

```
In [27]: import numpy as np
import pandas as pd
import scanpy as sc
import scirpy as ir
from matplotlib import pyplot as plt
```

```
In [28]: sc.logging.print_header()
```

```
scanpy==1.6.0 anndata==0.7.4 umap==0.4.6 numpy==1.18.5 scipy==1.5.0 pandas==
1.0.5 scikit-learn==0.23.1 statsmodels==0.11.1 python-igraph==0.7.1+5.3b99dbf
6 leidenalg==0.7.0
```

```
In [29]: adata = ir.datasets.wu2020_3k()
```

```
In [30]: adata.shape
```

```
Out[30]: (3000, 30727)
```

```
In [31]: adata.obs
```

```
Out[31]:
```

	cluster_orig	patient	sample	source	clonotype_orig	multi_chain
<b>LN1_GTAGGCCAGCGTAGTG-1-19</b>	4.4-FOS	Lung1	LN1	NAT	lung1.tn.C223	False
<b>RN2_AGAGCGACAGATTGCT-1-27</b>	4.4-FOS	Renal2	RN2	NAT	renal2.tnb.C1362	False
<b>LN1_GTCATTTCAATGAAAC-1-19</b>	8.2-Tem	Lung1	LN1	NAT	lung1.tn.C25	False
<b>LN2_GACACGCAGGTAGCTG-2-2</b>	8.6-KLRB1	Lung2	LN2	NAT	lung2.tn.C2452	False
<b>LN2_GCACTCTCAGGGATTG-2-2</b>	4.4-FOS	Lung2	LN2	NAT	lung2.tn.C5631	False
...	...	...	...	...	...	...
<b>RT3_GCAGTTAGTATGAAAC-1-6</b>	4.2-RPL32	Renal3	RT3	Tumor	renal3.tnb.C176	False
<b>LT1_GACGTGCTCTCAAGTG-1-24</b>	8.2-Tem	Lung1	LT1	Tumor	lung1.tn.C151	False
<b>ET3_GCTGGGTAGACCTTTG-1-3</b>	3.1-MT	Endo3	ET3	Tumor	endo3.tn.C76	False
<b>RT1_TAAGAGATCCTTAATC-1-8</b>	4.5-IL6ST	Renal1	RT1	Tumor	renal1.tnb.C83	False
<b>LN2_TCTGAGAAGGACACCA-2-2</b>	4.6b-Treg	Lung2	LN2	NAT	lung2.tn.C6211	False

```
3000 rows × 44 columns
```

```
In [32]: adata.obs.source
```

```
Out[32]: LN1_GTAGGCCAGCGTAGTG-1-19    NAT
         RN2_AGAGCGACAGATTGCT-1-27    NAT
         LN1_GTCATTTCAATGAAAC-1-19    NAT
         LN2_GACACGCAGGTAGCTG-2-2     NAT
         LN2_GCACTCTCAGGGATTG-2-2     NAT
         ...
         RT3_GCAGTTAGTATGAAAC-1-6     Tumor
         LT1_GACGTGCTCTCAAGTG-1-24    Tumor
         ET3_GCTGGGTAGACCTTTG-1-3     Tumor
         RT1_TAAGAGATCCTTAATC-1-8     Tumor
         LN2_TCTGAGAAGGACACCA-2-2     NAT
Name: source, Length: 3000, dtype: category
Categories (3, object): [Blood, NAT, Tumor]
```

```
In [33]: sc.pp.filter_genes(adata, min_cells=10)
         sc.pp.filter_cells(adata, min_genes=100)
```

```
In [34]: sc.pp.normalize_per_cell(adata, counts_per_cell_after=1000)
         sc.pp.log1p(adata)
```

```
In [35]: adata.obsm["X_umap"] = adata.obsm["X_umap_orig"]
```

```
In [36]: mapping = {
         "nan": "other",
         "3.1-MT": "other",
         "4.1-Trm": "CD4_Trms",
         "4.2-RPL32": "CD4_RPL32",
         "4.3-TCF7": "CD4_TCF7",
         "4.4-FOS": "CD4_FOS",
         "4.5-IL6ST": "CD4_IL6ST",
         "4.6a-Treg": "CD4_Treg",
         "4.6b-Treg": "CD4_Treg",
         "8.1-Teff": "CD8_Teff",
         "8.2-Tem": "CD8_Tem",
         "8.3a-Trm": "CD8_Trms",
         "8.3b-Trm": "CD8_Trms",
         "8.3c-Trm": "CD8_Trms",
         "8.4-Chrom": "other",
         "8.5-Mitosis": "other",
         "8.6-KLRB1": "other",
         }
         adata.obs["cluster"] = [mapping[x] for x in adata.obs["cluster_orig"]]
```

```
In [37]: adata.obs.patient
```

```
Out[37]: LN1_GTAGGCCAGCGTAGTG-1-19    Lung1
          RN2_AGAGCGACAGATTGCT-1-27    Renal2
          LN1_GTCATTTCAATGAAAC-1-19    Lung1
          LN2_GACACGCAGGTAGCTG-2-2     Lung2
          LN2_GCACTCTCAGGGATTG-2-2     Lung2
          ...
