



Bionano Solve Installation Guide

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Revision History

Revision	Notes
A	Initial release of document.
B	Revision to wget command
C	Add install step for new packages
D	Added install for Bionano Access Server Removed install for IrysSolve
E	Added section on Security Patches
F	Overview updated
G	Warnings and Notices updated
H	Modified install file name
J	Updated security patching procedure
K	Adding Docker pre-requisite
L	Modified python command syntax for bng-install

Overview

Bionano Solve are installed on Bionano Access Servers, Saphyr Compute Servers, and Bionano Compute Servers before server shipment and installation.

The Bionano Solve (folder “tools”) is located at the /home/bionano directory on the compute server. The folder contains various tools and scripts, including our computation pipeline Bionano Solve. Each tool is versioned independently. These tools together perform computation job on our compute server.

Install or Upgrade of Bionano Solve involves downloading a zipped file to the home/bionano directory and un-tarring the contents. Please refer to our Bionano Solve Release Note for details of the each update.

Warning

This installation is designed to overlay your existing /home/bionano/tools directory. **Do not move or delete the existing contents of that directory.** If you remove files from the tools directory your system may not function properly after this installation. Our installation process retains each version of the pipeline tools on your system automatically. There is no need to archive the existing contents.

Security Patches

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

security updates. Please be sure to reboot your system after applying system updates. For more information on security updates please refer to our [security patching status page](#).

Installation/Upgrade Instructions

As of version 1.6 Bionano Solve utilizes Docker. Using Docker container technology offers several advantages. We can easily deploy the 150+ software dependencies our pipeline requires with a single image and we can support sites that do not have internet access on their compute servers. Be aware the Docker installation requires root access. When you run the installation script you will receive an immediate acknowledgement, but it may take 15 minutes for the Docker images to be fully installed. Please be aware that the installation will replace any existing installation of Docker with the latest version.

Installation with Internet Access

Follow these installation instructions if your servers have Internet access. It will be used to download the Bionano Solve installation file and install Docker.

1. Use putty or other terminal software to connect (ssh) to your Bionano Access Server using the 'bionano' account. You will need to know the 'bionano' account credentials and the IP address for your Bionano Access Server to proceed:

```
ssh access
```

2. Download the installation file:

```
wget -N www.bnxinstall.com/access/tools/access.tools.tgz
```

3. Unzip the installation file:

```
tar -xvf access.tools.tgz
```

4. Give your session root privileges:

```
sudo su -
```

5. Run the installation script:

```
cd /home/bionano/tools/access/1.0  
python bng-install all
```

6. Close your root session:

```
exit
```

7. Close your bionano session:

```
exit
```

8. Repeat steps 1-6 on your Saphyr1a server.

Installation without Internet Access

Follow these installation instructions if you do not have Internet access on your servers. You will be required to download the Bionano Solve installation file and the Docker rpm files on a Centos or Redhat Linux based system and transfer them to your bionano servers to complete this installation. Use these commands to download the Bionano Solve installation file and the Docker rpm files.

```
wget -N www.bnxinstall.com/access/tools/access.tools.tgz  
sudo yum install docker --downloadonly --downloadaddir=/home/bionano/docker
```

These installation instructions assume that you have transferred the docker folder with rpm files and the Bionano Solve installation file to /home/bionano on the Bionano Access Server and the Saphyr1a compute server.

1. Use putty or other terminal software to connect (ssh) to your Bionano Access Server using the 'bionano' account. You will need to know the 'bionano' account credentials and the IP address for your Bionano Access Server to proceed:

```
ssh access
```

2. Unzip the installation file:

```
tar -xvf access.tools.tgz
```

3. Give your session root privileges:

```
sudo su -
```

4. Run the installation script:

```
cd /home/bionano/tools/access/1.0/  
python bng-install all
```

5. Close your root session:

```
exit
```

6. Close your bionano session:

```
exit
```

7. Repeat steps 1-6 on your Saphyr1a server.

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.

Type	Contact
Email	support@bionanogenomics.com
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