BV-BRC Test Report

A9. Service - MetaCATS

Item to test	MetaCATS Service using exemplar datasets
URL	https://www.bv-brc.org/app/MetaCATS
Prerequisites	Bacterial Fasta contig files in Workspace
References	https://www.bv-brc.org/docs/quick_references/services/metacats.html https://www.bv-brc.org/docs/tutorial/metacats/metacats.html
Tester(s)	Rebecca Wattam, Maulik Shukla
Test date	21-Apr-2022 (follow-up from original test)
Test result	Pass (minor issue reported)

Overview

- Test the service using exemplar datasets
- Test input options, i.e., feature groups and alignment files
- Test auto grouping using various metadata attributes
- For each job submitted, verify successful completion of the job, availability of the output files in the workspace, and quality of the results.

Test Data

Dataset	Rational	Input Format	Input
Spike protein – nonhuman	Interesting	Single	SARSCov2 Spike Protein -
mammals	use case	genome	Nonhuman Mammals
		group	
Spike protein – nonhuman	Interesting	Multiple	SARSCov2 Spike Protein - Cat
mammals	use case	SARSCov2 Spike Protein - Deer	
		groups	SARSCov2 Spike Protein - Minks
Spike protein – nonhuman	Interesting	Alignment file	SARSCov2 Spike Protein -
mammals	use case		Nonhuman Mammals - MSA.afa
			pike_protein_nonhuman_mammal
			_metadata.tsv

 All test datasets and corresponding job results are available in the following public workspace: https://www.bv-brc.org/workspace/BVBRC@patricbrc.org/BVBRC%20Tests/MetaCATS

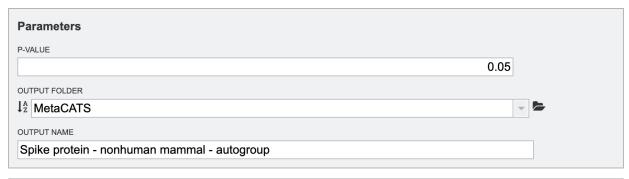
Test Results

- All MetaCATS jobs completed successfully, without any errors.
- · All jobs resulted in expected output files in corresponding job output directory, including

- chisqTable.tsv a tab separated value file with results for a "Chi-square Goodness" of fit test
 result, i.e. positions that have significant non-random distribution between the specified
 groups
- mcTable.tsv a tab separated value file with results for adjusted p-values for multiple comparisons.
- The interactive chi-square table provided option for filtering for only those positions that vary significantly across host groups.
- All test datasets and corresponding job results are available in the following public workspace: https://www.bv-brc.org/workspace/BVBRC@patricbrc.org/BVBRC%20Tests/MetaCATS
- Below are a series of screenshots showing successful completion of the jobs, availability of the result files in the workspace, the interactive chi-square table positions that vary significantly across host groups.
- Input genomes groups and jobs results in the workspace.

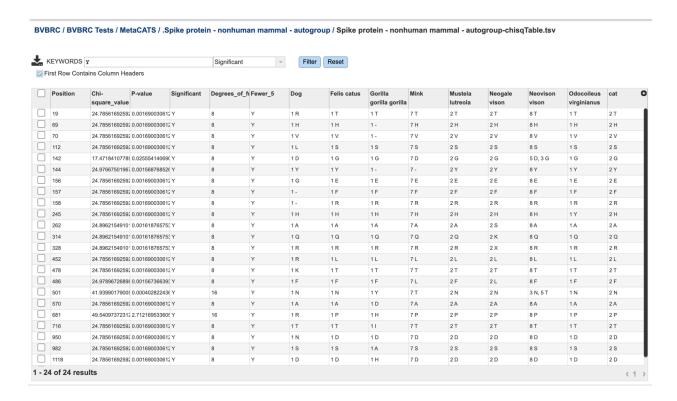


Spike protein – nonhuman mammals – auto grouping based on host names in genome metadata

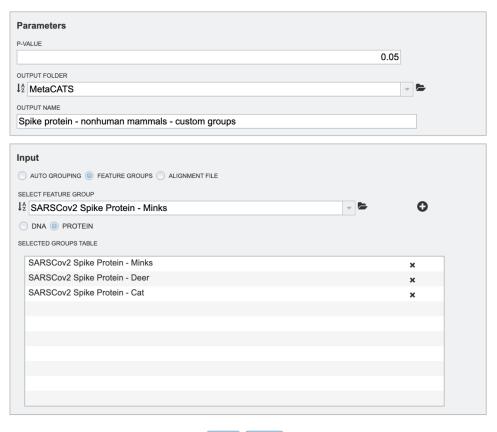




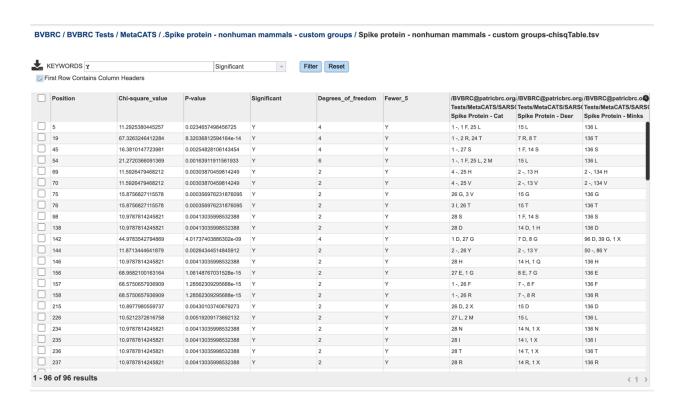
	Name	•	Size	Owner	Members	Created	0
t	Parent folder				-		
	Spike protein - nonhuman mammal - autogroup-chisqTable.tsv		34.1 kB	me	Public	5/7/22, 5:01 PM	
	Spike protein - nonhuman mammal - autogroup-mcTable.tsv		1.6 MB	me	Public	5/7/22, 5:01 PM	
	Spike protein - nonhuman mammal - autogroup.mafft.log		3.6 kB	me	Public	5/7/22, 5:01 PM	



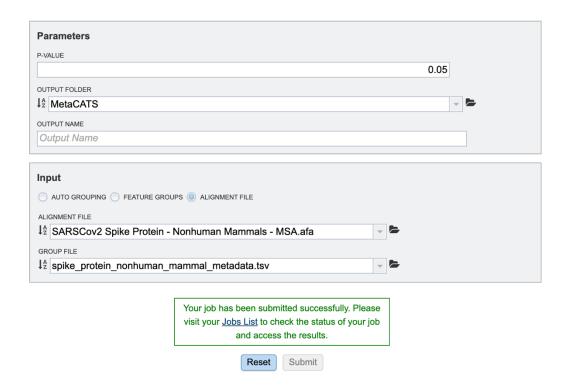
Spike protein – nonhuman mammals – manual grouping by using host specific genome groups



Reset Submit



 Spike protein – nonhuman mammals – manual grouping by using user supplied alignment file and group metadata file.



Note:

- Bug: The jobs failed when using user supplied alignment and group files as input.
- Resolution: The bug has been identified and being fixed. It will be deployed to production in the next release.

References

- Metadata-driven Comparative Analysis Tool (meta-CATS) Quick Reference Guide
- Metadata-driven Comparative Analysis Tool (meta-CATS) Tutorial