



# Bionano Access<sup>®</sup> Installation Guide

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## Introduction

The purpose of this document is to detail how to install and configure Bionano Access<sup>®</sup>. This document has been written for anyone who might install this product. This document will cover a variety of approaches for installation. It will cover multiple configurations including shared web server and standalone installations. It will also cover installation procedures for various operating systems including Linux, Mac, and Windows. The first part of this document will cover the process for a first time installation. The document also outlines some considerations specific to existing IrysView<sup>®</sup> customers.

If you will be integrating this web server with any compute servers, the compute servers should be deployed first. To complete the configuration of Bionano Access you will need the static IP address of those systems and the file share to be used for image transfer. Bionano engineers and customer IT operations staff will complete those installations and provide this information.

A single shared instance of Bionano Access per organization is the recommended installation. It is not recommended to install Bionano Access on each workstation. This would defeat the shared collaborative project based design of Bionano Access. It is possible to run Bionano Access on a workstation in standalone mode if you do not have an instrument, compute servers, or collaborators in order to visualize Bionano data.

## Compatibility

Bionano Access is compatible with data generated by a Saphyr<sup>®</sup> instrument and bioinformatics output from the Bionano Solve pipeline. Bionano Access has also been tested for compatibility with existing Irys data generated by Auto Detect 2.1.4 and IrysSolve 2.1 pipeline. Bionano Access can be run on a virtual server if needed. Bionano Access is currently supported on the following operating systems:

- CentOS 7.x
- RHEL 7.x
- Macintosh (OS X)
- Windows 7 or greater (64 bit only)

## System Requirements

8 GB of memory for standalone installations and 32 GB for shared web servers is recommended. For disk you can estimate approximately 5 GB per assembly you plan to retain on the web server. The web server is very lightweight and will run easily on most systems. If you have a large number of concurrent users or you are noticing performance issues contact support to help identify a configuration that will work best for your situation.

## Access Updates

Note, the prerequisite software packages (see Prerequisites section below) only need to be installed once. To update your Access, perform the Access installation again (see section Windows Installation or Linux/Macintosh Installation). The Bionano Access install can be run as many times as desired. It will not remove or overwrite any of your data, files, or configurations. You can determine the current version of Bionano Access installed by looking at the Access Help Page (<http://<servername>:3005/Help/HelpIndex.html>).

## Warning

If you have already installed Bionano Access, please note the required version of Nodejs has changed. We now require version 6 or greater instead of version 4.5. If you have an existing installation with version 4.5 or earlier you will need to update it. Follow the instructions below to install the latest version of Nodejs. You can check the version installed by issuing this command at the command prompt:

```
node --version
```

### For Windows:

- Stop your Bionano Access web server.
- Go to the control panel, select programs and features.
- Uninstall Nodejs
- Run the installation for [Node.js 8.9.4](#)

### For Mac:

- Stop your Bionano Access web server
- Run the installation for [Node.js 8.9.4](#).

### For Linux (Centos / Redhat):

- Stop your Bionano Access web server
- Issue the following commands. Please note, you may need to restart your terminal after issuing the curl command.

```
curl -o- https://raw.githubusercontent.com/creationix/nvm/v0.32.1/install.sh | bash
nvm install 8.9.4
nvm use 8.9.4
```

## Prerequisites

Bionano Access requires PostgreSQL 9.6, Perl 5, and nodejs 6 or greater. Links have been provided below to the appropriate installations instructions based on your operating system. Do not install different versions than what has been indicated. Be sure to perform these installations with administrator rights. During install, Stack Builder is not required and use default paths and ports during install.

### For Windows:

- [Perl 5.24](#)
- [PostgreSQL 9.6.2](#) (set password to “1rysvievw”, use port 5432)
- [Node.js 8.9.4](#)

### For Macintosh:

- MacOS Sierra 10.12
- [Perl 5.24](#)
- [Python 2.7.14](#) (required by PostgreSQL for Mac)
- [PostgreSQL 9.6.8](#) (set password to “1rysvievw”, use port 5432)

**Note:** Please make sure PostgreSQL bin is in your PATH environment variable before attempting the Bionano Access Install. Otherwise the createdb command in the installation script will fail. Example command to update your PATH environment variable:

```
export PATH=$PATH:/Users/wrodriguez/PostgreSQL/pg96/bin
```

Nodejs will be installed automatically by the mac installation script (install\_mac.sh). This is described later in the document.

