

```
In [1]: import json
gut_samples = [['chic_1', "mgm4440283.3"],
               ['chic_2', "mgm4440284.3"],
               ['chic_3', "mgm4440285.3"],
               ['chic_4', "mgm4440286.3"],
               ['cow_1', "mgm4441679.3"],
               ['cow_2', "mgm4441680.3"],
               ['cow_3', "mgm4441682.3"],
               ['mus_1', "mgm4440463.3"],
               ['mus_2', "mgm4440464.3"],
               ['fish_1', "mgm4441695.3"],
               ['fish_2', "mgm4441696.3"]]
```

```
In [2]: chic_1 = gut_samples[0][1]
chic_1_data = ! wget -q -O - "http://api.metagenomics.anl.gov/metagenome/$chic_1"
chic_1_obj = json.loads(chic_1_data[0])
print chic_1_obj['name']
print chic_1_obj['id']
print chic_1_obj['metadata']['sample']
```

```
Chicken Cecum A
mgm4440283.3
{'data': {'biome': u'animal-associated habitat', 'samp_mat_process': u'DNA
extraction', 'material': u'animal-associated habitat', 'geodetic_system':
u'wgs_84', 'samp_collect_device': u'Fourteen days post challenge, birds from two
pens (A&B) were euthanized and ceca collected for further analysis. Fresh cecal
samples from two (C. jejuni-inoculated and C. jejuni-uninoculated) 28-day old
chickens were analyzed. Cecal contents were collected using aseptic techniques.
Samples were stored at &#8722;80\xb0C until DNA extraction.', 'country': u'United
States of America', 'env_package': u'host-associated', 'feature': u'animal-
associated habitat', 'longitude': u'-88.2073', 'isol_growth_condt': u'18698407',
'location': u'Urbana, IL', 'latitude': u'40.1106', 'collection_timezone':
u'UTC', 'continent': u'north_america'}, 'name': u'mgs11882', 'id': u'mgs11882'}
```

```
In [3]: gut_ids = "&".join( map(lambda x: "id="+x[1], gut_samples) )
gut_data = ! wget -q -O - "http://api.metagenomics.anl.gov/matrix/function?$gut_ids"
gut_objs = json.loads(gut_data[0])
```

```
Biological Observation Matrix 1.0
[{'u'id': u'mgm4440283.3', 'u'metadata': None}, {'u'id': u'mgm4440284.3',
'u'metadata': None}, {'u'id': u'mgm4440285.3', 'u'metadata': None}, {'u'id':
u'mgm4440286.3', 'u'metadata': None}, {'u'id': u'mgm4440463.3', 'u'metadata': None},
{'u'id': u'mgm4440464.3', 'u'metadata': None}, {'u'id': u'mgm4441679.3', 'u'metadata':
None}, {'u'id': u'mgm4441680.3', 'u'metadata': None}, {'u'id': u'mgm4441682.3',
'u'metadata': None}, {'u'id': u'mgm4441695.3', 'u'metadata': None}, {'u'id':
u'mgm4441696.3', 'u'metadata': None}]
```

```
protein')]]},
{'id': u'SS00036',
 'metadata': {'ontology': [u'Carbohydrates',
```

```
In [5]: print gut_objs['matrix_type']  
print gut_objs['shape']  
print gut_objs['data'][:10]
```

```
sparse  
[8473, 11]  
[[0, 10, 1], [1, 0, 74], [1, 1, 37], [1, 2, 10], [1, 3, 3], [1, 4, 6], [1, 5, 6],  
[1, 6, 22], [1, 7, 7], [1, 8, 14]]
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In [5]:
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