

# 6\_python

December 13, 2020

## 1 Customize intercellular networks

### 1.0.1 Marton Olbei

### 1.0.2 10/12/2020

In this tutorial we show you how to query interactions from the intercellular interactions in OmniPath, and go over the various attributes accompanying them.

We'll start by importing libraries, first `omnipath`, and `pandas` for data wrangling.

```
[94]: import omnipath as op
import pandas as pd
```

The intercellular interactions in OmniPath are collated from a number of sources. When putting together a query, you can select all of these, or just a preferred subset of them. The `requests.Intercell.resources` function returns the list of datasets included in the database.

```
[95]: op.requests.Intercell.resources()
```

```
[95]: ('Adhesome',
      'Almen2009',
      'Baccin2019',
      'CSPA',
      'CellCellInteractions',
      'CellPhoneDB',
      'ComPPI',
      'DGIdb',
      'EMBRACE',
      'GO_Intercell',
      'GPCRdb',
      'Guide2Pharma',
      'HGNC',
      'HPA_secretome',
      'HPMR',
      'ICELLNET',
      'Integrins',
      'Kirouac2010',
      'LOCATE',
      'LRdb',
```

```

'MCAM',
'Matrisome',
'MatrixDB',
'Membranome',
'OPM',
'OmniPath',
'Phobius',
'Ramilowski2015',
'Ramilowski_location',
'Signalink_function',
'Surfaceome',
'TopDB',
'UniProt_keyword',
'UniProt_location',
'UniProt_topology',
'Zhong2015',
'iTALK')

```

These resources contain a large variety of actors we can use to build intercellular interactions. Take a peek at a generalized list of these categories by using the `requests.Intercell.generic_categories()` function.

This list is also accessible from the browser, at [https://omnipathdb.org/intercell\\_summary](https://omnipathdb.org/intercell_summary). Using the `requests.Intercell.categories()` command returns the complete list.

```
[96]: op.requests.Intercell.generic_categories()
```

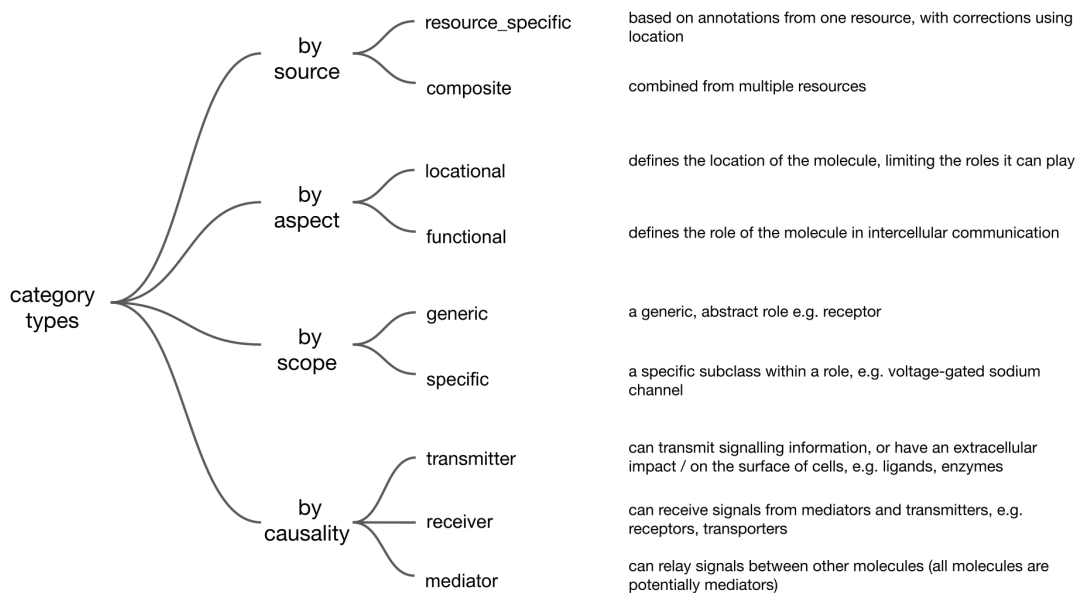
```

[96]: ('adherens_junction',
      'adhesion',
      'cell_adhesion',
      'cell_surface',
      'cell_surface_enzyme',
      'cell_surface_ligand',
      'cell_surface_peptidase',
      'desmosome',
      'ecm',
      'ecm_regulator',
      'extracellular',
      'extracellular_peptidase',
      'gap_junction',
      'intracellular',
      'intracellular_intercellular_related',
      'ion_channel',
      'ion_channel_regulator',
      'ligand',
      'ligand_regulator',
      'matrix_adhesion',
      'matrix_adhesion_regulator',

```

```
'peripheral',
'plasma_membrane',
'plasma_membrane_peripheral',
'plasma_membrane_regulator',
'plasma_membrane_transmembrane',
'receptor',
'receptor_regulator',
'secreted',
'secreted_enzyme',
'secreted_enzyme',
'secreted_peptidase',
'secreted_peptidase_inhibitor',
'secreted_receptor',
'sparc_ecm_regulator',
'tight_junction',
'transmembrane',
'transmembrane_predicted',
'transporter')
```

Now that we have seen the resources and categories, we have to go over a few definitions related to them to make sure everything is clear going forward.



