BaseSpace Variant Interpreter Beta Release Notes

BaseSpace Variant Interpreter Beta v.1.0.18455

May 25, 2017

Introduction

These Release Notes detail new features, known issues, and recently resolved issues for the BaseSpace Variant Interpreter Beta Testing software. For details on how to operate BaseSpace Variant Interpreter Beta Testing software, see the online help, which is available from the Help icon in the application.

New Features

- **Gene List Manager**

  The gene list manager is an improved and extended version of the existing gene list functionality. In the new gene list manager, users can create gene lists by:

  - Duplicating an existing gene list
  - Browsing to a local file and uploading one or more files
  - Merging two or more existing gene lists by
    - Union – summing of the lists
    - Intersect – selecting common genes between the lists
  - Manual addition of genes by
    - Typing in gene symbols
    - Copy and Pasting from another source
  - Phenotype-derived gene lists – find genes associated with one or more phenotypes (maximum of 3) by inputting HPO or SNOMED phenotype terms and choosing one or more supported sources to generate gene lists of up to 300 genes.

  Most actions in the gene list manager will populate the middle “working area” and the user can choose to move all or selected genes from this list to the “Final List” area to save the gene list. Gene symbols will be validated at the time of save and any errors will need to be corrected before the gene list can be saved.

  The number of genes in a gene-list has been increased from 1000 to 2000 genes to make gene lists more useful in filtering operations.

- **Inspect reads supporting variant calls using IGV**

  Users can now view the reads supporting a variant call in a web browser embedded version of IGV. In addition to viewing the reads, users can visualize along side overlapping variant calls from other external variant databases, such as ClinGen (ISCA http://dbsearch.clinicalgenome.org/search/) and Database of Genomic Variants (DGV http://dgv.tcag.ca/dgv/app/home). Functions include:

  - Linking variants to their respective positions and BAM files for read level inspection, *if the imported case was from BaseSpace Sequence Hub and the BAM file is located in the same folder as the VCF.*
  - Users can apply filters to reduce the number of overlapping variants displayed as tracks in IGV, to high confidence variants only.
  - Users can review overlapping copy number and structural variants from the same case alongside SNVs and Indels, to identify putative compound heterozygous variants spanning different variant types.
  - External variant databases supported include DGV, ISCA and DECIPHER (coming soon).

- **Record Gene-Transcript Choice during interpretation**

  Variant interpretation now includes the ability to precisely select the appropriate transcript for a variant instead of the default canonical transcript. The interpretation interface now has an additional dropdown that presents a list of all gene-transcript combinations available at the variant position being interpreted in the user's transcript space (Ensembl or RefSeq).

  In addition, the user is provided with the HGVSc notation of the variant as well as the predicted consequence relevant to the transcript. For intergenic regions or regions where no transcripts are available, the choice presented to the user is "Intergenic Region".

- **Custom Annotations**

  Users can now use advanced filtering for custom annotations for more efficient variant identification. These improvements include support for:

  - multi-column custom annotations filtering by sub-annotations
  - numerical queries for numeric type custom annotations
  - substring matching on string type custom annotations
  - AND/OR logical filtering for multiple conditions

- **Case Workflow Management**

  Users can now re-analyze multiple cases, saving time after a software upgrade. In addition, Privileged Users now have the ability to delete multiple cases.

  Users can also accelerate the setup of multiple cases for analysis by applying pre-saved filters to multiple cases. During bulk apply of a filter, each filter will be applied to the first applicable tab in each case. For cases where a saved filter cannot be applied (due to a missing variant type, for example), the user will be notified.

- **Knowledge Network - Curation Portal (Association Summary page)**

  Improved user experience for the association summary pages during the "Add" and "Edit" operations. The new pages are designed to align the two processes and streamline the ability for users to add and edit content within the Curation Portal (CP). In addition, new features support link-outs for PubMed and clinical trials (clinicaltrials.gov).

  Users can now perform the entire workflow (add/edit/enable/disable) for external associations on the Association Summary page.

- **Knowledge Network - Variant Interpreter (Variant Details page)**

  Users can now perform the entire workflow (add/edit/enable/disable) for external associations on the Variant Details page. In addition, new features support link-outs for clinical trials (clinicaltrials.gov).

