Bionano Access® v1.4 Release Notes

Document Number: 30272

Document Revision: E

Table of Contents

Legal Notice

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

Patents

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

Trademarks

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

Bionano Genomics®, Saphyr®, Saphyr Chip®, and Bionano Access® 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 Genomics is given or implied. Users are not permitted to use these trademarks without the prior written consent of Bionano Genomics. 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.

Revision History

Revision	Notes
A	Initial release of document
B	Release of 1.4.1 Update
C	Release of 1.4.2 Update
D	Release of 1.4.3 Update
E	Added Known Issues.

Bionano Access

This document describes the v1.4 release of Bionano Access®. In this document we will provide an overview of what is changing with this release so that you may better understand the impact of moving to this version of our visualization software. Should you have any questions please contact support@bionanogenomics.com.

Introduction

Bionano Access v1.4 is a new release of our Bionano Access product. Bionano Access supports Windows, Mac, and Linux systems. Data between users is shared using projects, and performance is much improved through rendering optimizations and graphics acceleration. This application is designed for install on a single centralized server that can be shared across an organization. For information about system requirements and installation please refer to our Installation Guide (P/N 30170).

Compatibility

Bionano Access is compatible with data generated on both Irys and Saphyr instruments. Existing Irys Data generated via Auto Detect v2.1.4 or IrysSolve v2.1 pipeline can be uploaded into Bionano Access. Bionano Access is compatible with Saphyr Control Software v3.1 and v4.8.

Bionano Access is designed to integrate directly with the Bionano Solve® v3.4 pipeline running on Saphyr Compute and Bionano Compute servers. Compute configurations which are not directly compatible will continue to be supported from the command line, with a manual import of results into Bionano Access.

Known Issues

Chimeric Score Filter Change

In Access v1.4.3, we repaired the chimeric score filter on variant annotations of *de novo* assemblies. In previous versions, this filter was not functional. In v1.4.3, the pass selection will only show records whose score is ‘pass’. The fail selection will only show records whose chimeric score is ‘fail’. The all selection will all records including those whose chimeric score is ‘not applicable’. Currently, the chimeric score for all insertion and deletion calls will be ‘not applicable’; those calls would only be shown when the all selection option is enabled.

Improvements

Below is a brief description of new features that have been added with this release. For more detailed information on these new features please refer to our user manuals and video tutorials.

Improvement	Description
Alerts	The Bionano Access system now sends alerts to notify system administrators of errors or system conditions that require attention. This is the foundation for proactive system diagnostics where the system can monitor itself and alert those responsible when action is needed. This feature works similar to the messaging and message center already built into Bionano Access. Messages are notifications sent to specific users regarding job status and other system events. Alerts are broadcast to all users with the 'Administrator' role. Alerts will appear in header of the Bionano Access website next to the existing Message Center Icon. The system will also post alerts sent by the instrument that pertain to a chip run on the dashboard.
Version Check	Each version of Bionano Access is designed to run with a specific version of Bionano Solve. Bionano Access will now check the installed version of Bionano Solve on startup to ensure the correct version is installed.
Image Preview	In the genome browser for *do novo* assemblies and variant annotations you have the ability to generate structural variant reports. When a variant is selected an image is captured of the variant that will appear in the report. A preview icon is now available to allow the user to view the image that was captured.
Toggle Bed Labels	The system will display the BED region name when you hover the mouse over a BED region. Now if you hold the shift key and click on the BED region the label will remain visible. If you shift click the BED region again the label will disappear. Turning on labels on BED regions of interest is useful to mark when you are creating an SV report.
Zip Support	Most Bionano Solve operations generate a compressed result file. Traditionally, these files were in tar.gz format. When these compressed files contain a large number of files, extracting specific files is slow. This caused performance issues with certain operations such as showing molecules in the genome browser. We have switched to using zip files instead. Individual files can be extracted from a zip file quickly, and zip files are smaller.
Maintenance Mode	It is now possible to put the system into Maintenance Mode. In maintenance mode, only users with the Administrator role can log into the system. This allows them to check system operation after upgrades before opening the system to general use.

Complex Passwords	The system is now able to enforce complex passwords on user accounts. Administrators can configure the degree of complexity desired.
Login Attempts	With this version of Bionano Access, users are only permitted a configured number of login attempts before their account is locked. Administrators can change how many attempts are granted.
Forgot Password	The Forgot User password workflow has been changed. The user must respond to an email sent by the system, and a challenge response form before passwords are reset.
Session Limit	To prevent shared accounts (a security concern according to most data protection guidelines including GDPR and FedRamp), the system only allow one web session per account. When logging into the system any existing sessions on other systems will be terminated automatically. It is possible to open multiple tabs to the web application on the same system.
Rare Variant Analysis	The new Bionano Solve operation Rare Variant Analysis to detect structural variants with low allelic fraction has been integrated into Bionano Access. It is possible to perform this operation and visualize the results.
NGS map colors	In the genome browser, it is now possible to change the color of the NGS maps when you are viewing scaffolds.

