



# **Bionano VIA™ System Requirements**

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## Revision History

REVISION	NOTES
A	Initial release.
B	Transferred document to rebranded template.
C	July 2023 update. Product name change to VIA.
D	March 2024 – update hardware requirements.

## VIA Architecture

The VIA system is designed as a truly scalable system that is easy to deploy and maintain by labs of any size, from a single user to a large enterprise. The key to this scalability is the modular design of the system. The core system is composed of three components: Clients, Server, and Processing Unit. Depending on the types of samples processed in VIA, additional utility software may need to be installed (**Figure 1**).

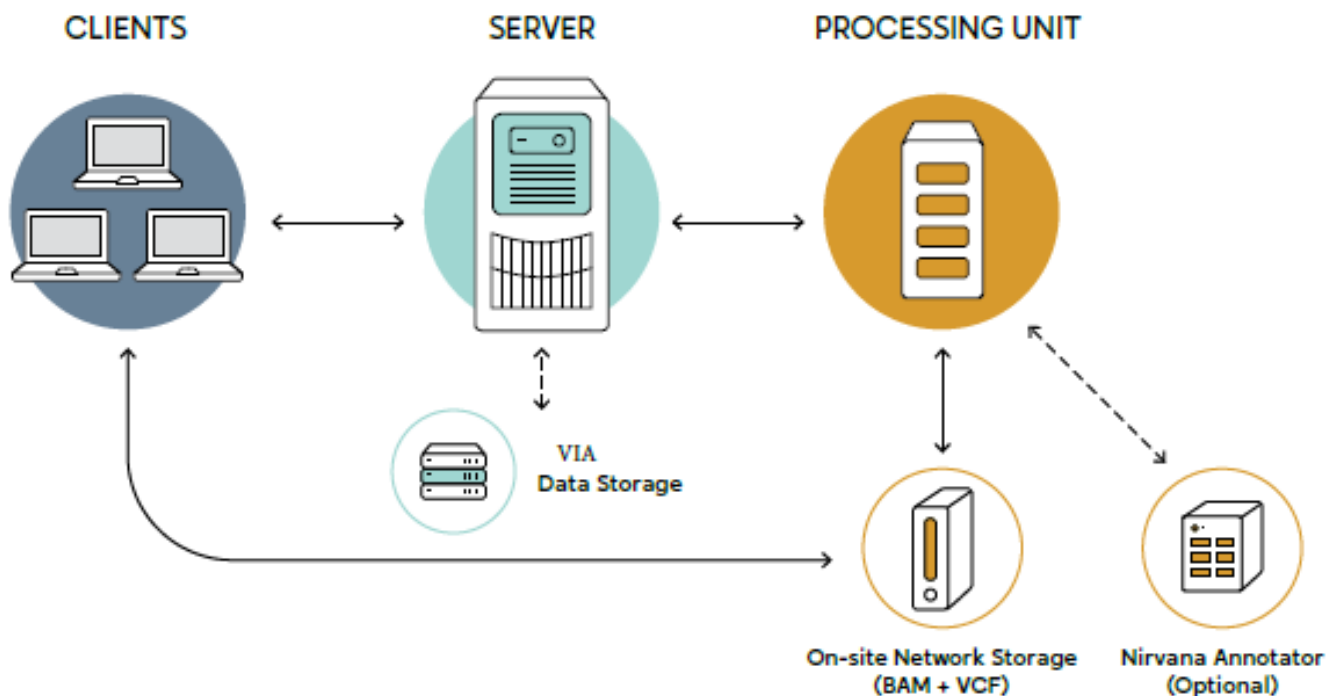
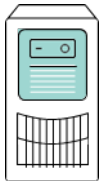


Figure 1. VIA Architecture



### Clients

The Client software is the Graphical User Interface (GUI) utilized by all users to access VIA. The Client software is installed on multiple computers, allowing multiple users to access VIA at the same time from within the network as well as remotely. After the initial installation, the system will be able to automatically update the client when the system administrator updates the software. This avoids manually updating each client.



### Server

The server is the heart of the system; it manages the data in the repository as well as all the resources (e.g., tracks, users, configurations, etc.). All data is stored on the server with exceptions for “raw” NGS data (see NGS section). The database storage component of the VIA server can be in the same directory as the server installation directory or hosted on a mounted drive. The server component can be installed on a physical server on premises or on a cloud (e.g., Amazon AWS) and all clients communicate with the server through a secure http connection. The server should be up and running all the time to service incoming requests from the clients and include a back-up policy to back up the content of the repository on a regular basis.



### Processing Servers

The processing server is used to process raw samples to make calls. It can be hosted on the same machine as the server, depending on the number and size of samples being processed; separate servers are recommended. For large scale deployments, the system can utilize multiple Processing Servers in cases where there is demand for processing many samples simultaneously. The Processing Server communicates with the server via a secure protocol. The VIA Admin can specify different processing servers for different types of samples for efficient processing; smaller files (e.g., panels/arrays) can be run on a less powerful processing server while WGS samples can be assigned to a much more powerful processing server. This unit does not require backups.

