Bionano Access® Installation Guide

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Revision History

REVISION	NOTES
AB	Installation and dependencies updated for Access release 1.7.
AC	Updated hyperlinks for MAC computer installations
AD	Added instruction in prerequisite section.
AE	Adding step to install instruction to remove previous Access-Install folder.
AF	Added additional instructions in the prerequisite section.
AG	Updated Software download link
AH	Updates for Bionano Access 1.8 release and additional data backup guidance
AI	Removing Mac Installation Support
AJ	Added Red Hat install instructions

Introduction

The purpose of this document is to detail how to install and configure Bionano Access®. This document will cover a variety of approaches to 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 and Windows. The first part of this document will cover the process for a first-time installation.

On startup Bionano Access will check the configuration for Compute servers. During startup Access will connect and verify that the proper Solve version is installed on any Compute server configured. If it cannot connect or verify the proper version of Bionano Solve, Bionano Access will not start. Therefore, users will want to update the Bionano Solve version on the Compute servers before upgrading Bionano Access. The Compute servers will signal the Bionano Access server when the job is complete. Be sure to assign the Bionano Access Server a static IP so the address the Compute servers use to communicate with the Access Server does not change.

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 to have one instance 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 a Saphyr instrument or Compute server is available 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 can be run on a virtual server if needed and is currently supported on the following operating systems:

- CentOS 7.x
- RHEL 9.x
- Windows 10

Installation on the Mac OS is no longer supported starting with Bionano Access 1.8.1.

System Requirements

16 GB of memory for standalone installations and 32 GB for shared web servers is recommended. For disk, and per each assembly to retain on the web server estimate approximately 10 GB. The web server is very lightweight and will run easily on most systems. If performance issues are noticed, contact support@bionano.com to help identify a configuration that will work best for the situation.

Access Updates

The prerequisite software packages (see "Prerequisites" section below) only need to be installed once. To update Access, perform the Access installation again (see "Windows Installation" or "Linux Installation" sections). The

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Bionano Access installation can be run as many times as desired. It will not remove or overwrite any user data, files, or configurations. To determine the current version of Bionano Access installed, see the **Access Help** page (http://<servername>:3005/Help/HelpIndex.html).

For Windows

1. Stop the Bionano Access web server.
2. Go to the control panel, select programs and features.
3. Uninstall Node.js.
4. Run the installation for Node.js 12.22.10.1.
5. From command prompt run: `npm install -g npm@8.10.0`

For CentOS

1. Stop the Bionano Access web server.
2. Issue the following commands.

    NOTE: User terminal may need to be restarted after issuing the curl command.

```
sudo yum remove nodejs

sudo yum install https://rpm.nodesource.com/pub_12.x/el/7/x86_64/nodejs-12.20.1-1nodesource.x86_64.rpm

sudo npm install npm@8.10.0 -g

sudo yum install java-11-openjdk-devel
```

Backup

Data backup is the responsibility of the end user facility and is strongly recommended on a recurring basis. Prior to updating the software, it is strongly recommended to conduct a backup of the data on the Bionano Access Server, including the databases for Access and VIA software. Administrator access for the server is required for database directory permissions, if not already established. Contact Support@Bionano.com for assistance. Bionano Support may not set up database backup for the end user however guidance can be provided. For additional details, please refer to the *Saphyr Site Preparation Guide* (CG-30145).

Rollback

If a backup system is in place, users can restore the backup to return the system to the previous version if needed. Bionano support should be contacted for assistance in the instance of needing to revert the Bionano Access Server (BAS) from a backup. Users should back up the environment on a regular basis.

Prerequisites

If the Bionano Access system will be integrated with a Compute cluster, Bionano Solve should be installed/updated in that environment first. Access will check that the correct version of the pipeline is installed before it starts.

Bionano Access requires PostgreSQL 12 , Perl 5, Java 11, and Node.js 12. Links to the appropriate installation instructions based on the operating system have been provided below. Do not install different versions than what has been indicated. Be sure to perform these installations with administrator rights. During installation, Stack Builder is not required and uses default paths and ports during install.

For Windows

PostgreSQL 12: https://www.enterprisedb.com/downloads/postgres-postgresql-downloads. Set password to "1rysview", use port 5432, and remember to update the path.

Perl 5: https://strawberryperl.com/

Java 11: https://www.oracle.com/java/technologies/javase/jdk11-archive-downloads.html. **NOTE**: User may be required to create an Oracle account to download the installer.