          RT3_GCAGTTAGTATGAAAC-1-6     Renal3
          LT1_GACGTGCTCTCAAGTG-1-24    Lung1
          ET3_GCTGGGTAGACCTTTG-1-3     Endo3
          RT1_TAAGAGATCCTTAATC-1-8     Renal1
          LN2_TCTGAGAAGGACACCA-2-2     Lung2
          Name: patient, Length: 3000, dtype: category
          Categories (14, object): [Colon1, Colon2, Endo1, Endo2, ..., Lung6, Renal1, R
          enal2, Renal3]
```

```
In [38]: adata.obs.sample
```

```

Out[38]: <bound method NDFrame.sample of
t sample source \
LN1_GTAGGCCAGCGTAGTG-1-19      4.4-FOS   Lung1     LN1     NAT
RN2_AGAGCGACAGATTGCT-1-27      4.4-FOS   Renal2    RN2     NAT
LN1_GTCATTTCAATGAAAC-1-19      8.2-Tem   Lung1     LN1     NAT
LN2_GACACGCAGGTAGCTG-2-2       8.6-KLRB1 Lung2     LN2     NAT
LN2_GCACTCTCAGGGATTG-2-2       4.4-FOS   Lung2     LN2     NAT
...
RT3_GCAGTTAGTATGAAAC-1-6       4.2-RPL32 Renal3    RT3     Tumor
LT1_GACGTGCTCTCAAGTG-1-24      8.2-Tem   Lung1     LT1     Tumor
ET3_GCTGGGTAGACCTTTG-1-3       3.1-MT    Endo3     ET3     Tumor
RT1_TAAGAGATCCTTAATC-1-8       4.5-IL6ST Renal1    RT1     Tumor
LN2_TCTGAGAAGGACACCA-2-2       4.6b-Treg Lung2     LN2     NAT

                                clonotype_orig multi_chain IR_VJ_1_locus \
LN1_GTAGGCCAGCGTAGTG-1-19      lung1.tn.C223      False      nan
RN2_AGAGCGACAGATTGCT-1-27      renal2.tnb.C1362   False      TRA
LN1_GTCATTTCAATGAAAC-1-19      lung1.tn.C25       False      TRA
LN2_GACACGCAGGTAGCTG-2-2       lung2.tn.C2452     False      nan
LN2_GCACTCTCAGGGATTG-2-2       lung2.tn.C5631     False      TRA
...
RT3_GCAGTTAGTATGAAAC-1-6       renal3.tnb.C176    False      TRA
LT1_GACGTGCTCTCAAGTG-1-24      lung1.tn.C151     False      TRA
ET3_GCTGGGTAGACCTTTG-1-3       endo3.tn.C76       False      nan
RT1_TAAGAGATCCTTAATC-1-8       renal1.tnb.C83     False      TRA
LN2_TCTGAGAAGGACACCA-2-2       lung2.tn.C6211    False      TRA

                                IR_VJ_2_locus IR_VDJ_1_locus IR_VDJ_2_locus ... \
LN1_GTAGGCCAGCGTAGTG-1-19      nan                TRB         TRB   ...
RN2_AGAGCGACAGATTGCT-1-27      nan                TRB         nan   ...
LN1_GTCATTTCAATGAAAC-1-19      nan                TRB         nan   ...
LN2_GACACGCAGGTAGCTG-2-2       nan                TRB         nan   ...
LN2_GCACTCTCAGGGATTG-2-2       nan                TRB         nan   ...
...
RT3_GCAGTTAGTATGAAAC-1-6       nan                TRB         nan   ...
LT1_GACGTGCTCTCAAGTG-1-24      nan                nan         nan   ...
ET3_GCTGGGTAGACCTTTG-1-3       nan                TRB         nan   ...
RT1_TAAGAGATCCTTAATC-1-8       nan                TRB         nan   ...
LN2_TCTGAGAAGGACACCA-2-2       nan                TRB         nan   ...

                                IR_VDJ_2_c_gene \
LN1_GTAGGCCAGCGTAGTG-1-19      TRBC2
RN2_AGAGCGACAGATTGCT-1-27      nan
LN1_GTCATTTCAATGAAAC-1-19      nan
LN2_GACACGCAGGTAGCTG-2-2       nan
LN2_GCACTCTCAGGGATTG-2-2       nan
...
RT3_GCAGTTAGTATGAAAC-1-6       nan
LT1_GACGTGCTCTCAAGTG-1-24      nan
ET3_GCTGGGTAGACCTTTG-1-3       nan
RT1_TAAGAGATCCTTAATC-1-8       nan
LN2_TCTGAGAAGGACACCA-2-2       nan

                                IR_VJ_1_cdr3_nt
\
LN1_GTAGGCCAGCGTAGTG-1-19      None
RN2_AGAGCGACAGATTGCT-1-27      TGTGCTGTGAGGGGAATAACAATGCCAGACTCATGTTT

