

# Connected Services and Pipes

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## service::dev\_human\_correlation

### Parameters

set	String	Data set name: rna_seq_genes, rna_seq_exons, exon_microarray_genes or exon_microarray_exons
donors	Array (optional)	Comma delimited list of Donor.id. Defaults to all donors.
structures	Array	Comma delimited list of Structure.id or Structure.acronym.
probes	Integer	Probe id to correlate against.
sort_order	String (optional)	'asc' for ascending order, or 'desc' for descending order. Defaults to descending.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

### Examples

```

http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::dev_human_correlation[set$eqrna_seq_genes][probes$eq1090294][structures$eq'CBC' ]

http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::dev_human_correlation[set$eqrna_seq_exons][probes$eq279330730][structures$eq'CBC' ]

Retrieve exon_microarray_genes correlation values for structure with the acronym, "CBC".

http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::dev_human_correlation[set$eqexon_microarray_genes][probes$eq9463][structures$eq'CBC' ]

http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::dev_human_correlation[set$eqexon_microarray_exons][probes$eq280550735][structures$eq'CBC' ]

```

## service::dev\_human\_differential

### Parameters

set	String	Data set name: rna_seq_genes, rna_seq_exons, exon_microarray_genes or exon_microarray_exons
donors1	Array (optional)	Comma delimited list of Donor.id. Defaults to all donors.
structures1	Array	Comma delimited list of Structure.id.
donors2	Array (optional)	Comma delimited list of Donor.id. Defaults to all donors.
structures2	Array	Comma delimited list of Structure.id.
sort_by	String (optional)	'p-value' or 'fold-change'. Defaults to 'p-value'.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

### Examples

```

http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::dev_human_differential[set$eq'rna_seq_genes' ][structures1$eqDFC][structures2$eqMFC]

http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::dev_human_differential[set$eq'rna_seq_genes' ][structures1$eqDFC][structures2$eqMFC]

http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::dev_human_differential[set$eq'exon_microarray_exons' ][structures1$eqDFC][structures2$eqMFC]

http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::dev_human_differential[set$eq'exon_microarray_genes' ][structures1$eqDFC][structures2$eqMFC]

```

## service::dev\_human\_expression

### Parameters

set	String	Data set name: rna_seq_genes, rna_seq_exons, exon_microarray_genes or exon_microarray_exons
probes	Integer	Probe.id to correlate against
donors	Integer (optional)	Comma delimited list of Donor.id to filter expression results.
structures	Integer (optional)	Comma delimited list of Structure.id to filter expression results.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.

num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.
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## Examples

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::dev_human_expression[set$eq'rna_seq_genes'] [probes$eq1090294]

http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::dev_human_expression[set$eq'rna_seq_exons'] [probes$eq279330730]

http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::dev_human_expression[set$eq'exon_microarray_genes'] [probes$eq9463]

http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::dev_human_expression[set$eq'exon_microarray_exons'] [probes$eq280550735]
```

## service::dev\_human\_microarray\_correlation

### Parameters

donors	Array (optional)	Comma delimited list of Donor.id. Defaults to all donors.
structures	Array	Comma delimited list of Structure.id or Structure.acronym.
probes	Integer	Probe id to correlate against
sort_order	String (optional)	'asc' or 'desc'. Defaults to 'desc'.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

### Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::dev_human_microarray_correlation[probes$eq1048426] [structures$eqSG]
```

## service::dev\_human\_microarray\_differential

### Parameters

donors1	Array (optional)	Comma delimited list of Donor.id. Defaults to all donors.
structures1	Array	Comma delimited list of Structure.id.
donors2	Array (optional)	Comma delimited list of Donor.id. Defaults to all donors.
structures2	Array	Comma delimited list of Structure.id.
sort_by	String (optional)	'p-value' or 'fold-change'. Defaults to 'p-value'.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

### Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::dev_human_microarray_differential[structures1$eqMZ] [structures2$eqCP]
```

## service::dev\_human\_microarray\_expression

### Parameters

probes	Integer	Comma delimited list of Probe.id to filter microarray expression results.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.
donors	Integer (optional)	Comma delimited list of Donor.id to filter microarray expression results.
structures	Integer (optional)	Comma delimited list of Structure.id to filter microarray expression results.

### Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::dev_human_microarray_expression[probes$eq1053223,1053224][donors$eq12566][structures$eq11587]
```