Node.js 12: https://nodejs.org/download/release/v12.22.10/node-v12.22.10-x64.msi. Upgrade npm to 8.10.0 after node installation by executing '`npm install npm@8.10.0 -g`' in the command prompt.

```
For CentOS 7 # install perl
sudo yum install -y perl


# install java
sudo yum install java-11-openjdk-devel


# 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


# update npm
sudo npm install npm@8.10.0 -g


# install postgresql
sudo yum install -y https://download.postgresql.org/pub/repos/yum/reporpms/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 '1rysview';"

sudo systemctl restart postgresql-12
```

For RHEL 9

```
sudo dnf groupinstall 'Development Tools' -y

curl -fsSL https://rpm.nodesource.com/setup_12.x | sudo bash -

sudo dnf install nodejs -y

sudo npm install npm@8.10.0 -g

sudo dnf install java-11-openjdk-devel -y

sudo dnf install perl -y

sudo dnf install python3 -y

sudo dnf -y install https://download.postgresql.org/pub/repos/yum/reporpms/EL-9-x86_64/pgdg-redhat-repo-latest.noarch.rpm

sudo dnf install postgresql14-server postgresql14-contrib

sudo postgresql-14-setup initdb

sudo cp /var/lib/pgsql/14/data/pg_hba.conf /var/lib/pgsql/14/data/pg_hba.conf.orig

sudo bash -c 'echo "local all all peer">/var/lib/pgsql/14/data/pg_hba.conf'

sudo bash -c 'echo "host all all 127.0.0.1/32 md5" >>/var/lib/pgsql/14/data/pg_hba.conf'

sudo bash -c 'echo "host all all ::1/128 md5" >>/var/lib/pgsql/14/data/pg_hba.conf'

sudo systemctl enable --now postgresql-14

sudo systemctl start postgresql-14

sudo -i -u postgres psql -U postgres -d postgres -c "alter user postgres with password '1rysview';"

sudo systemctl restart postgresql-14

wget http://www.bnxinstall.com/access/Access-Install.tar.gz

tar -zxf Access-Install.tar.gz

cd Access-Install

sudo ./install.sh

chmod +x /home/bionano/access/web/Server/StartAccess.sh

sudo systemctl restart access
```

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RSA keys and keyless login to any Linux servers that will be used for detection or assembly servers before running the installation the first time should be established. To generate new RSA keys, employ this command as the user:

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

To set up keyless login for the Bionano account use this command where `<<servername>>` is the DNS name for that server or the IP address. Evaluate with an SSH connection afterwards. Users will not be prompted for a password if it worked.

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

> **WARNING:** Please make sure both PostgreSQL and Java are in the user path before attempting the Bionano Access Install. This can be assessed by trying the 'psql' or 'java' commands at a command prompt. If they are not recognized the path will need to be updated. Example commands to update the path environment variable have been provided below, but they may vary depending on the exact system.
>
> **Linux:**
>
> ```
> export PATH=$PATH:/usr/pgsql-12/bin/
> ```
>
> **Windows:**
>
> 1. Right click in Windows Explorer and click **Properties**.
> 2. Select **Advanced System Settings**.
> 3. Click **Environment Variables** button.
> 4. Under system variables (not user variables) select **Path**.
> 5. Click the **Edit** button.
> 6. Add (if not already there) `C:\Program Files\PostgreSQL\12\bin`
> 7. Add (if not already there) `C:\Program Files\Java\jdk-11\bin`
> 8. 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 prerequisites are installed and PostgreSQL and Java are added to PATH (see "Prerequisites" section). Make sure the active account has administrator rights.
3. Download the Bionano Access Windows Setup **(Access_Setup.exe)** from the Bionano Software Download page (https://bionano.com/software-downloads/).
4. Right click on the `Access_Setup.exe` file and select **Run as Administrator**.

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Linux Installation

Most testing is performed using CentOS. As such CentOS is the recommended operating system. However, it is known that other organizations often prefer other versions of Linux which are likely to be compatible as well but have not been validated for use at this time. The following instructions will guide users on how to install Bionano Access on a Linux system.

If not already applying security updates to the user system on a regular basis Bionano recommends running 'yum update' on the Linux operating system prior to installing the latest version of Bionano Access. This operation requires Internet access and will update the libraries on the system to the latest versions including various security updates. Be sure to reboot the system after applying the latest patches when the user system is idle.