### CentOS 7 and RHEL 7:

The commands to install the required prerequisite software on Centos and RedHat have been provided below.

```
# install perl
sudo yum install -y perl

#install nodejs
curl --silent --location https://rpm.nodesource.com/setup\_8.x | sudo bash -
sudo yum install -y nodejs

#install postgresql

(Centos only)
sudo yum install https://download.postgresql.org/pub/repos/yum/9.6/redhat/rhel-7-x86_64/pgdg-centos96-9.6-3.noarch.rpm

(Redhat only)
sudo yum install https://download.postgresql.org/pub/repos/yum/9.6/redhat/rhel-7-x86_64/pgdg-redhat96-9.6-3.noarch.rpm

sudo yum install postgresql96-server postgresql96-contrib
sudo /usr/pgsql-9.6/bin/postgresql96-setup initdb
sudo cp /var/lib/pgsql/9.6/data/pg_hba.conf /var/lib/pgsql/9.6/data/pg_hba.conf.orig
sudo bash -c 'echo "local all all peer">/var/lib/pgsql/9.6/data/pg_hba.conf'
sudo bash -c 'echo "host all all 127.0.0.1/32 md5" >>/var/lib/pgsql/9.6/data/pg_hba.conf'
sudo bash -c 'echo "host all all ::1/128 md5" >>/var/lib/pgsql/9.6/data/pg_hba.conf'

#start postgresql service
sudo systemctl start postgresql-9.6
sudo systemctl enable postgresql-9.6
sudo -i -u postgres psql -U postgres -d postgres -c "alter user postgres with password '1rysv1ew';"
sudo systemctl restart postgresql-9.6
```

## Windows Installation

64 bit Windows 7 or greater is supported. Follow the instructions below to complete a Windows installation.

### Installation Steps:

1. Make sure the system has Internet access.
2. Make sure the active account has administrator rights.
3. Download the Bionano Access Windows Setup (Access\_Setup.exe) from the [Bionano Software Download page](#).
4. Right click on the Access\_Setup.exe file and select 'Run as Administrator'.

## Linux / Macintosh Installation

### CentOS / RedHat Installation Steps:

The majority of our in house testing is performed using CentOS. As such CentOS is the recommended operating system. However it is known that other organizations often prefer other flavors of Linux. Testing has been performed using RedHat, Ubuntu, and Darwin (Macintosh). Other versions of Linux are likely to be compatible as well, but have not been validated for use at this time. The following instructions will guide you how to install Bionano Access on a Linux system.

If you are not already applying security updates to your system on a regular basis we recommend running 'yum update' on your linux operating system prior to installing the latest version of Bionano Access. This operation requires Internet access and will update the libraries on your system to the latest versions including various security updates.

1. Verify the installation system has internet access.
2. Create a bionano user account that has sudo privileges.
3. Download the Bionano Access Linux/Mac Installation (Access-Install.tar.gz) from the [Bionano Software Downloads page](#).
4. Extract the file to /home/bionano:  
tar -zxf Access-Install.tar.gz -C /home/bionano
5. Run installation script:  
sudo /home/bionano/Access-Install/install.sh

### Mac Installation Steps:

Mac installations are intended for standalone use only. We do not intend for mac systems to function as shared web servers. You may be prompted for your Mac admin password during the installation. The install script will install nodejs if it is not already on your system.

1. Verify the installation system has internet access.
2. Download the Bionano Access Linux/Mac Installation (Access-Install.tar.gz) from the [Bionano Software Downloads page to your home directory](#).
3. Open a terminal window and go to your home directory (cd ~/).
4. Extract the install file in your home directory (tar -xvf Access-Install.tar.gz)
5. Go into the Access-Install directory
6. Run this command:  
./install\_mac.sh

## Configuration

A configuration file is used to specify your Bionano Access setup. This file tells Bionano Access where to find files and what compute servers it should communicate with. Specify the configuration file by name when you start the web server. If you plan to run Bionano Access in standalone mode with no instruments or compute servers you do not have to perform any configuration steps and you can skip the balance of the Configuration section.

Bionano Access can be configured to work with a combination of Saphyr instruments and or compute servers. You need to create an access.txt file in the ../bionano/access/web/Server/Config folder for your specific configuration. In the Config folder we provided various template files you can use as a starting point. An access.txt file is not provided in the installation so that we do not overwrite your configuration during future updates.

### Example access.txt Configuration File

```
{
  "psfDetectServer": "193.168.50.31",
  "assemblyServer1": "193.168.50.31",
  "assemblyServer2": "193.168.50.31",
  "icsShare": "\\193.168.50.31\share",
  "webServerShare": "\\193.168.50.31\share",
  "irysSolveShare": "/home/bionano/access/share",
  "icsShareRelPath": "chips",
  "webServerShareJobs": "jobs",
  "webServerRelLocalFiles": "",
  "webServerPort": "3005",
  "solveServerUser": "bionano",
  "scriptDir": "/home/bionano/tools/access/1.0",
  "refAlignerDir": "tools/pipeline/1.0/REFALIGNER/1.0",
  "irysSolveListenIP": "10.10.1.13"
}
```

### Configuration Settings

Adjust the following properties in your access configuration file to establish proper connections with the Saphyr Instrument Control Software and your compute servers.