## service::dev\_mouse\_agea

### Parameters

seed_age	String	Age.id
map_age	String	Age.id
seed_point	Array	Comma delimited list of integers representing a point in the age's space.
seed_threshold	Array	Pair of floating point values representing the correlation seed age threshold.
map_threshold	Array	Pair of floating point values representing the correlation map age threshold.
contrast_threshold	Array (optional)	Pair of integer values representing the contrast domain threshold.
target_threshold	Array (optional)	Pair of integer values representing the target domain threshold.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

### Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::dev_mouse_agea[seed_age$eq'E18.5'][map_age$eq'E15.5'][seed_point$eq4200,2380,2360]
[map_threshold$eq0.467,0.657][seed_threshold$eq0.811,0.924]
```

## service::dev\_mouse\_correlation

### Parameters

row	Integer	DataSet.id or Gene.id to correlate against.
structures	Array (optional)	Comma delimited list of Integer Structure.id or String Structure.acronym.
ages	Array (optional)	Comma delimited list of Age.name.
sort_order	String (optional)	'asc' or 'desc'. Defaults to 'desc'.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.

num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.
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## Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::dev_mouse_correlation[row$eq13267][structures$eq'NP'][ages$eq'P14','P28']
```

## service::gbm\_correlation

### Parameters

donors	Array (optional)	Comma delimited list of Donor.id. Defaults to all donors.
structures	Array	Comma delimited list of Structure.id or Structure.acronym.
probes	Integer	Probe id to correlate against
sort_order	String (optional)	'asc' or 'desc'. Defaults to 'desc'.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

## Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::gbm_correlation[probes$eq3551][structures$eqGBM]
```

## service::gbm\_differential

### Parameters

donors1	Array (optional)	Comma delimited list of Donor.id. Defaults to all donors.
structures1	Array	Comma delimited list of Structure.id.
donors2	Array (optional)	Comma delimited list of Donor.id. Defaults to all donors.
structures2	Array	Comma delimited list of Structure.id.
sort_by	String (optional)	'p-value' or 'fold-change'. Defaults to 'p-value'.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

## Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::gbm_differential[structures1$eqGBM][structures2$eqCTpan]
```

## service::gbm\_expression

### Parameters

probes	Integer	Comma delimited list of Probe.id to filter microarray expression results.
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start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.
donors	Integer (optional)	Comma delimited list of Donor.id to filter gbm expression results.
structures	Integer (optional)	Comma delimited list of Structure.id to filter gbm expression results.

## Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::gbm_expression[probes$eq3551][donors$eq703393][structures$eqGBM]
```

## service::gbm\_ish\_differential

### Parameters

structures 1	Array	Comma delimited list of Structure.id.
structures 2	Array	Comma delimited list of Structure.id.
threshold1	Array (optional)	Comma delimited Integer pair indicating thresholds for domain 1.
threshold2	Array (optional)	Comma delimited Integer pair indicating thresholds for domain 2.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

### Examples

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::gbm_ish_differential[structures1$eqCTpnn][structures2$eqIT]
```

## service::gbm\_ish\_expression

### Parameters

structures	Array	Comma delimited list of Structure.id.
threshold	Array (optional)	Comma delimited Integer pair indicating thresholds.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

### Examples

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::gbm_ish_expression[structures$eqCTpnn][threshold$eq0,100000]
```

## service::human\_microarray\_correlation

### Parameters

donors	Array (optional)	Comma delimited list of Donor.id. Defaults to all donors.
structures	Array	Comma delimited list of Structure.id or Structure.acronym.
probes	Integer	Probe.id to correlate against.
sort_order	String (optional)	'asc' or 'desc'. Defaults to 'desc'.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

## Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::human_microarray_correlation[probes$eq1048426][structures$eq'FL']
```

## service::human\_microarray\_differential

### Parameters

donors1	Array (optional)	Comma delimited list of Donor.id. Defaults to all donors.
structures1	Array	Comma delimited list of Structure.id.
donors2	Array (optional)	Comma delimited list of Donor.id. Defaults to all donors.
structures2	Array	Comma delimited list of Structure.id.
sort_by	String	'p-value' or 'fold-change'. Defaults to 'p-value'.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

### Examples

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::human_microarray_differential[structures1$eq4005][structures2$eq4006]
```

## service::human\_microarray\_expression

### Parameters

probes	Integer	Comma delimited list of Probe.id to filter microarray expression results.
donors	Integer (optional)	Comma delimited list of Donor.id to filter microarray expression results.
structures	Integer (optional)	Comma delimited list of Structure.id to filter microarray expression results.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

### Examples

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::human_microarray_expression[probes$eq1014952][donors$eq9861,10021][structures$eq4079]
```



