



# **Bionano VIA™ System Requirements**

DOCUMENT NUMBER:

CG-30577

DOCUMENT REVISION:

C

Effective Date:

07/20/2023

## Table of Contents

<b>Legal Notice</b>	<b>3</b>
Patents	3
Trademarks	3
<b>Revision History</b>	<b>4</b>
<b>VIA Architecture</b>	<b>5</b>
Clients	6
Server	<b>Error! Bookmark not defined.</b>
Processing Server(s)	<b>Error! Bookmark not defined.</b>
Microarrays	6
NGS	6
<b>VIA Additional Utility Software</b>	<b>7</b>
Nirvana Annotator	7
BAM MultiScale Reference Builder	7
VIA Sample Importer	7
<b>Hardware Recommendation</b>	<b>7</b>
<b>Technical Assistance</b>	<b>9</b>

---

## Legal Notice

### **For Research Use Only. Not for use in diagnostic procedures.**

This material is protected by United States Copyright Law and International Treaties. Unauthorized use of this material is prohibited. No part of the publication may be copied, reproduced, distributed, translated, reverse-engineered or transmitted in any form or by any media, or by any means, whether now known or unknown, without the express prior permission in writing from Bionano Genomics, Inc. Copying, under the law, includes translating into another language or format. The technical data contained herein is intended for ultimate destinations permitted by U.S. law. Diversion contrary to U. S. law prohibited. This publication represents the latest information available at the time of release. Due to continuous efforts to improve the product, technical changes may occur that are not reflected in this document. Bionano Genomics, Inc. reserves the right to make changes to specifications and other information contained in this publication at any time and without prior notice. Please contact Bionano Genomics, Inc. Customer Support for the latest information.

BIONANO GENOMICS, INC. DISCLAIMS ALL WARRANTIES WITH RESPECT TO THIS DOCUMENT, EXPRESSED OR IMPLIED, INCLUDING BUT NOT LIMITED TO THOSE OF MERCHANTABILITY OR FITNESS FOR A PARTICULAR PURPOSE. TO THE FULLEST EXTENT ALLOWED BY LAW, IN NO EVENT SHALL BIONANO GENOMICS, INC. BE LIABLE, WHETHER IN CONTRACT, TORT, WARRANTY, OR UNDER ANY STATUTE OR ON ANY OTHER BASIS FOR SPECIAL, INCIDENTAL, INDIRECT, PUNITIVE, MULTIPLE OR CONSEQUENTIAL DAMAGES IN CONNECTION WITH OR ARISING FROM THIS DOCUMENT, INCLUDING BUT NOT LIMITED TO THE USE THEREOF, WHETHER OR NOT FORESEEABLE AND WHETHER OR NOT BIONANO GENOMICS, INC. IS ADVISED OF THE POSSIBILITY OF SUCH DAMAGES.

### **Patents**

Products of Bionano Genomics® may be covered by one or more U.S. or foreign patents.

### **Trademarks**

The Bionano logo and names of Bionano products or services are registered trademarks or trademarks owned by Bionano Genomics, Inc. ("Bionano") in the United States and certain other countries.

Bionano™, Bionano Genomics®, Saphyr®, Saphyr Chip®, Bionano Access™, VIA™ software, and Bionano EnFocus™ are trademarks of Bionano Genomics, Inc. All other trademarks are the sole property of their respective owners.

No license to use any trademarks of Bionano is given or implied. Users are not permitted to use these trademarks without the prior written consent of Bionano. The use of these trademarks or any other materials, except as permitted herein, is expressly prohibited and may be in violation of federal or other applicable laws.

© Copyright 2023 Bionano Genomics, Inc. All rights reserved.

## Revision History

REVISION	NOTES
A	Initial release.
B	Transferred document to rebranded template.
C	July 2023 update. Product name change to VIA.