```

```

LN1_GTCATTTCAATGAAAC-1-19          TGTGCTGTGAGGTTGGGTAACCAAGTTCTATTTT
LN2_GACACGCAGGTAGCTG-2-2          None
LN2_GCACTCTCAGGGATTG-2-2          TGTGCAGCAAGCGACCCACGGTCGAGGCAGGAAGTCTCTGATCTTT
...
RT3_GCAGTTAGTATGAAAC-1-6          TGTGCTGCGATGGATAGCAACTATCAGTTAATCTGG
LT1_GACGTGCTCTCAAGTG-1-24          TGTGCTTATAGGAGTTCCCTTGGTGGTGCTACAAACAAGCTCATCTTT
ET3_GCTGGGTAGACCTTTG-1-3          None
RT1_TAAGAGATCCTTAATC-1-8          TGTGCAATGAGCGAGATTTCTGGTGGCTACAATAAGCTGATTTTT
LN2_TCTGAGAAGGACACCA-2-2          TGTGCTACGGAGGAATATGGAAACAAGCTGGTCTTT
    
```

IR\_VJ\_2\_cdr3\_nt \

```

LN1_GTAGGCCAGCGTAGTG-1-19          None
RN2_AGAGCGACAGATTGCT-1-27          None
LN1_GTCATTTCAATGAAAC-1-19          None
LN2_GACACGCAGGTAGCTG-2-2          None
LN2_GCACTCTCAGGGATTG-2-2          None
...
RT3_GCAGTTAGTATGAAAC-1-6          None
LT1_GACGTGCTCTCAAGTG-1-24          None
ET3_GCTGGGTAGACCTTTG-1-3          None
RT1_TAAGAGATCCTTAATC-1-8          None
LN2_TCTGAGAAGGACACCA-2-2          None
    
```

IR\_VDJ\_1\_cdr3\_nt

```

\
LN1_GTAGGCCAGCGTAGTG-1-19          TGTGCCAGCAGCTTAATGCGGCTAGCGGGAGATACGCAGTATTTT
RN2_AGAGCGACAGATTGCT-1-27          TGTGCCAGCAGCTTTGGAACGGTGGCTGAAGCTTTCTTT
LN1_GTCATTTCAATGAAAC-1-19          TGCAGTGCTAGAGATGGAGGGGGGGGAACACTGAAGCTTTCTTT
LN2_GACACGCAGGTAGCTG-2-2          TGTGCCAGCAGCCAAGGTCAGGGACAGGATTTTAACTACGAGCAGT...
LN2_GCACTCTCAGGGATTG-2-2          TGTGCCAGCAGCTTGACCGTTAACACTGAAGCTTTCTTT
...
RT3_GCAGTTAGTATGAAAC-1-6          TGTGCCACCAAGGACAGGGAAGACACCGGGGAGCTGTTTTTT
LT1_GACGTGCTCTCAAGTG-1-24          None
ET3_GCTGGGTAGACCTTTG-1-3          TGTGCCAGCAGCCGGACAGGGGGGATTCCGGGGAGCTGTTTTTT
RT1_TAAGAGATCCTTAATC-1-8          TGTGCCTGGAGTGACAGGTCAGACGAGCAGTACTTC
LN2_TCTGAGAAGGACACCA-2-2          TGTGCCAGCAGCTTTCTACCTTTGGGAGATACGCAGTATTTT
    
```