## service::mouse\_agea

### Parameters

set	String	Data set name: mouse_coronal.
seed_age	String	An age identifier. P56.
map_age	String	An age identifier. P56.
seed_point	Array	A comma delimited triple indicating the coordinates of a point in 3-D SectionDataSet space.
correlation_threshold 1	Float (optional)	Correlation threshold for domain 1.
correlation_threshold 2	Float (optional)	Correlation threshold for domain 2.
threshold1	Array (optional)	Comma delimited Integer pair defining the threshold for domain 1.
threshold2	Array (optional)	Comma delimited Integer pair defining the threshold for domain 2.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

### Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::mouse_agea[set$eqmouse_coronal][seed_age$eqP56][map_age$eqP56][seed_point$eq6800,4200,5600]
[correlation_threshold1$eq0.84][correlation_threshold2$eq0.93]
```

## service::mouse\_correlation

### Parameters

set	String	Data set name: mouse or mouse_coronal.
structures	Array (optional)	Comma delimited list of Structure.id or Structure.acronym.
row	Integer	DataSet.id to correlate against.
sort_order	String (optional)	'asc' or 'desc'. Defaults to 'desc'.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

### Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::mouse_correlation[set$eqmouse][row$eq68918934]

http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::mouse_correlation[set$eqmouse_coronal][row$eq357096]
```

## service::mouse\_differential

### Parameters

set	String	Data set name: mouse or mouse_coronal.
structures 1	Array	Comma delimited list of Structure.id.
structures 2	Array	Comma delimited list of Structure.id.

threshold1	Array (optional)	Comma delimited Integer pair indicating thresholds for domain 1.
threshold2	Array (optional)	Comma delimited Integer pair indicating thresholds for domain 2.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

## Examples

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::mouse_differential[set$eq'mouse'] [structures1$eq8] [structures2$eq315]

http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::mouse_differential[set$eq'mouse_coronal'] [structures1$eq8] [structures2$eq315]
```

## service::mouse\_connectivity\_correlation

### Parameters

row	Integer	SectionDataSet.id to correlate against.
structures	Array (optional)	Comma delimited list of Integer Structure.id or String Structure.acronym.
hemisphere	String (optional)	Structure's hemisphere. Use 'Right' or 'Left'. Defaults to both hemispheres.
transgenic_lines	Array (optional)	Comma delimited list of Integer TransgenicLine.id or String TransgenicLine.name. Specify ID 0 to exclude all TransgenicLines.
injection_structures	Array (optional)	Comma delimited list of Integer Structure.id or String Structure.acronym.
primary_structure_only	String (optional)	'true' or 'false'
sort_order	String (optional)	'asc' or 'desc'. Defaults to 'desc'.
product_ids	Array (optional)	Comma delimited list of Integer Product.ids.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

### Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::mouse_connectivity_correlation[row$eq112162251] [structures$eqTH] [hemisphere$eqright] [num_rows$eq100]
[transgenic_lines$eq0,177838259]
```

## service::mouse\_connectivity\_injection\_coordinate

Search for injection sites near a set of 3-D coordinates, ranking the results by their distance from the coordinates.

### Parameters

seed_point	Array	A comma delimited triple indicating the coordinates of a point in 3-D space.
transgenic_lines	Array (optional)	Comma delimited list of Integer TransgenicLine.id or String TransgenicLine.name. Specify ID 0 to exclude all TransgenicLines.
injection_structures	Array (optional)	Comma delimited list of Integer Structure.id or String Structure.acronym.
primary_structure_only	String (optional)	'true' or 'false'
product_ids	Array (optional)	Comma delimited list of Integer Product.ids.