## VIA Data File Types

### Microarrays

All data including raw array data is stored on the server. Hardware requirements vary based on the type and size of data being processed and managed.

### NGS

VIA can store and process different types of NGS data. BAM files are processed to derive copy number and BAF. They are also used to process, and display read depth and individual reads in the genome browser. VCF files are used for sequence variants.

Processed data from VCF and BAM files is stored in the repository, but the original files are not copied to the server and are kept in their original on-site network storage location. The server keeps track of where these files

are located by storing the file path to the files and updating this if the files move. It is recommended to store these files on the same network as the server for best performance. If the files are located on a different network, then performance could be impacted greatly. As NGS data can be quite large and assume a lot of space, the use of external drives connected to the server is a good solution for storage of these files.

NGS data comes in many formats (VCF files, BAM files from targeted panels, BAM from WES, BAM from WGS) and the size of these files varies. Hardware requirements vary based on the type and size of data being processed and managed. For example, to process deep WGS data, more RAM and faster processing are needed.

## VIA Additional Utility Software

### Nirvana Annotator

VIA uses the Illumina **Nirvana Annotation** tool to annotate VCF files in a single seamless workflow beginning with loading of files into VIA. The **Nirvana** tool is installed separately from the VIA system. It is recommended that Nirvana be installed on the same machine as the Processing Server. The installation files are rather large and require at least 60GB of space (including supplementary databases).

### BAM MultiScale Reference Builder

The **BAM MultiScale Reference Builder** is a separately installed application that is used to generate reference files to be used with the VIA software when processing BAM files to derive copy number from NGS platforms.

Building a reference file with this utility may only need to be done once, if the same reference file will be used for all the experimental NGS samples. This utility should be installed on a user machine that has access to BAM files. Hardware requirements vary based on the size of BAM files that will be used for creating the reference file. For a small NGS panel, 8GB RAM is minimum, but more RAM (up to 32GB) will be needed for deep WGS. The required space for this utility is 6GB.

### VIA Sample Importer

The **VIA Sample Importer** is an optional command line utility that streamlines and automates sample loading and processing for VIA software. It requires as input the sample descriptor file that specifies samples, location, and processing settings. This utility should be installed on a user machine. The installation space required for this utility is ~500MB in size. **NOTE:** See hardware recommendations in the next section.

## Hardware Recommendation

**Table 1** lists minimum hardware recommendations. Adjust the RAM and CPU based on expected volume and type of data being processed and expand disk space as the database grows. **NOTE:** File sizes can widely vary. Use the following to estimate the amount of disk space needed: 100–500MB per sample for VIA database storage.

**Table 1.** Hardware Recommendations

	OS	RAM	CPU	Disk Space
Client	64bit Windows, Mac OS X (Java 1.8)	16GB recommended (minimum 8GB) solely for Client application. Physical RAM should be higher than memory allocated to the Client. Higher amount of RAM might be needed to view and review sequence variants.		<b>500MB</b>
Processing Unit	64bit Windows; Ubuntu LTS, CentOS 7 or 8, RHEL 9* (Java 1.8)	8GB (16GB if using WGS) recommended (4GB minimum) solely for Processing Server process. Higher amount of RAM and disk space might be needed depending on throughput and data types.	Dual core	500MB
Server	64bit Windows; Ubuntu LTS, CentOS 7 or 8, RHEL 9* (Java 1.8)	8GB recommended solely for the Server process. Higher amount of RAM and disk space might be needed depending on throughput and data types.	Quad core	Varies (recommen ed 500Gb minimum)
Nirvana (optional)	64bit Windows; CentOS 7 or 8, RHEL 9* Needs to be installed on same machine as Processing	32GB recommended (16GB minimum) Higher amount of RAM and disk space might be needed depending on throughput and data types.	CPU with AVX support. AVX was introduced on Intel with the Sandy Bridge architecture, so Xeons after around 2011 should support it. If using VMWare and if VMWare vMotion is at EVC level L3 (Westmere) or below, increase to at least L4 (Sandybridge).	60GB minimum
BAM MultiScale Reference Builder (optional)	64bit Windows, Mac OS X, Ubuntu LTS, CentOS 7 or 8, RHEL 9*(Java 1.8)	16GB (32GB if using WGS) recommended (8GB minimum)		6 GB
VIA Sample Importer (optional)	64bit Windows; Ubuntu LTS, CentOS 7 or 8, RHEL 9*	8GB recommended (minimum 4GB) solely for Client application		500MB

\*with SELinux disabled

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## Technical Assistance

For technical assistance, contact Bionano Technical Support.

You can retrieve documentation on Bionano products, SDSs, 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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