IR\_VDJ\_2\_cdr3\_nt

```

\
LN1_GTAGGCCAGCGTAGTG-1-19          TGTGCAAGTCGCTTAGCGGTTTTATCGACTAGCGGGAGTGTCGGAG...
RN2_AGAGCGACAGATTGCT-1-27          None
LN1_GTCATTTCAATGAAAC-1-19          None
LN2_GACACGCAGGTAGCTG-2-2          None
LN2_GCACTCTCAGGGATTG-2-2          None
...
RT3_GCAGTTAGTATGAAAC-1-6          None
LT1_GACGTGCTCTCAAGTG-1-24          None
ET3_GCTGGGTAGACCTTTG-1-3          None
RT1_TAAGAGATCCTTAATC-1-8          None
LN2_TCTGAGAAGGACACCA-2-2          None
    
```

	has_ir	batch	n_genes	n_counts	cluster
LN1_GTAGGCCAGCGTAGTG-1-19	True	19	582	1188.0	CD4_FOSS
RN2_AGAGCGACAGATTGCT-1-27	True	27	740	1712.0	CD4_FOSS
LN1_GTCATTTCAATGAAAC-1-19	True	19	1264	3195.0	CD8_Tem
LN2_GACACGCAGGTAGCTG-2-2	True	2	1844	5518.0	other
LN2_GCACTCTCAGGGATTG-2-2	True	2	2086	6866.0	CD4_FOSS

```

...
RT3_GCAGTTAGTATGAAAC-1-6 True 6 574 1773.0 CD4_RPL32
LT1_GACGTGCTCTCAAGTG-1-24 True 24 1087 2711.0 CD8_Tem
ET3_GCTGGGTAGACCTTTG-1-3 True 3 693 1382.0 other
RT1_TAAGAGATCCTTAATC-1-8 True 8 673 1977.0 CD4_IL6ST
LN2_TCTGAGAAGGACACCA-2-2 True 2 1200 2539.0 CD4_Treg

```

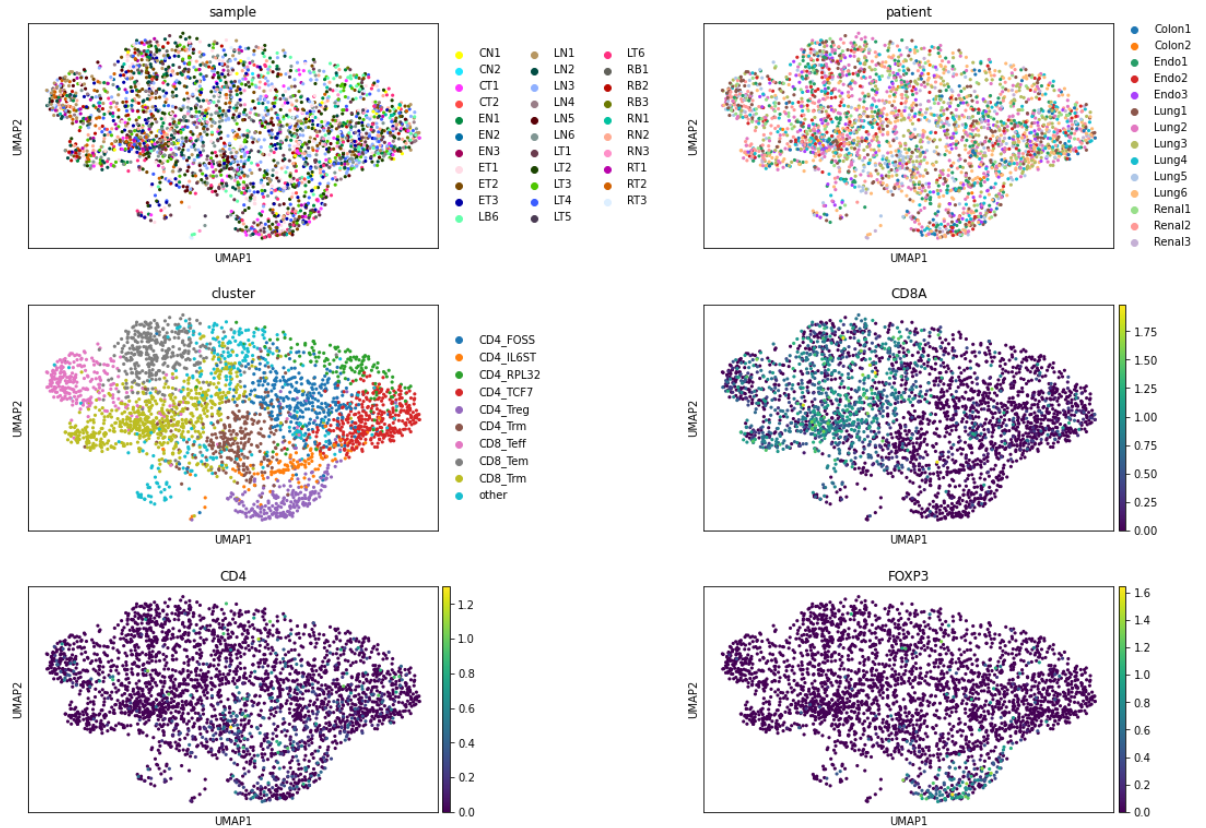
[3000 rows x 47 columns]>

```

In [39]: sc.pl.umap(
    adata,
    color=["sample", "patient", "cluster", "CD8A", "CD4", "FOXP3"],
    ncols=2,
    wspace=0.5,
)