start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

## Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::mouse_connectivity_injection_coordinate[seed_point$eq6600,5400,4800][transgenic_lines$eq0]
```

## service::mouse\_connectivity\_injection\_structure

Search by injection structures, ranking the results the results by signal in the target structures.

### Parameters

injection_structures	Array	Comma delimited list of Integer Structure.id or String Structure.acronym.
target_domain	Array (optional)	Comma delimited list of Integer Structure.id or String Structure.acronym.
injection_hemisphere	String (optional)	'Right' or 'Left'. Defaults to both hemispheres.
target_hemisphere	String (optional)	'Right' or 'Left'. Defaults to both hemispheres.
transgenic_lines	Array (optional)	Comma delimited list of Integer TransgenicLine.id or String TransgenicLine.name. Specify ID 0 to exclude all TransgenicLines.
injection_domain	Array (optional)	Comma delimited list of Integer Structure.id or String Structure.acronym.
primary_structure_only	String (optional)	'true' or 'false'
product_ids	Array (optional)	Comma delimited list of Integer Product.ids.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

## Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::mouse_connectivity_injection_structure[injection_structures$eqTH][injection_hemisphere$eqRight]
[target_domain$eqVIS][target_hemisphere$eqRight][transgenic_lines$eq0]
```

## service::mouse\_connectivity\_target\_spatial

Displays all SectionDataSets with projection signal density  $\geq 0.1$  at the seed point. This service also returns the path along the most dense pixels from the seed point to the center of each injection site.

### Parameters

seed_point	Array	A comma delimited triple indicating the coordinates of a point in 3-D SectionDataSet space.
transgenic_lines	Array (optional)	Comma delimited list of Integer TransgenicLine.id or String TransgenicLine.name. Specify ID 0 to exclude all TransgenicLines.
section_data_set	Integer (optional)	SectionDataSet.id to filter the results.
injection_structures	Array (optional)	Comma delimited list of Integer Structure.id or String Structure.acronym.
primary_structure_only	String (optional)	'true' or 'false'
product_ids	Array (optional)	Comma delimited list of Integer Product.ids.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

## Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::mouse_connectivity_target_spatial[seed_point$eq6600,5400,4800][start_row$eq25][num_rows$eq50]
```

## service::nhp\_lmd\_microarray\_correlation

### Parameters

donors	Array (optional)	comma separated list of integers Donor ids. Defaults to all donors.
structures	Array	Comma delimited list of Structure.id.
probes	Integer	Probe.id to correlate against.
sort_order	String (optional)	'asc' or 'desc'. Defaults to 'asc'.
start_row	Integer (optional)	starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	number of rows of data for paging purposes. Defaults to 2000.

## Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::nhp_lmd_microarray_correlation[probes$eq30357][structures$eqBN]
```

## service::nhp\_lmd\_microarray\_differential

### Parameters

donors1	Array (optional)	Comma delimited list of Donor.id. Defaults to all donors.
structures1	Array	Comma delimited list of Structure.id.
donors2	Array (optional)	Comma delimited list of Donor.id. Defaults to all donors.
structures2	Array	Comma delimited list of Structure.id.
sort_by	String (optional)	'p-value' or 'fold-change'. Defaults to 'p-value'.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

## Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::nhp_lmd_microarray_differential[structures1$eqHF][structures2$eqBN]
```

## service::nhp\_lmd\_microarray\_expression

### Parameters

probes	Integer	Probe.id to correlate against.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

## Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::nhp_lmd_microarray_expression[probes$eq15815]
```

## service::nhp\_macro\_microarray\_correlation

### Parameters

donors	Array (optional)	Donor.id. Defaults to all donors.
structures	Array	Comma delimited list of Structure.id.
probes	Integer	Probe.id to correlate against.
sort_order	String (optional)	'asc' or 'desc'. Defaults to 'asc'.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

## Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::nhp_macro_microarray_correlation[probes$eq49067][structures$eqBN]
```

## service::nhp\_macro\_microarray\_differential

### Parameters

donors1	Array (optional)	Donor.id. Defaults to all donors.
structures1	Array	Comma delimited list of Structure.id.
donors2	Array (optional)	Donor.id. Defaults to all donors.
structures2	Array	Comma delimited list of Structure.id.
sort_by	String (optional)	'p-value' or 'fold-change'. Defaults to 'p-value'.
start_row	Integer (optional)	starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

## Examples

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::nhp_macro_microarray_differential[structures1$eqHF][structures2$eqBN]
```

## service::nhp\_macro\_microarray\_expression

### Parameters

probes	Integer	Probe.id to correlate against.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

## Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::nhp_macro_microarray_expression[probes$eq15815]
```

## service::tbi\_correlation

### Parameters

donors	Array (optional)	Comma delimited list of Donor.id. Defaults to all donors.
structures	Array	Comma delimited list of Structure.id or Structure.acronym.
probes	Integer	Probe id to correlate against
sort_order	String (optional)	'asc' or 'desc'. Defaults to 'desc'.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

## Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::tbi_correlation[structures$eqHIP][probes$eq499304660]
```