To import an intercellular network we call the `interactions.import_intercell_network()` function.

In this example below we generate a large intercellular network, where we are attempting to connect ligands to receptors.

- first, we define the datasets to import from `include`

- following that, we will specify the qualities of the transmitting proteins, such as which categories they should belong to, what should be their scope, source, aspect and so on under `transmitter_param`
- once we are done with that, we should specify the same for the receiving molecules under `receiver_param`

These steps can be individually traced back through URLs:

1. interaction parameters: <https://omnipathdb.org/interactions?genesymbols=yes&datasets=omnipath,pathwayextra>
2. transmitter parameters: <https://omnipathdb.org/intercell?scope=generic&categories=ligand&causality=transmitter>
3. receiver parameters: <https://omnipathdb.org/intercell?scope=generic&categories=receptor&causality=receiver>

```
[97]: intercell = op.interactions.import_intercell_network(
      include=['omnipath', 'pathwayextra', 'ligreextra'].
      transmitter_params(category_intercell_source = )# define categories
    )
```

```
[100]: op.interactions.import_intercell_network(
      include=['omnipath', 'pathwayextra', 'ligreextra'],
    )
```

```
-----
AttributeError                                Traceback (most recent call last)
<ipython-input-100-9bddab7f73b1> in <module>
----> 1 op.interactions.import_intercell_network.get()

AttributeError: 'function' object has no attribute 'get'
```

```
[98]: intercell_filtered = intercell[
      (intercell['category_intercell_source'] == 'ligand') & # set transmitters_
      ↪to be ligands
      (intercell['category_intercell_target'] == 'receptor') # set receivers to_
      ↪be receptors
    ]
intercell_filtered
```

```
[98]:
```

	source	target	is_stimulation	is_inhibition	consensus_direction	\
9	P23560	P48995	True	False	True	
17	P48061	P04899	True	False	True	
21	P02776	P04899	True	False	True	
90	P19235	Q13507	True	False	True	
96	P19235	P01588	False	True	False	
...	...	...	...	...	...	
30113	Q8NFY4	Q9NZC2	False	False	False	
30117	Q5SRR4	Q9HCN3	False	False	False	
30118	P35247	P11226	True	False	True	
30148	P24001	P34995	True	False	True	

30150	Q8NHL6	Q8IYS5	False	True	True
-------	--------	--------	-------	------	------

	consensus_stimulation	consensus_inhibition	\
9	True	False	
17	True	False	
21	True	False	
90	True	False	
96	False	False	
...	...	...	
30113	False	False	
30117	False	False	
30118	True	False	
30148	True	False	
30150	False	True	

	dip_url	curation_effort	\
9	None	0	
17	None	0	
21	None	0	
90	None	3	
96	<a href="http://dip.doe-mbi.ucla.edu/dip/DIPview.cgi?IK...">http://dip.doe-mbi.ucla.edu/dip/DIPview.cgi?IK...</a>	21	
...	...	...	
30113	None	2	
30117	None	0	
30118	None	0	
30148	None	0	
30150	None	0	

	references	...	\
9	NaN	...	
17	NaN	...	
21	NaN	...	
90	TRIP:18276585;TRIP:19074769;TRIP:21757714	...	
96	BioGRID:10318834;BioGRID:15358619;BioGRID:1732...	...	
...	...	...	
30113	LRdb:16715077;Ramilowski2015:16715077	...	
30117	NaN	...	
30118	NaN	...	
30148	NaN	...	
30150	NaN	...	

	category_source_intercell_target	uniprot_intercell_target	\
9	resource_specific	P48995	
17	resource_specific	P04899	
21	resource_specific	P04899	
90	resource_specific	Q13507	
96	resource_specific	P01588	