```

... storing 'cluster' as categorical



In [40]: adata

Out[40]: AnnData object with n\_obs × n\_vars = 3000 × 11850  
 obs: 'cluster\_orig', 'patient', 'sample', 'source', 'clonotype\_orig', 'muti\_chain', 'IR\_VJ\_1\_locus', 'IR\_VJ\_2\_locus', 'IR\_VDJ\_1\_locus', 'IR\_VDJ\_2\_locus', 'IR\_VJ\_1\_cdr3', 'IR\_VJ\_2\_cdr3', 'IR\_VDJ\_1\_cdr3', 'IR\_VDJ\_2\_cdr3', 'IR\_VJ\_1\_junction\_ins', 'IR\_VJ\_2\_junction\_ins', 'IR\_VDJ\_1\_junction\_ins', 'IR\_VDJ\_2\_junction\_ins', 'IR\_VJ\_1\_expr', 'IR\_VJ\_2\_expr', 'IR\_VDJ\_1\_expr', 'IR\_VDJ\_2\_expr', 'IR\_VJ\_1\_v\_gene', 'IR\_VJ\_2\_v\_gene', 'IR\_VDJ\_1\_v\_gene', 'IR\_VDJ\_2\_v\_gene', 'IR\_VJ\_1\_d\_gene', 'IR\_VJ\_2\_d\_gene', 'IR\_VDJ\_1\_d\_gene', 'IR\_VDJ\_2\_d\_gene', 'IR\_VJ\_1\_j\_gene', 'IR\_VJ\_2\_j\_gene', 'IR\_VDJ\_1\_j\_gene', 'IR\_VDJ\_2\_j\_gene', 'IR\_VJ\_1\_c\_gene', 'IR\_VJ\_2\_c\_gene', 'IR\_VDJ\_1\_c\_gene', 'IR\_VDJ\_2\_c\_gene', 'IR\_VJ\_1\_cdr3\_nt', 'IR\_VJ\_2\_cdr3\_nt', 'IR\_VDJ\_1\_cdr3\_nt', 'IR\_VDJ\_2\_cdr3\_nt', 'has\_in', 'batch', 'n\_genes', 'n\_counts', 'cluster'  
 var: 'gene\_ids', 'feature\_types', 'n\_cells'  
 uns: 'log1p', 'sample\_colors', 'patient\_colors', 'cluster\_colors'  
 obsm: 'X\_umap\_orig', 'X\_umap'

In [41]: ir.tl.chain\_qc(adata)

