



# Bionano Solve<sup>®</sup>

## Software Installation Guide

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## Introduction

Here are notes on installing the latest Bionano Solve® software on a Saphyr Compute, Bionano Compute, IrysSolve® or a compatible server. To better understand the release details, please review the Bionano Solve Release Notes.

In this document, we only describe how to install Bionano Solve as standalone tools. For installation of Bionano Solve in conjunction with Bionano Access, please see the Bionano Tools Installation Guide (PN#30182).

## Set up Bionano Solve Pipeline on a Compute Server

Bionano Solve runs on a Linux server with x86-64 processors. While fully tested on Ubuntu 12.04 and CentOS, the pipeline may run on other \*NIX operating systems with the following prerequisites:

1. python 2.7.5
2. perl 5.14.X or 5.16.X
3. R 3.1.2 or greater with R libraries data.table, igraph, intervals, MASS, parallel, XML (which requires a Linux system library libxml2), and argparser
4. glibc >= 2.14 and gcc libraries (for older CPUs without AVX)
5. minimum RAM size is 256 GB on at least 1 node, 32 GB on all nodes

Running the assembly pipeline on a cluster requires a job submission system (such as Sun Grid Engine) that supports the Distributed Resource Management Application API (DRMAA). We require the Python DRMAA module on the submission host for the cluster.

## Installation Steps

### 1. Download the .tar.gz file

The .tar.gz file can be downloaded at the following URL:  
[http://bnxinstall.com/solve/Solve3.3\\_10252018.tar.gz](http://bnxinstall.com/solve/Solve3.3_10252018.tar.gz)

### 2. Select the pipeline installation location

Select a pipeline root directory; it can be a shared location or under one's home directory. Make sure the installation user has write permission to the selected pipeline root directory.

### 3. Unpack the .tar.gz file command

Run the following command on the Linux command line to decompress and unpack the .tar.gz file (note: replace *Solve.tar.gz* below with the path to the latest tar.gz):

```
tar -xvf Solve.tar.gz -C <PipelineRootDirectory>
```

After unpacking the downloaded file as above, the following folders/files are created:

- cohortQC
- HybridScaffold
- Pipeline
- RefAligner
- RefGenome
- SVMerge
- UTIL
- VariantAnnotation
- VCFCConverter

## Descriptions of Installation Structure

### 1. General description

**CohortQC:** scripts for generating MQR and other cohort-based metrics

**HybridScaffold:** scripts for single-enzyme and two-enzyme hybrid scaffold tools

**Pipeline:** scripts for *de novo* assembly pipeline

**RefAligner:** binary tools for alignment and assembly

**RefGenome:** cmap files for human reference builds hg19 and hg38

**SVMerge:** script for merging single-enzyme SV calls

**UTIL:** utility shell scripts for running *de novo* assembly (to be modified based on your own installation and application)

**VariantAnnotation:** tools for annotating and validating SV calls

**VCFCConverter:** scripts for converting SMAP and SVMerge output to VCF format

### 2. Cluster argument XML files for assembly

A cluster argument file has to be created for your particular compute environment. Pre-built cluster argument files are packaged with the pipeline. For more help, please contact Bionano Support.

### 3. Arguments XML files for assembly

Pre-built assembly arguments files, which contain recommended RefAligner parameters for different applications are packaged with RefAligner.

### 4. Configuration XML files for Hybrid Scaffold

Pre-build Hybrid Scaffold configuration files are under the main Hybrid Scaffold directory for single-enzyme hybrid scaffold and under the TGH directory for two-enzyme hybrid scaffold.

## Technical Assistance

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For technical assistance, contact Bionano Genomics Technical Support.

You can retrieve documentation on Bionano products, SDS's, certificates of analysis, frequently asked questions, and other related documents from the Support website or by request through e-mail and telephone.

Type	Contact
Email	<b>support@bionanogenomics.com</b>
Phone	<b>Hours of Operation:</b>  <b>Monday through Friday, 9:00 a.m. to 5:00 p.m., PST</b>  <b>US: +1 (858) 888-7600</b>
Website	<b><a href="http://www.bionanogenomics.com/support">www.bionanogenomics.com/support</a></b>