...	...	...
30113	resource_specific	Q9NZC2
30117	resource_specific	Q9HCN3
30118	resource_specific	P11226
30148	resource_specific	P34995
30150	resource_specific	Q8IYS5

	genesymbol_intercell_target	entity_type_intercell_target	\
9	TRPC1	protein	
17	GNAI2	protein	
21	GNAI2	protein	
90	TRPC3	protein	
96	EPO	protein	
...	...	...	
30113	TREM2	protein	
30117	TMEM8A	protein	
30118	MBL2	protein	
30148	PTGER1	protein	
30150	OSCAR	protein	

	consensus_score_intercell_target	transmitter_intercell_target	\
9	1	False	
17	1	False	
21	1	False	
90	1	False	
96	1	False	
...	...	...	
30113	9	False	
30117	1	False	
30118	1	False	
30148	5	False	
30150	1	False	

	receiver_intercell_target	secreted_intercell_target	\
9	True	False	
17	True	False	
21	True	False	
90	True	False	
96	True	True	
...	...	...	
30113	True	True	
30117	True	False	
30118	True	True	
30148	True	False	
30150	True	True	

plasma\_membrane\_transmembrane\_intercell\_target \

```

9           False
17          False
21          False
90          False
96          False
...
30113      True
30117      True
30118      False
30148      True
30150      False

```

```

      plasma_membrane_peripheral_intercell_target
9           False
17          False
21          False
90          False
96          False
...
30113      False
30117      False
30118      False
30148      False
30150      False

```

[7604 rows x 46 columns]

This results in 7604 interactions. Let's narrow it down by restricting it with some of the categorical data outlined above.

```

[99]: intercell_filtered = intercell_filtered[
      (intercell_filtered['category_source_intercell_target'] ==
      → 'resource_specific')
      ]
intercell_filtered

```

```

[99]:   source  target  is_stimulation  is_inhibition  consensus_direction  \
9      P23560  P48995           True           False           True
17     P48061  P04899           True           False           True
21     P02776  P04899           True           False           True
90     P19235  Q13507           True           False           True
96     P19235  P01588           False          True           False
...
30113  Q8NFY4  Q9NZC2           False          False           False
30117  Q5SRR4  Q9HCN3           False          False           False
30118  P35247  P11226            True           False           True
30148  P24001  P34995            True           False           True
30150  Q8NHL6  Q8IYS5           False          True           True

```

	consensus_stimulation	consensus_inhibition	\
9	True	False	
17	True	False	
21	True	False	
90	True	False	
96	False	False	
...	...	...	
30113	False	False	
30117	False	False	
30118	True	False	
30148	True	False	
30150	False	True	

	dip_url	curation_effort	\
9	None	0	
17	None	0	
21	None	0	
90	None	3	
96	<a href="http://dip.doe-mbi.ucla.edu/dip/DIPview.cgi?IK...">http://dip.doe-mbi.ucla.edu/dip/DIPview.cgi?IK...</a>	21	
...	...	...	
30113	None	2	
30117	None	0	
30118	None	0	
30148	None	0	
30150	None	0	

	references	...	\
9	NaN	...	
17	NaN	...	
21	NaN	...	
90	TRIP:18276585;TRIP:19074769;TRIP:21757714	...	
96	BioGRID:10318834;BioGRID:15358619;BioGRID:1732...	...	
...	...	...	
30113	LRdb:16715077;Ramilowski2015:16715077	...	
30117	NaN	...	
30118	NaN	...	
30148	NaN	...	
30150	NaN	...	

	category_source	intercell_target	uniprot_intercell_target	\
9	resource_specific		P48995	
17	resource_specific		P04899	
21	resource_specific		P04899	
90	resource_specific		Q13507	
96	resource_specific		P01588	
...	...		...	



30113	resource_specific	Q9NZC2
30117	resource_specific	Q9HCN3
30118	resource_specific	P11226
30148	resource_specific	P34995
30150	resource_specific	Q8IYS5

	genesymbol_intercell_target	entity_type_intercell_target	\
9	TRPC1	protein	
17	GNAI2	protein	
21	GNAI2	protein	
90	TRPC3	protein	
96	EPO	protein	
...	...	...	
30113	TREM2	protein	
30117	TMEM8A	protein	
30118	MBL2	protein	
30148	PTGER1	protein	
30150	OSCAR	protein	

	consensus_score_intercell_target	transmitter_intercell_target	\
9	1	False	
17	1	False	
21	1	False	
90	1	False	
96	1	False	
...	...	...	
30113	9	False	
30117	1	False	
30118	1	False	
30148	5	False	
30150	1	False	

	receiver_intercell_target	secreted_intercell_target	\
9	True	False	
17	True	False	
21	True	False	
90	True	False	
96	True	True	
...	...	...	
30113	True	True	
30117	True	False	
30118	True	True	
30148	True	False	
30150	True	True	

	plasma_membrane_transmembrane_intercell_target	\
9	False	

17	False
21	False
90	False
96	False
...	...
30113	True
30117	True
30118	False
30148	True
30150	False

	plasma_membrane_peripheral_intercell_target
9	False
17	False
21	False
90	False
96	False
...	...
30113	False
30117	False
30118	False
30148	False
30150	False

[7589 rows x 46 columns]

*In this tutorial we learned:*

- the data sources used to generate intercellular interactions
- the qualities of intercellular interactors
- the functions to generate and specify intercellular interactions