



Bionano Access[®]

Installation Guide

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Revision History

Revision	Released	Notes
AB	10/20/2021	Installation and dependencies updated for Access release 1.7.
AC	12/15/2021	Updated hyperlinks for MAC computer installations
AD	2/9/2022	Added instruction in prerequisite section.
AE	06/17/2022	Adding step to install instruction to remove previous Access-Install folder.

Introduction

The purpose of this document is to detail how to install and configure Bionano Access®. 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® customers.

If you will be integrating this web server with any compute servers, Bionano Tools should be installed on the compute servers first. To complete the configuration of Bionano Access you will need the static IP address of compute system which is used to submit computation jobs.

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

Compatibility

Bionano Access is compatible with data generated by a Saphyr® 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 (Catalina)
- Windows 10

System Requirements

16 GB of memory for standalone installations and 32 GB for shared web servers is recommended. For disk you can estimate approximately 10 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 are noticing performance issues, contact support to help identify a configuration that will work best for your situation.

Access Updates

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>).

For Windows:

- Stop your Bionano Access web server.
- Go to the control panel, select programs and features.
- Uninstall Node.js
- Run the installation for [Node.js 12.22.10.1](#)

For Mac:

- Stop your Bionano Access web server
- Run the installation for [Node.js 12.22.10](#)
 - Apple may prevent install. Go to System Preferences > Security & Privacy to run installer.

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.

```
sudo yum remove nodejs  
sudo yum install https://rpm.nodesource.com/pub_12.x/el7/x86_64/nodejs-12.20.1-1nodesource.x86_64.rpm
```

Rollback

Take a backup of your environment first if you have an existing installation of Bionano Access and would like the option to rollback your installation to the previous version after the installation process. You can then restore your backup to return the system to the previous version if needed. You should be backing up your environment on a regular basis. For more information on backups refer to the Saphyr Site Preparation Guide (PN 30145).

Prerequisites

If your Bionano Access system will be integrated with a compute cluster you should install / update Bionano Solve on that environment first. Access will check the correct version of the pipeline is installed before it will start.

Bionano Access requires PostgreSQL 9.6, Perl 5, and Node.js 12. Links have been provided below to the appropriate installation 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:

- [Strawberry Perl](#)
- [PostgreSQL 12](#) (set password to “1rysviiew”, use port 5432, and remember to update your path)
- [Node.js 12.22.10](#)
- [Java 1.8](#)

For Macintosh:

- [Perl 5](#)
- [Python 2.7.15](#) (required by PostgreSQL for Mac)
- [PostgreSQL 11](#) (set password to “1rysviiew”, use port 5432, and do not install Stack Builder)
- [Node.js 12.22.10](#)
- [Java 1.8](#)

For 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 java
sudo yum install -y java-1.8.0-openjdk

# install python3
sudo yum install -y python3

#install nodejs
curl --silent --location https://rpm.nodesource.com/setup/12.x | sudo bash -
sudo yum install -y nodejs

#install postgresql
sudo yum install -y https://download.postgresql.org/pub/repos/yum/reporepms/EL-7-x86_64/pgdg-redhat-repo-
latest.noarch.rpm

sudo yum install -y postgresql12 postgresql-12-server postgresql12-contrib
sudo /usr/pgsql-12/bin/postgresql-12-setup initdb
sudo cp /var/lib/pgsql/12/data/pg_hba.conf /var/lib/pgsql/12/data/pg_hba.conf.orig
sudo bash -c 'echo "local all all peer">/var/lib/pgsql/12/data/pg_hba.conf'
sudo bash -c 'echo "host all all 127.0.0.1/32 md5" >>/var/lib/pgsql/12/data/pg_hba.conf'
sudo bash -c 'echo "host all all ::1/128 md5" >>/var/lib/pgsql/12/data/pg_hba.conf'

#start postgresql service
sudo systemctl start postgresql-12
sudo systemctl enable postgresql-12
sudo -i -u postgres psql -U postgres -d postgres -c "alter user postgres with password 'lrysviue';"
sudo systemctl restart postgresql-12
```

You will also need to establish RSA keys and keyless login to any servers that will be used for detection or assembly servers before running the install the first time. To generate new RSA keys use this command as the Bionano user:

```
ssh-keygen -t rsa
```

To setup keyless login for the Bionano account use this command where <<servername>> is the DNS name for that server or the IP address. Test it with an SSH connection afterwards. You should not be prompted for a password if it worked.

```
ssh-copy-id <<servername>>
```


WARNING: Please make sure both PostgreSQL and Java are in your path before attempting the Bionano Access Install. You can test this by trying the 'psql' or 'java' commands at a command prompt. If they are not recognized you need to update your path. Example commands to update your path environment variable have been provided below, but they may vary depending on your exact system. Please note Mac Catalina OS requires PATH to be added while in bash.

Mac:

```
PATH="/Library/PostgreSQL/11/bin:$PATH"
```

Linux:

```
export PATH=$PATH:/usr/pgsql-12/bin/
```

Windows:

- Right click your computer in Windows Explorer and click properties
- Select Advanced system settings
- Click Environment Variables button
- Under system variables (not user variables) select Path
- Click the Edit button
- Add (if not already there) C:\Program Files\PostgreSQL\12\bin
- Add (if not already there) C:\Program Files (x86)\Java\jdk1.8.0_161\bin
- Click Ok (x3)

Windows Installation

64-bit Windows 10 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 Installation

The majority of our 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. 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. Be sure to reboot your system after applying the latest patches when your system is idle.

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](#). Be sure to delete previous installation tar files before downloading the latest installation tar file.
4. Delete previous install folder:
`rm -rf Access-Install`
5. Extract the file to /home/bionano:
`tar -zxf Access-Install.tar.gz -C /home/bionano`
6. Run installation script:
`sudo /home/bionano/Access-Install/install.sh`

Macintosh Installation

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. Run this command: `bash`
5. Extract the install file in your home directory (`tar -xvf Access-Install.tar.gz`)
6. Go into the Access-Install directory (`cd ./Access-Install`)
7. Run this command: `./install_mac.sh`
8. Enter user password and PostgreSQL password (“1rysvie”) accordingly

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",
  "assemblyServers": ["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
psfDetectServer	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"
irysSolveListenIP	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"
icsShare	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"
webServerShare	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"
assemblyServers	Input the static IP address of compute node that can take SGE job submissions.	["193.168.50.31"]
webServerPort	The TCP port used by the Access application	3005
proxyServer	url of proxyserver for internet access	http://192.168.48.21:3128

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=16384 server default
```

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

```
node --max-old-space-size=32768 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.

You can add ‘https’ to the end of either command above if you install an ssl certificate on the server. You will need a key.pem and cert.pem in your access/web/Server directory. Contact our support team for instructions how to generate and or acquire an ssl certificate for your environment. We recommend using an SSL certificate for https communication to protect your data.

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. When you enable https the port will be the value of the webServerPort setting plus one. 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=32768 server access & disown
```

Please be aware:

The first time you start Bionano Access 1.7 after upgrading from a previous version, several BED files will be jsonized. This process may take several minutes to complete. This conversion will only happen once and your Bionano Access webserver may not be responsive during this conversion.

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 strongly 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 and it violates security guidelines for clinical environments. 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 Irys Solve 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

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.

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