Tickets

Updates

Version	Summary	Ticket
1.4.1	Failed to find AutoNoise1_rescaled.bnx.gz	IW-4796
1.4.1	Reference missing for Variant Annotation on Rare Variant objects	IW-4787
1.4.1	Get chip stats totals are incorrect	IW-4788
1.4.2	User undefined error when importing molecules	IW-4840
1.4.2	Options links missing when there are no assembly servers in configuration.	IW-4841 IW-4842
1.4.2	Part 20319 throughput limit increased to 1300Gbp	IW-4843 IW-4912
1.4.2	Type error when launching BNX filter operation	IW-4845
1.4.2	Scaffold links active before job completed	IW-4772
1.4.2	Dual label prep display issue during experiment definition	IW-4786
1.4.2	Route user to home screen after password change	IW-4989 IW-4332
1.4.3	Proxy support for Compute on Demand	IW-5115
1.4.3	Bed File not showing	IW-5183
1.4.3	Alignment options active before completion	IW-5169
1.4.3	Circos failed to load	IW-5131 IW-5168
1.4.3	Hide masked copy number variant segments	IW-5156
1.4.3	Disable chimeric score filter for variant annotation objects	IW-5157
1.4.3	Gaps in copy number, baseline missing	IW-5172
1.4.3	Update Opt Arg files	IW-5199
1.4.3	Add cnv mask BED files to for display	IW-5189

User Stories

Summary	Ticket
[Alerts] Add server name to alert messages	IW-3328
[Alerts] Add health icon to header	IW-3348
[Alerts] Show run specific alerts on dashboard	IW-3524
[Alerts] Send email alerts to administrators	IW-3525
[Alerts] Check tools version on startup	IW-3964
[Annotation] Add Image Preview for SV Report	IW-3587
[Annotation] Include masked SVs in VCF Export	IW-3949
[BNX] Add label count filter	IW-3389
[BNX] Change default merge selections	IW-3919
[Circos] Toggle BED labels	IW-3352
[Circos] Clear BED labels	IW-4018
[Experiment Design] Add SV Mask to Auto Assembly	IW-3335
[Experiment Design] Capture target amount to collect	IW-3865
[Experiment Design] Show target progress on dashboard	IW-3877
[Import] Add zip support	IW-4135
[Security] Maintenance mode	IW-101
[Security] Detect caps lock	IW-517
[Security] Add logout to side menu	IW-1521
[Security] Complex passwords	IW-1889
[Security] Password attempts	IW-1891
[Security] Password expiration	IW-1893
[Security] Login retry attempts	IW-3916
[Security] Improved forgot password workflow	IW-3988
[Security] Session limit	IW-4163
[Security] Reset password on first login	IW-4132
[Single Molecule] Add aneuploidy tab	IW-3296
[Single Molecule] Rare Variant Analysis Operation	IW-3297
[Single Molecule] Rare Variant Visualization	IW-3298
[Single Molecule] Create annotation parameter file	IW-4075
[Single Molecule] Import Rare Variant Analysis	IW-4328
[Variant Annotation] Add support for Rare Variant Analysis annotation	IW-4282
[Viewer] Allow user to change color on NGS maps	IW-3260
[Viewer] Add scale for copy number	IW-3401
[Viewer] Add filter for chimeric assembly score	IW-3904
[Viewer] Add named filter for copy number confidence	IW-4044
[Viewer] Update keyboard shortcuts	IW-4204
[Viewer] Add filter for copy number size	IW-3865

Defects

Summary	Ticket
[Alert] Disable disk check on startup	IW-4021
[Alignment] Inverting molecules does not invert labels	IW-3924
[BNX Filter] some fields allow negative values	IW-4383
[Database] Anchor table is too large	IW-4527
[Experiment Design] Long sample names cause issues	IW-3985
[Experiment Design] Make dashboard always show scans	IW-3982
[Experiment Design] Back button resets project selection	IW-4138
[Experiment Design] Experiment module navigation changed	IW-4091
[Experiment Design] Dashboard not showing multiplex correctly	IW-4126
[Experiment Design] Users can see all experiments	IW-4271
[Experiment Design] Allow experiment edits for unused flow cells on sealed chips	IW-4411
[Import] Failed due to too many connections	IW-4093
[Project Browser] Maps to Molecules link not active	IW-4034
[Project Browser] Renamed object shows old name in viewer	IW-4052
[Project Browser] Give Project Lead access to named filters	IW-3967
[Project Browser] Possible to create duplicate named filters	IW-3920
[Project Browser] Prevent mismatched enzymes	IW-4516
[Project Browser] Remember object page number	IW-3752
[Project Browser] Tag is selected instead of added when hitting enter	IW-4031
[Project Browser] De novo assembly tags not saved with new object	IW-4293
[Project Browser] Deleting copied object deletes original object as well	IW-4397
[Settings] BED Files with spaces in filename cause errors	IW-3841
[Settings] Known canonical system BED files updated	IW-4080
[Settings] Keep system warning during install	IW-4021
[Variant Annotation] Cannot display more than on SV at a time	IW-3571
[Variant Annotation] Need all option for Found in Parents filter	IW-3968
[Viewer] Change default copy number size filter to 500Gbp	IW-4014
[Viewer] Hide circos icon for scaffolds	IW-4015
[Viewer] BED filter not applied if chromosome has no BED regions	IW-4024
[Viewer] Viewing molecules is slow	IW-4059
[Viewer] Anchor selection in circos plot not working	IW-3750
[Viewer] Bookmark not working for genome browser	IW-4004
[Viewer] Changed filter dialog labels for clarity	IW-4013

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**
Phone	**Hours of Operation:** **Monday through Friday, 9:00 a.m. to 5:00 p.m., PST** **US: +1 (858) 888-7663**
Website	**www.bionanogenomics.com/support**

Bionano Genomics, Inc.
9540 Towne Centre Drive, Suite 100
San Diego, CA 92121