1. Verify the installation system has internet access.

2. Make sure prerequisites are installed and PostgreSQL is added to PATH7 (see "Prerequisites" section).

3. Create a Bionano user account that has sudo privileges.

4. Download the Bionano Access Linux Installation (`Access-Install.tar.gz`) from the Bionano Software Downloads page (https://bionano.com/software-downloads/). Be sure to delete previous installation tar files before downloading the latest installation tar file.

5. Delete previous install folder:
   ```
   rm -rf Access-Install
   ```

6. Extract the file to /home/bionano:
   ```
   tar –zxf Access-Install.tar.gz –C /home/bionano
   ```

7. Cd Run installation script:
   ```
   sudo /home/bionano/Access-Install/install.sh
   ```

Configuration

A configuration file is used to specify the Bionano Access setup. This file tells Bionano Access where to find files and what Compute servers with which it should communicate. Specify the configuration file by name when starting the web server. If planning to run Bionano Access in standalone mode with no instruments or Compute servers it is not necessary to perform any configuration steps and users can skip the balance of this Configuration section.

Bionano Access can be configured to work with a combination of Saphyr instruments and or Compute servers. Create an `access.txt` file in the ~/bionano/access/web/Server/Config folder for the specific configuration. In the Config folder various template files to use as a starting point have been provided. An `access.txt` file is not provided in the installation so that user configuration during future updates is not overwritten.

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, shown in **Table 1**, in the Access configuration file to establish proper connections with the Saphyr Instrument Control Software and user Compute servers.

Table 1. Connection properties

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 proxy server for internet access	**http://192.168.48.21:3128**
referenceListDisplay	Access ships with a variety of references for common studied species. It is possible to use this setting to limit references to human only. You can also limit references to only those that were provided with Bionano Access (not user uploaded).	**"human;system"**

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 the user 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 which used to be optimized for larger data files. 'server' is the starting nodejs file and the final parameter (access or default) is the configuration file to use.

Add 'https' to the end of either command above if an ssl certificate is installed on the server. It will need a key.pem and cert.pem in the access/web/Server directory. Please follow *How to enable HTTPS in Bionano Access* (CG-30377) to set up https for Access. Using an SSL certificate for https communication to protect user data is recommended.

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 Bionano's default port. Change the port for the web server in the configuration file by changing the 'webServerPort' setting. When enabling https, the port will be the value of the webServerPort setting plus one. If using port 80 it is not necessary to add a port number to the 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 the Web Server's IP address or DNS is unknown, contact the 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 the machine.

Ex.: `http://192.168.48.57:3005, http://bionano-227:3005/`

On CentOS and RedHat if closing the SSH session, the server will stop. Use the following commands to detach from the process and allow it to continue running after exit. When running 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
```

The first time Bionano Access 1.8 is started after upgrading from Access 1.6 or a previous version, several BED files will be jsonized. This process may take several minutes to complete. This conversion will only happen once and the Bionano Access webserver may not be responsive during this conversion. **NOTE**: To start the web server in Linux, users can only use the "bionano" account which 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 the Bionano Access web server (see **Table 2**). First, if firewall security is present, allow the following traffic from the Bionano Access web server. Generally, if running in standalone these considerations would not apply. The Compute On Demand endpoints will depend on the Compute region selected when activating the service. Contact Support if the exact endpoints for these systems are required.

Table 2. Security System 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/HTTPS (port is set as webServerPort in config file)
Compute On Demand	https://*.bionanostratus.com/ http://*.bionanostratus.com/ https://platform.rescale.com/ https://*.amazonaws.com/	TCP:3000 TCP:3001 TCP: 443

User Accounts

When first accessing the web server, log in following the prompt. A default user account is provided to access the system. Once logged in, user accounts for all team members can be created. **WARNING**: It is suggested that the user create a new user account and NOT use the default account for analysis. It is also strongly recommended to disable or modify the default account once user accounts have been created. Do not use shared accounts between users, as this defeats how the notification scheme is designed to operate. It also violates security guidelines for clinical environments. If changing the default account please notify Bionano Support or provide them with an account to use when servicing the system.

Default Account

`Username: bionanoadmin`

`Password: admin`

Technical Assistance

For technical assistance, contact Bionano 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	support@bionano.com
Phone	Hours of Operation: Monday through Friday, 9:00 a.m. to 5:00 p.m., PST US: +1 (858) 888-7663 Monday through Friday, 9:00 a.m. to 5:00 p.m., CET UK: +44 115 654 8660 France: +33 5 37 10 00 77 Belgium: +32 10 39 71 00
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