THE ARK

OPEN SOURCE SOFTWARE
FOR MEDICAL RESEARCH

User Acceptance Test (UAT) Plan

Cloud-based Bioinformatics Tools

Genotypic Data Management

Document Version: 1.1

Date: 12/10/2013

Contents

1   Document Management

1.1   Contributors

Role	Group	Name
Owner	The Ark	Paul White
Developer	GOHaD	Chris Ellis
Tester/	GOHaD	Travis Endersby
User	WA DNA Bank	Dr Tegan McNab
Business Analyst / Scientific Advisor	GOHaD	Dr Philip Melton

1.2   Version Control

Date	Version	Author	Section	Amendment
25/06/2012	1.0	Paul White		Initial version
12/10/2013	1.1	Travis Endersby		Update with info and list one outstanding JIRA
12/10/2013	1.2	Travis Endersby		Upon NECTAR recommendation added independent tester

2   USER ACCEPTANCE TESTING

2.1   User Acceptance Definition

User Acceptance Testing should ensure that the application performs at an acceptable level for the Customer.

2.2   UAT Responsibilities

Role	Name	Responsibilities
Project Manager	Paul White & Travis Endersby	Communication with users responsible to agree format and scope of UAT Agree acceptance criteria with the Steering Committee nominee and designated UAT test personnel prior to commencing UAT Ensure that a detailed test plan is available for test users Ensure that bugs identified during UAT are logged in the Jira Issues Log Ensure testing takes place within agreed timeframes
Steering Committee Nominee	Winthrop Professor Eric Moses	Ensure appropriate UAT personnel to conduct testing are identified and available. Signoff final test results
UAT Testers	Travis Endersby – followed by independent testing by Dr Tegan McNab (WA DNA Bank)	Conduct UAT tests
Business Analyst / Scientific Advisor	Philip Melton	Ensuring test criteria match the expected use of a system that will manage the storage and pipelines of genotypic data.

3 UAT STRATEGY

The User Acceptance Test Plan should be used to record the Steering Committee Nominee(s) sign off of the documented scenarios. It is recommended that detailed test plans be used to record the results of user testing.

3.1 Test Approach

The purpose of this test case is to validate the Subject Management and Laboratory Information Management System modules and to validate the approach taken to migrate the existing production data over to the new production system.

3.2 Assumptions & Constraints

The following is assumed:
1. The test user can successfully access an UAT environment & production environment
2. The test user has a valid login to The Ark
3. The test user has been granted access to the Subject Management and LIMS modules to cross check data and Reporting Module to modify and submit Genotypic Data Managements
4. The production WARTN data has been migrated

3.3 Test Scenarios

Test Scenarios are laid out in the attached document (a scanned condensed 20 page print out for sign off and the original document with all of the previous test runs and communications will be available as an xls spreadsheet).

4   USER TESTING

PLEASE SEE ATTACHED DOCUMENTS

Any failed issues identified during UAT should be added to The Ark Issues Log in Jira. It may be agreed that UAT can be signed off while some feature requests remain – please add the Jira reference to the appropriate section above if this is the case.

The following request has been made for a future release. This work must and will be completed this year as part of what the Centre needs working for future projects but are willing to sign off now and make this item to do.

https://the-ark.atlassian.net/browse/ARK-1127; ARK-1127 - Provide a non-uploader method of editing Genotypic data management fields
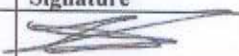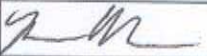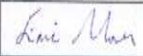
5 UAT RESULTS

5.1 Open Issues

Please insert a copy of any open issues from Jira, together with details of why these issues remain open at the sign off of the Acceptance Stage.

No issues were found which caused the delay of acceptance / sign-off but there has been one feature requests specified in the attached document. This will be prioritized as a number one priority of the developer and should be developed within 5 days.

5.2 Document Sign Off

Role	Name	Signature	Date
UAT Test Manager	Travis Endersby		12/10/2013
UAT Tester	Dr Tegan McNab		12/10/2013
Steering Committee Nominee	Winthrop Professor Eric Moses		12/10/2013

APPENDIX A: Attached test results (following pages);

Result coding: 1 = Pass (full functionality with no unexpected errors), 0 = Fail (lack of required functionality or reproducible error during testing), 9 = Conditional (partial functionality, error during testing which cannot be reproduced, poor user experience or other constraints) X = Functionality which is desirable

#	Test description	Pass (all items)	Fail (on any item)	User	Test time	Result
	Genotypic functionality					
1	A user with sufficient access can view genotypic module.	genotypic module/functti on is shownand write enabled if appropriate	genotypic function is not shown or is not write enabled	tmcnab	10/12/2013	1
2	A user with sufficient access can the data extraction module.	Data extraction module is shown and write enabled if appropriate	Data extraction module is NOT shown or NOT write enabled where appropriate	tmcnab	10/12/2013	1
3	A user without sufficient access should not be able to access or write to the data extraction module.	User without access is not allowed to see data.	User with innapropriate access level is able to see or manipulate search / data extraction page	tmcnab	10/12/2013	1

4	Clicking the "include Geno" checkbox on the Data extraction modification page should be saved upon click save	click checkbox... cliclick save, exit page, come back. "Include geno" should be selected... and vica versa	click checkbox on and off... cliclick save, exit page, come back. If the checkbox did not maintain its state...we have an error	tmcnab	10/12/2013	1
5	Run data extraction on a search result that does NOT have "include geno" selected	no geno results should appear in the downloads popup after the search	download appears or any other part of search fails to result as it normally would	tmcnab	10/12/2013	1
6	Run data extraction on a search result that DOES have "include geno" selected	Geno results should appear in the downloads popup after the search. File produced should be a valid csv.	download does not appear or is an invalid download link or file format.	tmcnab	10/12/2013	1

