

Detailed Description of Sentieon DNaseq, TNseq, and TNscope

**Sentieon DNaseq**

- Identical mathematics as Broad Institute's BWA-GATK Best Practice Workflow, 10X faster FASTQ-to-VCF, 20X faster BAM-to-VCF, measured in core-hours
- No run-to-run difference, no down-sampling in high coverage regions
- >200K samples joint-calling without intermediate file merging
- Centers for Common Disease Genomics (CCDG) functionally equivalent
- Pure software solution running on any generic-CPU-based system

**Sentieon TNseq**

- Identical mathematics as Broad Institute's Mutect and MuTect2, 10X faster FASTQ-to-VCF, measured in core-hours
- No run-to-run difference, no down-sampling in high coverage regions
- Pure software solution running on any generic-CPU-based system

**Sentieon TNscope**

- Complete tumor-normal somatic variant detection suite, calling SNV, INDEL, and SV
- No run-to-run difference, no down-sampling in high coverage regions
- Pure software solution running on any generic-CPU-based system
- Leads ICGC-TCGA DREAM Mutation Calling Challenge

applications such as liquid biopsies since Sentieon TNseq can process regions with coverage depths over 100K+ without down-sampling.

By design, Sentieon TNseq is inherently multi-threaded and is distributed-processing ready.

Sentieon **TNscope**, for accurate comprehensive tumor characterization

Key features:

- Comprehensive somatic variant detection calling SNV, INDEL, and SV on tumor-only or tumor-normal samples
- No run-to-run difference, no down-sampling in high coverage regions
- Pure software solution running on any generic-CPU-based systems
- Leads **ICGC-TCGA Dream Mutation Calling Challenge 6 in all three categories(SNV, INDEL, SV)**

Sentieon **TNscope** builds upon and improves the mathematical models used in MuTect and MuTect2. Employing sophisticated signal processing techniques to accumulate signal while canceling noise, TNscope enhances signal-to-noise ratio in variant detection, achieving higher sensitivity and specificity than comparable tools. All categories of variants are detected and characterized simultaneously, including SNV, INDEL, and structure variants eliminating the need to run multiple variant calling tools.

Sentieon participated in the ICGC-TCGA organized DREAM Challenge benchmarking tumor-normal somatic variant calling accuracy, using the engineering version of TNscope, and is leading with a solid margin in all 3 categories: SNV, INDEL, and SV. [On the final leaderboard](#), Sentieon achieved an F-score of 98.57% in SNV, 98.14% in INDEL, and 100% in SV.

Sentieon **TNscope** is inherently multi-threaded and distributed-processing ready.

Request Software

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Which Sentieon tools are you interested in *

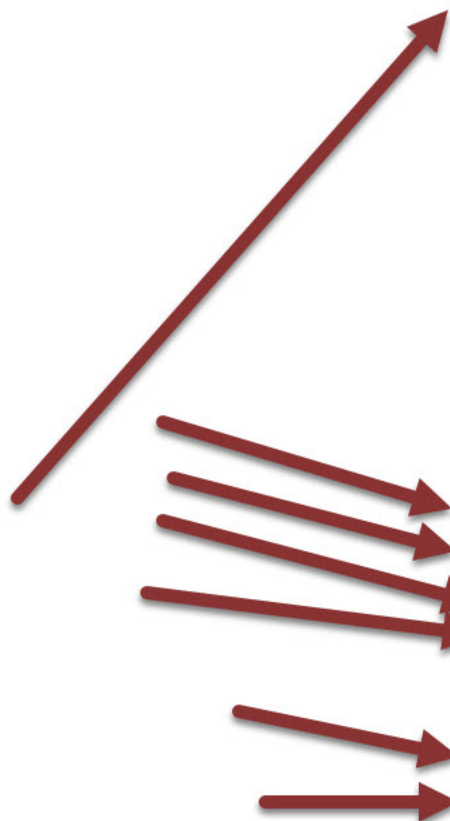
- Sentieon DNaseq
- Sentieon DNAscope
- Sentieon TNseq
- Sentieon TNscope

Where do you plan to run the Sentieon software *

- Cloud
- Local Compute
- Possibly Both

Comment

Submit





Wed 2/5/2020 8:36 AM
Rafael Aldana <rafael.aldana@sentieon.com>

Sentieon software package and evaluation license



To
Cc Brendan Gallagher

Hi :
<EITHER>
I believe Brendan mentioned that I would be contacting you about running our software.
I am very excited that you will evaluate our products. We hope our products will make your work more productive.
<OR>
It is very nice meeting you, and I am very excited that you will evaluate our products. We hope our products will make your work more productive.
Thanks a lot for sending me the information about your server.

You can download the license file for your system from <WEBSERVER_LINK>; the license file is valid until <LICENSE_EXPIRE>.
You will also need to download the software package. You can get it from <https://s3.amazonaws.com/sentieon-release/software/sentieon-genomics-201911.tar.gz>
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You can access and download the manual for our software from <https://support.sentieon.com/manual>

<EITHER>
In order to run our software in your system, you first need to start the license server in <HEADNODE>; running the following command will setup the license server as a running daemon in your system:
<SENTIEON_DIR>/bin/sentieon licensvr --start --log <LOCATION_OF_LOG_FILE> <LICENSE_FILE>
To run our software in the computing nodes, you need to set an environmental variable to tell our software the location of the license server and port. You can add this to your bash profile or to the scripts that will drive your pipelines:
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After the software is installed on your server, you may want to run a small quick start test to make sure everything is working properly. To do that, you can follow the instructions contained in https://support.sentieon.com/quick_start/downloads/Sentieon_QuickStart.pdf, and you will need to download the quick start package from: https://s3.amazonaws.com/sentieon-release/other/sentieon_quickstart.tar.gz

You may want to use and modify the shell script that comes with the quick start package, and use it to run our software with your data.
Alternatively, the software package also has some example shell scripts in the doc directory.
In addition, if you have pipelines using GATK, you may be interested in a document describing the argument correspondence between Sentieon and GATK; this document will help you convert your existing pipelines to using our tools. You can access it from <https://support.sentieon.com/appnotes/arguments>.

Also, if you plan on using DNAscope following the documentation in https://support.sentieon.com/appnotes/dnascope_ml/, you will need to download the machine learning model necessary to perform variant calling with higher accuracy by improving the candidate detection and filtering. You can find the latest version of the model at <https://s3.amazonaws.com/sentieon-release/other/SentieonDNAScopeModelBeta0.5.model>

The license I sent you allows for our software to be run in up to <NUM_CORES> threads run in parallel in your cluster. I hope this will enable you to evaluate our software, but if you need additional cores, I can send you an updated license. If you try running in multiple servers in more than <NUM_CORES> cores, our tools will be slowed down while waiting for free licenses, and you will get a warning in the log saying "No more license available for Sentieon". Again, if that is the case, do not hesitate on asking for a license for more cores.

Please do not hesitate to contact me with any questions or concerns you may have.

Thanks
Rafael