In [42]: adata

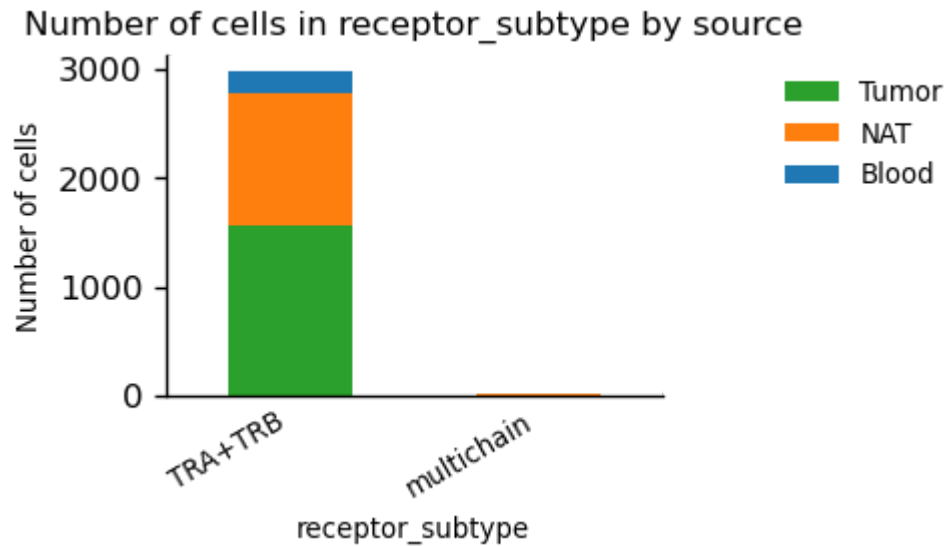
Out[42]: AnnData object with n\_obs × n\_vars = 3000 × 11850  
 obs: 'cluster\_orig', 'patient', 'sample', 'source', 'clonotype\_orig', 'muti\_chain', 'IR\_VJ\_1\_locus', 'IR\_VJ\_2\_locus', 'IR\_VDJ\_1\_locus', 'IR\_VDJ\_2\_locus', 'IR\_VJ\_1\_cdr3', 'IR\_VJ\_2\_cdr3', 'IR\_VDJ\_1\_cdr3', 'IR\_VDJ\_2\_cdr3', 'IR\_VJ\_1\_junction\_ins', 'IR\_VJ\_2\_junction\_ins', 'IR\_VDJ\_1\_junction\_ins', 'IR\_VDJ\_2\_junction\_ins', 'IR\_VJ\_1\_expr', 'IR\_VJ\_2\_expr', 'IR\_VDJ\_1\_expr', 'IR\_VDJ\_2\_expr', 'IR\_VJ\_1\_v\_gene', 'IR\_VJ\_2\_v\_gene', 'IR\_VDJ\_1\_v\_gene', 'IR\_VDJ\_2\_v\_gene', 'IR\_VJ\_1\_d\_gene', 'IR\_VJ\_2\_d\_gene', 'IR\_VDJ\_1\_d\_gene', 'IR\_VDJ\_2\_d\_gene', 'IR\_VJ\_1\_j\_gene', 'IR\_VJ\_2\_j\_gene', 'IR\_VDJ\_1\_j\_gene', 'IR\_VDJ\_2\_j\_gene', 'IR\_VJ\_1\_c\_gene', 'IR\_VJ\_2\_c\_gene', 'IR\_VDJ\_1\_c\_gene', 'IR\_VDJ\_2\_c\_gene', 'IR\_VJ\_1\_cdr3\_nt', 'IR\_VJ\_2\_cdr3\_nt', 'IR\_VDJ\_1\_cdr3\_nt', 'IR\_VDJ\_2\_cdr3\_nt', 'has\_in', 'batch', 'n\_genes', 'n\_counts', 'cluster', 'receptor\_type', 'receptor\_subtype', 'chain\_pairing'  
 var: 'gene\_ids', 'feature\_types', 'n\_cells'  
 uns: 'log1p', 'sample\_colors', 'patient\_colors', 'cluster\_colors'  
 obsm: 'X\_umap\_orig', 'X\_umap'



```
In [43]: ir.pl.group_abundance(adata, groupby="receptor_subtype", target_col="source")
```

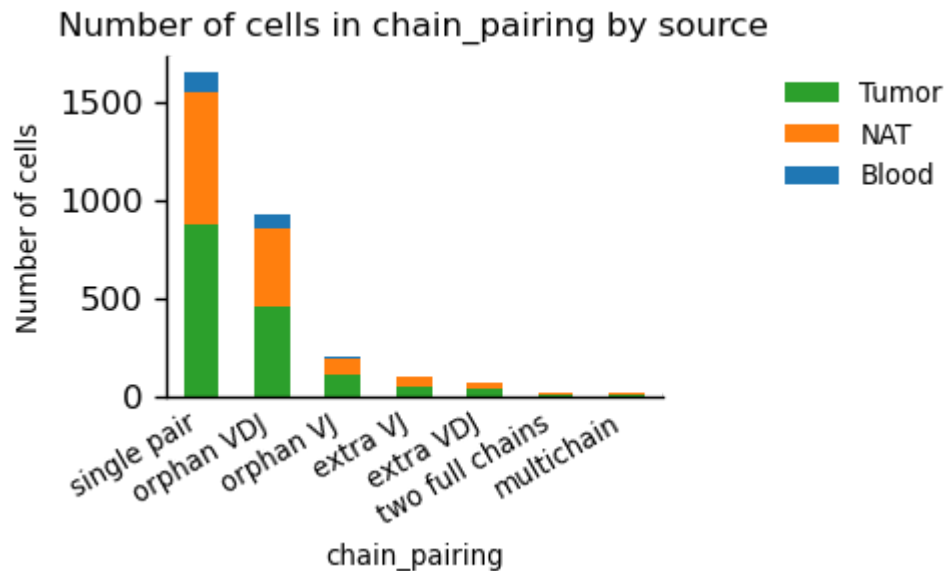
```
... storing 'receptor_type' as categorical
... storing 'receptor_subtype' as categorical
... storing 'chain_pairing' as categorical
```

```
Out[43]: <AxesSubplot:title={'center':'Number of cells in receptor_subtype by source'}, xlabel='receptor_subtype', ylabel='Number of cells'>
```



```
In [44]: ir.pl.group_abundance(adata, groupby="chain_pairing", target_col="source")
```

```
Out[44]: <AxesSubplot:title={'center':'Number of cells in chain_pairing by source'}, xlabel='chain_pairing', ylabel='Number of cells'>
```



