

Arvados - Feature #14168

[Running a workflow] Input presets

09/05/2018 03:16 PM - Moritz Gilsdorf

Status: New	Start date:
Priority: Normal	Due date:
Assigned To:	% Done: 0%
Category:	Estimated time: 0.00 hour
Target version:	
Description	
User Story	
As a Scientist	
I can use stored presets for workflows from the "Run a Pipeline" page so that I can switch easily between common resource bundles (e.g. different genome assemblies and depending annotations)	
This should be part of the input selection. Basically the idea is that a part of the input fields can be populated by selecting a preset from a e.g. dropdown menu. It needs to be clarified how these presets could be stored in the backend.	
Example: We have a RNAseq pipeline that requires, apart from the NGS reads as input, a bundle of other input data like an index and annotation data (call this resource bundle). We want to provide different bundles for different assemblies and species so that we don't have to register the same workflow several times for each preset.	

History

#1 - 09/05/2018 03:23 PM - Moritz Gilsdorf

- Description updated

#2 - 09/19/2018 07:14 AM - Chrystian Klingenberg

- Target version set to sprint 9

#3 - 09/19/2018 07:15 AM - Chrystian Klingenberg

- Target version deleted (sprint 9)

#4 - 10/23/2018 02:25 PM - Tom Morris

- Project changed from Arvados Workbench 2 to Arvados

- Target version set to To Be Groomed

This came from the Workbench 2 project, but is tightly involved with CWL, so we should discuss what's needed to support it.

#5 - 12/12/2018 04:30 PM - Peter Amstutz

This has come up in the CWL community chats. SBG has a very similar use case for their platform and wants a way to describe "suggested" inputs for a workflow (which is slightly different from defaults).

#6 - 07/06/2021 09:09 PM - Peter Amstutz

- Target version deleted (To Be Groomed)