RESOLVED ISSUES

Issue Key	Issue Category	Description
BSVI-24939	Audit Log	Validation status is not currently stored in the audit log.
BSVI-24943	Exports	Exported population frequencies for 1000 Genomes data are only for all populations.
BSVI-24942	Exports	Exported Clinvar Variants included non allele-specific RCVs.
BSVI-23555	Variant Details	The “Back to Case” button does not take the user back to the same tab on the variant grid.
BSVI-24935	Variant Grid	Applied Structural Variant filters do not show in the filter summary. Please view the filter dialog instead to verify.
WAC-730	Workgroups	In some instances, the bulk edit of user permissions checkboxes does not work. Log out/log in to resolve this, or edit users individually.

KNOWN ISSUES

Issue Key	Issue Category	Description
BSKN-3475	Associations	Importing associations from BSKN for retired ontology terms require users to select a current ontology term.
BSVI-24043	Case Management	When a case is in a non-actionable state (Failed, Action Required, etc), the case needs to be re-analyzed or re-uploaded prior to updating the case status or owner.
BSVI-25693	Case Management	Users are unable to add a sibling where the sibling's sex is set to unknown.
BSVI-25720	Case Registry	Checkbox selections do not clear when switching workgroups. When using bulk actions after a workgroup change, refresh the page before selecting new cases.
BSVI-22349	Case Registry	Users may have recently experienced failed VCF uploads that require re-analysis or re-upload. Please contact support if re-uploading these VCFs is not successful.
ON-636	Gene lookup	API should give back an appropriate error message when a given parameter value does not exist.
ON-639	Gene lookup	Gene auto-complete API: inconsistent sorting behavior for returned lists of matching genes.
ON-734	Gene lookup	GeL PanelApp and Phenolyzer diseases are not yet supported as a source for gene lists.
BSVI-12422	Import	If a user tries to upload a VCF file that is not properly formatted, the upload fails with an ambiguous error message. The file shows a status of fail, and the user can then delete it. Consequently, the variant grid does not appear.
BSVI-16408	Import	Uploading of multiple GRCh38 .vcf files occasionally results in an error. The error can be cleared by deleting the failed upload and retrying.
BSVI-23521	Variant Grid	Mode of inheritance calculation is occasionally inaccurate if family members are removed from original pedigree.
ON-345	Variant Grid	Autocomplete box shows results marked as 'obsolete' by nomenclature authority.
ON-432	Variant Grid	Expansion to related phenotypes sometimes yields results that are too distant.
ON-516	Variant Grid	Results in autocomplete pop-up might be sorted inconveniently (subjective).
BSVI-21855	Variant Grid	VCF name truncation to analysis result name may not match expectation (subjective).
BSVI-26024	Variant Grid	Inherited variants may not properly be associated with family members when structural variants are present, affecting Zygosity and Family-Based Filters.

Issue Key	Issue Category	Description
BSVI-24136	Visualization	The mutational signature plot is optimized for WGS, however there is no messaging to the user that analysis on any other platform may yield inaccurate findings or why a plot is not generated for any case with less than 200 SNVs.
BSVI-24137	Visualization	The dynamic visualization is located separate from the visualization panel, which may be misleading to users.
BSVI-25609	Visualization	The karyotype for some chromosomes fail to render on GRCh38 samples on the track level genome browser.
BSVI-25613	Visualization	The track level genome browser fails to load BAMs for samples generated from the Tumor-Normal workflow.
BSVI-25249	Visualization	Some read pop-up content may not correspond to details for the selected read in the track level genome browser.
WAC-767	Workgroups	Workgroup Administrators cannot revoke a pending invitation at this time, however Workgroup Administrators can still remove members from the workgroup.
BSVI-26324	Workgroups	New users to Variant Interpreter cannot access the Workgroups Administration Console unless they are added to an existing workgroup.
BSVI-24655	Zygosity	Zygosity text for variants on sex chromosomes does not account for pseudoautosomal regions
BSVI-24656	Zygosity	Pedigree diagrams reflect familial inheritance only for “PASS” variants