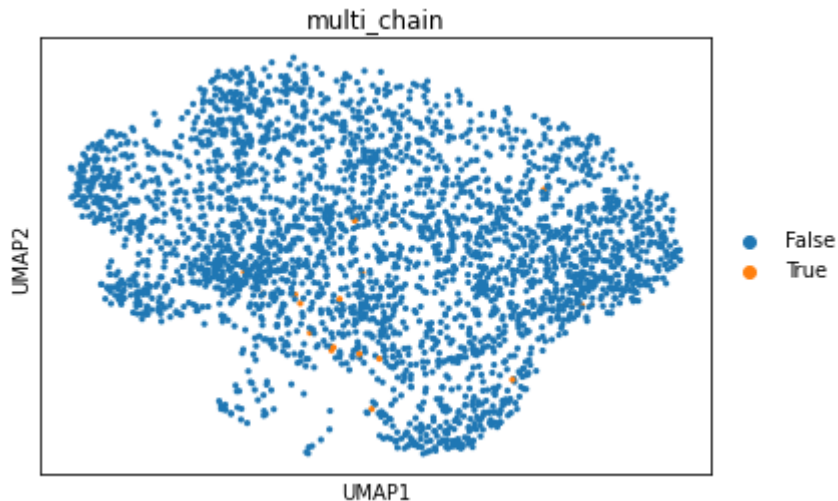
```
In [45]: print(
    "Fraction of cells with more than one pair of TCRs: {:.2f}".format(
        np.sum(
            adata.obs["chain_pairing"].isin(
                ["extra VJ", "extra VDJ", "two full chains"]
            )
        )
        / adata.n_obs
    )
)
```

Fraction of cells with more than one pair of TCRs: 0.06

```
In [46]: results_file = './Scirpy_learn.h5ad'
```

```
In [47]: adata.write(results_file)
```

```
In [48]: sc.pl.umap(adata, color="multi_chain")
```



```
In [49]: adata = adata[adata.obs["multi_chain"] != "True", :].copy()
```

```
In [50]: # using default parameters, `ir_neighbors` will compute nucleotide sequence id
entity
ir.pp.ir_neighbors(adata, receptor_arms="all", dual_ir="primary_only")
ir.tl.define_clonotypes(adata)
```

```
100%|██████████| 1643/1643 [00:00<00:00, 17114.68it/s]
100%|██████████| 2186/2186 [00:00<00:00, 112054.51it/s]
100%|██████████| 8887/8887 [00:00<00:00, 90558.27it/s]
```

```
In [51]: ir.tl.clonotype_network(adata, min_size=2)
         ir.pl.clonotype_network(adata, color="clonotype", legend_loc="none")
```

```
-----
ValueError                                Traceback (most recent call last)
<ipython-input-51-3dfa3846bb6e> in <module>
----> 1 ir.tl.clonotype_network(adata, min_size=2)
      2 ir.pl.clonotype_network(adata, color="clonotype", legend_loc="none")

~\AppData\Local\Continuum\anaconda3\lib\site-packages\scirpy\_tools\_clonotyp
es.py in clonotype_network(adata, sequence, metric, min_size, layout, layout_
kwargs, neighbors_key, key_clonotype_size, key_added, inplace, random_state)
    307     layout_kwargs = default_layout_kwargs if layout_kwargs is None el
se layout_kwargs
    308     if layout == "components":
--> 309         coords = layout_components(graph, **layout_kwargs)
    310     else:
    311         coords = graph.layout(layout, **layout_kwargs).coords

~\AppData\Local\Continuum\anaconda3\lib\site-packages\scirpy\util\graph.py in
layout_components(graph, component_layout, arrange_boxes, pad_x, pad_y)
     95     ]
     96     # get vertexes back into their original order
--> 97     coords = np.vstack(component_layouts)[vertex_sorter, :]
     98     return coords
     99

<__array_function__ internals> in vstack(*args, **kwargs)

~\AppData\Local\Continuum\anaconda3\lib\site-packages\numpy\core\shape_base.p
y in vstack(tup)
    281     if not isinstance(arrs, list):
    282         arrs = [arrs]
--> 283     return _nx.concatenate(arrs, 0)
    284
    285

<__array_function__ internals> in concatenate(*args, **kwargs)

ValueError: need at least one array to concatenate
```

