

BCFtools 1.8 merge VCF

BCFtools 1.8 merge VCF

Merge multiple VCF/BCF files from non-overlapping sample sets to create one multi-sample file.

Quick Start

- To use **BCFtools 1.8 merge VCF**, import your data in bgzip format along with the corresponding .csi index file.
- **Resources:** <https://github.com/samtools/bcftools>

Test Data



Test data for this app appears directly in the Discovery Environment in the Data window under *Community Data* -> *iplantcollaborative* -> *example_data* -> *BCFtools_merge*

Input File(s)

Use the following files from the directory above as test input.

Input VCF/BCF files:

- **SRR946914.vcf.gz**
- **SRR946916.vcf.gz**

Index files:

- **SRR946914.vcf.gz.csi**
- **SRR946916.vcf.gz.csi**

Parameters Used in App

When the app is run in the Discovery Environment, use the following parameters with the above input file(s) to get the output provided in the next section below.S

- Set the output file name to '14_16_merged.vcf'
- Choose 'uncompressed VCF' as the output file type
- All other parameters may be left as default.

Output File(s)

Expect **14_16_merged.vcf** as output.

Tool Source for App

- <https://github.com/samtools/bcftools>