## 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**).

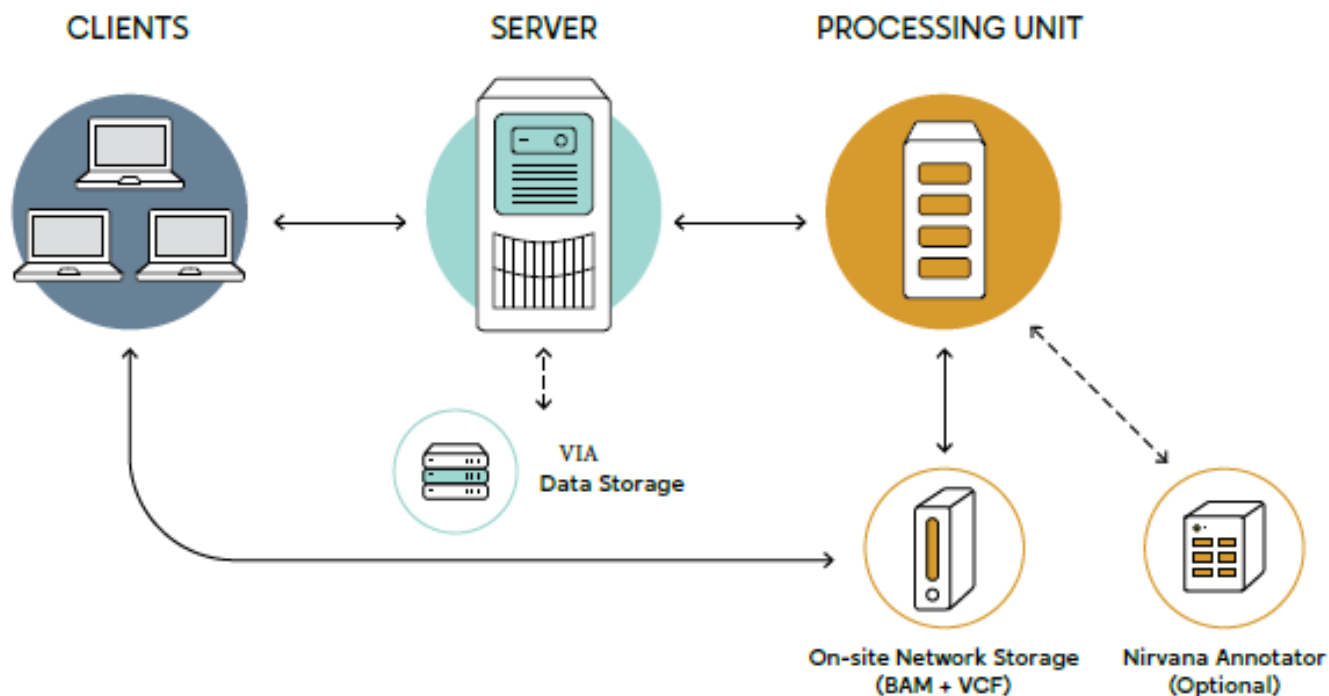
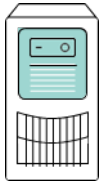


Figure 1. VIA Architecture



## 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, processing 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 recommendation on the next page.

## Hardware Recommendation

Below are minimum hardware recommendations (**Table 1**). 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: 10–170MB per sample for VIA database storage.

**Table 1.** Hardware Recommendation

	OS	RAM	CPU	Disk Space
Client	64bit Windows, Mac OS X (Java 1.8)	16GB recommended (minimum 8GB) solely for Client application 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 (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 (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 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 (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	8GB recommended (minimum 4GB) solely for Client application		500MB



## Technical Assistance

For technical assistance, contact Bionano Genomics 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.

TYPE	CONTACT
Email	<a href="mailto:software-support@bionano.com">software-support@bionano.com</a>
Phone	Hours of Operation: Monday through Friday, 9:00 a.m. to 5:00 p.m., PST US: +1 (858) 888-7663
Website	<a href="http://www.bionano.com/support">www.bionano.com/support</a>
Address	Bionano Genomics, Inc. 9540 Towne Centre Drive, Suite 100 San Diego, CA 92121