

caArray 094 - Handling Array Designs

Question: How Do I Associate An Imported Array Design With An Experiment?

Topic: Working With Array Design Files

Release: v2.0 and above

Date entered: April 24, 2012

Answer

In caArray, before an experiment can be successfully created, the array design(s) for platforms used in that experiment have to be imported first. Afterwards, the corresponding array designs must be associated with the experiment when the experiment is created, as shown in Figure 1 below.

Experiment: New Experiment

Overview

Overall Experiment Characteristics

The Overall Experiment Characteristics represent the minimum set of attributes required to submit an experiment for review. Required fields are marked with ***asterisks***.

Experiment Title*:

Experiment Description:

Status: In Progress

Experiment Identifier:

Assay Type*:

Assay Type*		Selected Assay Type
<input type="checkbox"/>	Exon	<input checked="" type="checkbox"/> Gene Expression
<input type="checkbox"/>	Gene Expression	
<input type="checkbox"/>	Methylation	
<input type="checkbox"/>	microRNA	
<input type="checkbox"/>	SNP	

Provider*:

Array Designs:

Organism*:

Figure 1. On the caArray 'New Experiment' page, the 'Array Designs' box lists all the array designs that have been imported into the experiment. Any designs you select from this list will become associated with the experiment and all the data files uploaded to it.

By selecting the corresponding array design(s) on the 'New Experiment' page, you are telling caArray that the selected array design(s) correspond to the data files to be uploaded. If only one array design is selected, caArray will associate all uploaded data files with that array design and will parse the data accordingly.

If more than one array design is selected, and if the data and sample annotations are in the MAGE-TAB format, additional information needs to be provided in the form of a SDRF metadata file, which is in the CSV file format. In the SDRF file, which lists all the experiment's samples, a column named "Array Design REF" shows the array design reference for each sample, as shown in Figure 2 below. This allows caArray to associate the correct array design with its corresponding array data files.

	T	U	V	W	X	Y	Z
1	Protocol REF	Term Source REF	Labeled Extract Name	Label	Protocol REF:Affymetrix:Protocol:	Hybridization Name	Array Design REF
2	P-AFFY-2	ArrayExpress	TK6 replicate 1	biotin	Hybridization-EukGE-WS2v5	H_TK6 replicate 1	Affymetrix.com:PhysicalArrayDesign:Test3
3	P-AFFY-2	ArrayExpress	TK6 replicate 1	biotin	Hybridization-EukGE-WS2v6	H_TK6 replicate 2	Affymetrix.com:PhysicalArrayDesign:HG-U133_Plus

Figure 2. The 'Array Design REF' column in the SDRF metadata file shows the array design LSID references for each listed sample from the experiment.

When entering the array design information into the SDRF file, be sure to pay attention to the syntax of the LSID reference. The correct reference syntax for most array designs supported by caArray can be found on the NCI instance of caArray at <https://array.nci.nih.gov/caarray/home.action>. Once you log in, click "Manage Array Designs", then click on the array design that your data files use, and capture the value for "Array Design LSID", as shown in Figures 3 and 4 below.

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Manage Array Designs

Array Designs

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Array Design Name	Provider	Assay Type	Version Number
012391_D_F_20120130	Agilent	Gene Expression	1
014693_D_F_20090929	Agilent	aCGH	1.0
014850_D_20070820	Agilent	Exon , Gene Expression , Methylation	08/20/2007

Figure 3. To find the LSID reference for an array design, first log in to the NCI caArray instance, then click on 'Manage Array Designs' (highlighted in red) in the left-hand navigation pane and click on the desired array design.

Manage Array Designs

012391_D_F_20120130

Some details of this array design may not be modified because it is already associated with an existing experiment.

Array Design Details

Array Design Name: 012391_D_F_20120130

Array Design LSID: URN:LSID:Agilent.com:PhysicalArrayDesign:012391_D_F_20120130

Description: Whole Human Genome Oligo Microarray

*Assay Type Gene Expression

Provider*: Agilent

Version Number*: 1

Feature Type*: in_situ_oligo_features (MO)

Organism*: Homo sapiens (ncbitax)

GEO Accession:

Figure 4. For the array design you selected from the 'Manage Array Designs' page, the 'Array Design Details' heading lists several attributes of the array design, including the LSID reference (highlighted in red). This reference can be captured and entered into your SDRF file.

Remember to remove the "URN:LSID:" prefix before you add the array design reference to the SDRF file column. For example, if the original LSID is:

URN:LSID:Agilent.com:PhysicalArrayDesign:012391_D_F_20120130

then the corresponding value to be entered into the SDRF file is:

Agilent.com:PhysicalArrayDesign:012391_D_F_20120130

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