#						
7	Run data extraction on a search result that DOES have "include geno" selected. Should have absolu no effect on the 4 other download files	Compare demographic, pheno, biospecimen and collection files from searches that both do and do not include geno results. These other tests should have ZERO differences in their results	The slightest difference in any other file suggests an error, as genotypic data extraction should NOT affect any other result	tmcnab	10/12/2013	1
8	A user with sufficient access can view (from the genotypic tab) AND extract (from the data extraction tab) ALL of the following fields:	pass only if both functionalities are as expected	fail if either tab does not display the correct results	tmcnab		
9		field is present and has correct value	field is missing or has incorrect value	tmcnab	10/12/2013	1
	pipeline Id					
10		field is present and has correct value	field is missing or has incorrect value	tmcnab	10/12/2013	1
	pipeline Name					
11		field is present and has correct value	field is missing or has incorrect value	tmcnab	10/12/2013	1
	pipeline Description					

12		field is present and has correct value. For subsequent processes will have an _forProcess_<index> suffix as the header	fields is missing or incorrect value or header is not adequately labeled with suffix as expected	tmcnab	10/12/2013	1
	processId for one or multiple processes					
13		field is present and has correct value. For subsequent processes will have an _<index> suffix as the header	fields is missing or incorrect value or header is not adequately labeled with suffix as expected	tmcnab	10/12/2013	1
	processName for one or multiple processes					
14		field is present and has correct value. For subsequent processes will have an _<index> suffix as the header in the extraction file	fields is missing or incorrect value or header is not adequately labeled with suffix as expected	tmcnab	10/12/2013	1
	processDescription for one or multiple processes					
15		field is present and has correct value. For subsequent processes will have an _<index> suffix as the header in the extraction file	fields is missing or incorrect value or header is not adequately labeled with suffix as expected	tmcnab	10/12/2013	1
	startTime for one or multiple processes					

16		field is present and has correct value. For subsequent processes will have an _<index> suffix as the header in the extraction file	fields is missing or incorrect value or header is not adequately labeled with suffix as expected	tmcnab	10/12/2013	1
	endTime for one or multiple processes					
17		field is present and has correct value. For subsequent processes will have an _<index> suffix as the header in the extraction file	fields is missing or incorrect value or header is not adequately labeled with suffix as expected	tmcnab	10/12/2013	1
	commandName for one or multiple processes					
18		field is present and has correct value. For subsequent processes will have an _<index> suffix as the header in the extraction file	fields is missing or incorrect value or header is not adequately labeled with suffix as expected	tmcnab	10/12/2013	1
	commandLocation for one or multiple processes					

19 commandServer Url for one or multiple processes	field is present and has correct value. For subsequent processes will have an _<index> suffix as the header in the extraction file	fields is missing or incorrect value or header is not adequately labeled with suffix as expected	tmcnab	10/12/2013	1
20 inputServer for one or multiple processes	field is present and has correct value. For subsequent processes will have an _<index> suffix as the header in the extraction file	fields is missing or incorrect value or header is not adequately labeled with suffix as expected	tmcnab	10/12/2013	1
21 inputLocation for one or multiple processes	field is present and has correct value. For subsequent processes will have an _<index> suffix as the header in the extraction file	fields is missing or incorrect value or header is not adequately labeled with suffix as expected	tmcnab	10/12/2013	1

22	field is present and has correct value. For subsequent processes will have an _<index> suffix as the header in the extraction file	fields is missing or incorrect value or header is not adequately labeled with suffix as expected	tmcnab	10/12/2013	1
inputFileHash for one or multiple processes					
23	field is present and has correct value. For subsequent processes will have an _<index> suffix as the header in the extraction file	fields is missing or incorrect value or header is not adequately labeled with suffix as expected	tmcnab	10/12/2013	1
inputFileType for one or multiple processes and for one or multiple inputs or outputs					
24	field is present and has correct value. For subsequent processes will have an _<index> suffix as the header in the extraction file	fields is missing or incorrect value or header is not adequately labeled with suffix as expected	tmcnab	10/12/2013	1
outputKept for one or multiple processes and for one or multiple inputs or outputs					

25	outputServer for one or multiple processes and for one or multiple inputs or outputs	field is present and has correct value. For subsequent processes will have an _<index> suffix as the header in the extraction file	fields is missing or incorrect value or header is not adequately labeled with suffix as expected	tmcnab	10/12/2013	1
26	outputLocation for one or multiple processes and for one or multiple inputs or outputs	field is present and has correct value. For subsequent processes will have an _<index> suffix as the header in the extraction file	fields is missing or incorrect value or header is not adequately labeled with suffix as expected	tmcnab	10/12/2013	1
27	outputFileHash for one or multiple processes and for one or multiple inputs or outputs	field is present and has correct value. For subsequent processes will have an _<index> suffix as the header in the extraction file	fields is missing or incorrect value or header is not adequately labeled with suffix as expected	tmcnab	10/12/2013	1

28	outputFileType for one or multiple processes and for one or multiple inputs or outputs	field is present and has correct value. For subsequent processes will have an _<index> suffix as the header in the extraction file	fields is missing or incorrect value or header is not adequately labeled with suffix as expected	tmcnab	10/12/2013	1
29	outputKept for one or multiple processes and for one or multiple inputs or outputs	field is present and has correct value. For subsequent processes will have an _<index> suffix as the header in the extraction file	fields is missing or incorrect value or header is not adequately labeled with suffix as expected	tmcnab	10/12/2013	1