

IVC on HPC

What is ISAAC?

Isaac Variant Caller (IVC) is an analysis package designed to detect SNVs and small indels from the aligned sequencing reads of a single diploid sample.

Links:

[GitHub](#)

[Documentation](#)

Versions Available:

The following versions are available on the cluster:

- IVC-1.0,7

How to load IVC?

To load IVC, use the following commands:

```
#Load the IVC module  
module load bio/ivc/1.0.7
```

To verify if the module and dependencies are loaded correctly, use the following command.

```
#Show all the modules loaded
module list
```

This should list all the IVC dependencies that are loaded- perl , gcc,and IVC.

How to use IVC?

To see the command line arguments for the program,

```
# CMD Args
configureWorkflow.pl --help
```

To copy input data for this demonstration, use the following commands:

```
# Copy input data
cp -r /share/apps/isaac_variant_caller/1.0.7/bin/demo ~/test/
```

To run IVC, use the following threaded slurm script,'

```
#!/bin/bash
#SBATCH --job-name=isaac_alignment
#SBATCH -p main
#SBATCH --qos main
#SBATCH --nodes=1
#SBATCH --ntasks=1
#SBATCH --cpus-per-task=8
#SBATCH --mem=16GB

# Load the ISAAC module
module load bio/ivc

# Set the number of threads to use
export OMP_NUM_THREADS=$SLURM_CPUS_PER_TASK

# Run ISAAC with the desired options
```

```
configureWorkflow.pl --bam
~/test/demo/data/NA12891_dupmark_chr20_region.bam --ref
~/test/demo/data/chr20_860k_only.fa --config
~/test/demo/ivc_demo_config.ini

# go to the output dir and make the dir
cd ivcOutput

make -j $OMP_NUM_THREADS
```

The output should be in the same directory.

Where to find help?

If you are stuck on some part or need help at any point, please contact OIT at the following address.

<https://ua-app01.ua.edu/researchComputingPortal/public/oitHelp>