## service::tbi\_differential

### Parameters

donors1	Array (optional)	Comma delimited list of Donor.id. Defaults to all donors.
structures1	Array	Comma delimited list of Structure.id.
donors2	Array (optional)	Comma delimited list of Donor.id. Defaults to all donors.
structures2	Array	Comma delimited list of Structure.id.
sort_by	String (optional)	'p-value' or 'fold-change'. Defaults to 'p-value'.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

## Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::tbi_differential[structures1$eqFWM][structures2$eqTCx]
```

## service::tbi\_expression

### Parameters

probes	Integer	Comma delimited list of Probe.id to filter microarray expression results.
start_row	Integer (optional)	Starting row of data for paging purposes. Defaults to 0.
num_rows	Integer (optional)	Number of rows of data for paging purposes. Defaults to 2000.

donors	Integer (optional)	Comma delimited list of Donor.id to filter gbm expression results.
structures	Integer (optional)	Comma delimited list of Structure.id to filter gbm expression results.

## Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::tbi_expression[donors$eq309335438][structures$eqPCx][probes$eq499304660]
```

## service::text\_search

### Parameters

query_string	String	String to search for (* is a wildcard)
k	String	The model that is the type of object to search for (i.e. Gene)

## Example

```
http://api.brain-map.org/api/v2/data/query.xml?criteria=
service::text_search[query_string$eq'abat'][k$eqGene]
```

## pipe::list

### Input

The output from the previous pipeline stage in json format.

### Parameters

(left hand side of parameter)	The variable id to be set in the pipeline namespace.
(right hand side of parameter)	A string using simple path syntax.

## Response

A comma separated list made up of the values found according to the path is assigned to the variable. More than one variable may be assigned in a single list pipe.

## Notes

A pipe may not be used at the beginning or end of a query pipeline. Pipe::list may be used between model and service stages in any combination. The scope of a variable in a pipe::list stage is from the pipe to the end of the pipeline. Prefix a pipe list variable with a dollar sign (\$) to reference it. Use the \$in operator when referencing a pipeline variable set by pipe::list because the output is a list.

## Fragment

```
pipe::list[gene_ids$eq'id'][probe_ids$eq'probes/probe/id']
```

## Example

```
http://api.brain-map.org/api/v2/data/query.json?criteria=
model::Organism[name$il'*sapiens'],
pipe::list[xorganism_id$eq'id'],
model::Gene[organism_id$in$xorganism_id]
```

## pipe::replace

### Input

The constant string or variable passed into the input parameter

### Parameters

pattern	Regular expression pattern to match against
replacement	String to replace the strings in input that match pattern.
input	Variable obtained from pipe::list or a constant string.
output	Name of a variable to assign the results to.

### Response

A string with the substitutions applied is assigned to the output variable.

### Fragment

```
pipe::replace[pattern$eq'a'] [replacement$eq'b'] [input$in'abcd'] [output$eqexample]
```

### Example

```
http://api.brain-map.org/api/v2/data/query.json?criteria=
model::Structure[acronym$eq'HiF'] [ontology_id$eq7],
pipe::list[path$eq'structure_id_path'],
pipe::replace[pattern$eq'$'] [replacement$eq'*'] [input$in$path] [output$eq'descendants'],
model::Structure[structure_id_path$il$descendants] [ontology_id$eq7]
```

## pipe::split

### Input

The constant string or variable passed into the input parameter

### Parameters

pattern	A regular expression pattern to match against.
input	A variable obtained from pipe::list or a constant string.
output	The name of a variable to assign the results to.

### Response

An comma-separated list of input string split where the pattern matched.

### Fragment



```
pipe::split[pattern$eq'x'] [input$in'axbxcxd'] [output$eqexample]
```

## Example

```
http://api.brain-map.org/api/v2/data/query.json?criteria=  
model::Structure[acronym$eq'HiF'] [ontology_id$eq7], pipe::list[path$eq'structure_id_path'],  
pipe::replace[pattern$eq'(^\\/)|(\\/$)'] [replacement$eq' ' ] [input$in$path] [output$eq'path'],  
pipe::split[pattern$eq'/'] [input$in$path] [output$eq'ancestors' ], model::Structure[id$in$ancestors]  
[ontology_id$eq7]
```

SectionDataSet