

# OneRoof: Base-, Variant-, and Consensus-calling under One Proverbial Roof

## Table of contents

Overview .....	1
Quick Start .....	2
Detailed Setup Instructions .....	2
Configuration .....	2
Developer Setup .....	2
Pipeline Steps .....	3
Contributing .....	3
Citation .....	3

## Overview

oneroof is a pipeline designed to take a common series of bioinformatic tasks (see below) and put them under “one roof”. We mean this quite literally: the pipeline will perform at its best when run on networked devices in the same building.

oneroof was originally developed at the very early stages of the United States Bovine Highly Pathogenic Avian Influenza (HPAI) outbreak of 2024, when we wanted one, configurable, easy-to-run pipeline that would do all of the following:

1. Handle super-accuracy basecalling with GPU acceleration on pod5-formatted Nanopore signal files.
2. Demultiplex BAM-formatted reads that come out of basecalling.
3. Perform the above two steps as signal files become available, either locally or remotely.
4. Accept raw read BAMs or FASTQs if basecalling and demultiplexing have already been performed elsewhere.
5. Accept paired Illumina reads in addition to Nanopore reads.
6. Use forward and reverse primer sequences to select only those reads that represent complete amplicons.
7. Trim away primers—and also any bases that are upstream of the forward primer or downstream of the reverse primer.
8. Align to a custom reference with the proper presets for the provided data.
9. Call variants and consensus sequences with appropriate settings for the provided data.
10. Perform tree building with nextclade, quality introspection with multiQC, and error correction based on the input sequence platform.

Though many excellent pipelines currently exist, e.g. nf-core/viralrecon, epi2me-labs/wf-amplicon, and nf-core/nanoseq, none of these pipelines quite handled all of the above. oneroof

seeks to handle these requirements while remaining highly configurable for users, highly modular for developers, and easy to control in the command line for both.

Overall, oneroof can be summarized as a pipeline written in and managed by Nextflow. Its software dependencies are provided through containers or through an environment assembled by pixi. To run it on your own Nanopore pod5s, simply run something like:

```
nextflow run nrminor/oneroof \
--pod5_dir my_pod5_dir \
--primer_bed my_primers.bed \
--refseq my_ref.fasta \
--ref_gbk my_ref.gbk \
--kit "SQK-NBD114-24"
```

These are the core elements required to run on Nanopore data: a directory of pod5 files, a BED file of primer coordinates, a reference sequence in FASTA and Genbank format, and the Nanopore barcoding kit used.

And for Illumina paired-end reads, it's even simpler:

```
nextflow run nrminor/oneroof \
--illumina_fastq_dir my_illumina_reads/
```

## Quick Start

## Detailed Setup Instructions

### Configuration

Most users should configure oneroof through the command line via the following parameters:

### Developer Setup

oneroof depends on software packages supplied through various conda registries as well as through PyPI, the Python Package Index. To unify these various channels, we used the relatively new pixi package and environment manager, which stores all dependencies from both locations in the file `pyproject.toml`.

To reproduce the environment required by this pipeline, make sure you are on a Mac with an x86\_64 (Intel) processor, a 64-bit linux machine, or a 64-bit Windows machine using Windows Subsystem for Linux (Apple Silicon coming soon!). Then, to reproduce the environment, install pixi with:

```
curl -fsSL https://pixi.sh/install.sh | bash
```

Download the pipeline with:

```
git clone https://github.com/nrminor/onerroof.git && cd oneroof
```

And then open a pixi subshell within your terminal with:

```
pixi shell
```

As long as you are using a supported system, the pipeline should run within that subshell. You can also run the pipeline within that subshell without containers using the “containerless” profile:

```
nextflow run nrminor/onerroof \  
-profile containerless \  
--pod5_dir my_pod5_dir \  
--primer_bed my_primers.bed \  
--refseq my_ref.fasta \  
--ref_gbk my_ref.gbk \  
--kit "SQK-NBD114-24"
```

Especially on Macs, this will reduce the overhead of using the Docker Virtual Machine and allow the pipeline to invoke tools installed directly within the local project environment.

## Pipeline Steps

## Contributing

## Citation