:GU:TU  1985:5:5:5  1779:221:0:0
chr0       9  .   A    C    .     PASS    COAF=1.318;CAAF=11.736  AU:CU:GU:TU  1976:8:8:8  1769:231:0:0
```