Property	Value	Example
<b>psfDetectServer</b>	This should be the IP address on the Saphyr Compute Server accessible to the Bionano Access Web Server. If you have more than one instrument it would be the primary Saphyr Compute server in your cluster. This value must be a static IP address.	"193.168.50.31"
<b>irysSolveListenIP</b>	This should be set to the IP address for the Bionano Access Web server that is accessible to all the compute servers. In some cases the web server may be dual homed so that the compute servers can be within an isolated VLAN. In this case the web server may have more than one IP address. The compute servers will curl http requests to the web server to update job status using this IP address. This value must be a static IP address.	"10.10.1.13"
<b>icsShare</b>	This is the path where the Saphyr Instrument Control Software will write images captured from the instrument for image detection. This path should be relative to the instrument control PC.	"\\193.168.50.31\share"
<b>webServerShare</b>	This is the path to the share for images from the instrument and output for the pipeline. If the web server is running on a Windows machine this value should be the same as the icsShare property. If the web server is running on a Linux system it should be the same as the irysSolveShare property.	Windows: "\\193.168.50.31\share"  Linux: "/home/bionano/access/share"
<b>assemblyServers</b>	Input the IP address where to send computational jobs.	["193.168.50.31"]

**Note:** The Bionano Access software is designed to load balance computational jobs between two clusters (assemblyServer1 and assemblyServer2). Both the assemblyServer1 and assemblyServer2 settings must have values. If you only have one cluster just enter the same IP address into both settings. Bionano Access is only compatible with compute servers running Bionano Solve v3.2 with our approved SGE configuration.



## Starting the Web Server

First open a command prompt and navigate to the following directory:

(Windows) `c:\bionano\access\web\Server`

(Linux) `/home/bionano/access/web/Server`

To start Bionano Access Web Server in standalone mode issue the following command:

```
node --max-old-space-size=4096 server default
```

To start Bionano Access Web Server with your access.txt configuration issue this command:

```
node --max-old-space-size=4096 server access
```

“node” is the command to start nodejs. The “--max-old-space-size” argument increases the V8 JavaScript engine memory use to be optimized for our larger data files. ‘server’ is our starting nodejs file and the final parameter (access or default) is the configuration file to use.

The web server should then be accessible from a browser using the IP address or DNS name for the webserver plus the port the server is running on. 3005 is our default port. You can change the port for the web server in the configuration file by changing the ‘webServerPort’ setting. If you use port 80 you will not need to add a port number to your URL, but there are known issues with curl responses from the compute servers routing to port 80 on some networks due to security restrictions. If you do not know your Web Server’s IP address or DNS, contact your IT department for details, and if using standalone mode on a local machine such as a desktop or laptop, use ‘localhost’ in place of an IP address. Other users would require the IP address or DNS name instead of localhost to access your machine.

Ex. <http://192.168.48.57:3005>, <http://bionano-227:3005/>

On CentOS and RedHat if you close your SSH session the server will stop. You can use the following commands to detach from the process and allow it to continue running after you exit. When you run this command the console output will be logged to the nohup.out file in the .../bionano/access/web/Server directory.

```
nohup node --max-old-space-size=4096 server access & disown
```

### **Important note:**

To start access the web server in Linux, you can only use the “bionano” account and the bionano account must have sudo privilege. Please do not start the access web server using the root account in Linux.

## Firewall

There are a few security considerations with your Bionano Access web server. First if you have firewall security you will need to allow the following traffic from the Bionano Access web server. Generally if you are running in standalone these considerations would not apply.

**Firewall information:**

Source System	Target System	Protocol
Bionano Access Web Server	psfDetectServer assemblyServers	SSH port 22
All compute servers Saphyr Instrument Control PC Workstation Browsers	Bionano Access Web Server	HTTP (port is set as webServerPort in config file)

## User Accounts

When you first access the web server you will be prompted to log in. There is a default user account (below) provided you can use to access the system. Once you have logged in, create user accounts for your team members. We recommend that you disable or modify the default account once you have finished creating user accounts for your organization. Do not use shared accounts between users, that defeats how the notification scheme is designed to operate. If you change the default account please notify Bionano Support or provide them an account you want them to use when servicing your system.

**Default Account:**

Username: [bionoadmin](#)

Password: [admin](#)

## IrysView Customers

Customers with an existing Irys instrument will continue to use Auto Detect 2.1.4 for image detection. They will then import the generated bnx files manually into a project in Bionano Access. The Experiment Design module and dashboards for real time monitoring in Bionano Access are not compatible with the Irys instrument. Existing Irys data can be imported into Bionano Access using the import feature. Complex objects such as assemblies and scaffolds must be tar zipped into a single file in the correct format. Scripts to compress and zip existing Irys data for upload along with detailed instructions can be found on our [AccessImportUtils](#) project on GitHub.

It is recommended that Irys owners install the Bionano Access software on their existing workstation dedicated to Auto Detect. That system has sufficient computing resources to handle the web server. Existing IrysSolve servers can be converted to Irys Compute servers running Bionano Solve v3.0, but this process requires Bionano Technical Support involvement. The system will be reimaged so any data on the system will be erased. Important data should be archived before the system is re-imaged.

## 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>

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