In [52]: `pip freeze`

```
airr==1.3.0
alabaster==0.7.12
anaconda-client==1.7.2
anaconda-navigator==1.9.12
anaconda-project==0.8.3
anndata==0.7.4
annoy @ file:///D:/bld/python-annoy_1589264717844/work
argh==0.26.2
asn1crypto @ file:///C:/ci/asn1crypto_1594339244757/work
astroid @ file:///C:/ci/astroid_1592481955828/work
astropy==4.0.1.post1
atomicwrites==1.4.0
attrs==19.3.0
Automat==0.8.0
autopep8 @ file:///tmp/build/80754af9/autopep8_1592412889138/work
Babel==2.8.0
backcall==0.2.0
backports.shutil-get-terminal-size==1.0.0
bbknn==1.3.12
bcrypt==3.1.7
beautifulsoup4==4.9.1
biopython==1.78
bitarray @ file:///C:/ci/bitarray_1594753961793/work
bkcharts==0.2
bleach==3.1.5
bokeh @ file:///C:/ci/bokeh_1593179283802/work
boto==2.49.0
Bottleneck==1.3.2
brotlipy==0.7.0
certifi==2020.6.20
cffi==1.14.0
changeo==1.0.0
chardet==3.0.4
click==7.1.2
cloudpickle @ file:///tmp/build/80754af9/cloudpickle_1594141588948/work
clyent==1.2.2
colorama==0.4.3
comtypes==1.1.7
conda==4.8.4
conda-build==3.17.8
conda-package-handling==1.7.0
Note: you may need to restart the kernel to use updated packages.conda-verify
==3.1.1
constantly==15.1.0
contextlib2==0.6.0.post1
cryptography==2.9.2

cssselect==1.1.0
cyclers==0.10.0
Cython @ file:///C:/ci/cython_1594834055134/work
cytoolz==0.10.1
dask @ file:///tmp/build/80754af9/dask-core_1594156306305/work
decorator==4.4.2
defusedxml==0.6.0
descartes==1.1.0
diff-match-patch @ file:///tmp/build/80754af9/diff-match-patch_1594828741838/
work
```

distributed @ file:///C:/ci/distributed\_1594319358820/work  
docutils==0.16  
entrypoints==0.3  
et-xmlfile==1.0.1  
fastcache==1.1.0  
filelock==3.0.12  
flake8==3.8.3  
Flask==1.1.2  
fsspec==0.7.4  
future==0.18.2  
get-version==2.1  
gevent @ file:///C:/ci/gevent\_1593010757573/work  
glob2==0.7  
gmpy2==2.0.8  
greenlet==0.4.16  
h5py==2.10.0  
HeapDict==1.0.1  
html5lib @ file:///tmp/build/80754af9/html5lib\_1593446221756/work  
hyperlink==19.0.0  
idna @ file:///tmp/build/80754af9/idna\_1593446292537/work  
imageio @ file:///tmp/build/80754af9/imageio\_1594161405741/work  
imagesize==1.2.0  
importlib-metadata @ file:///C:/ci/importlib-metadata\_1593446525189/work  
incremental==17.5.0  
intervaltree @ file:///tmp/build/80754af9/intervaltree\_1594361675072/work  
ipykernel @ file:///C:/ci/ipykernel\_1595342053367/work/dist/ipykernel-5.3.3-py3-none-any.whl  
ipython @ file:///C:/ci/ipython\_1593433781269/work  
ipython-genutils==0.2.0  
ipywidgets==7.5.1  
isort==4.3.21  
itemadapter @ file:///home/conda/feedstock\_root/build\_artifacts/itemadapter\_1593694453559/work  
itsdangerous==1.1.0  
jdcal==1.4.1  
jedi @ file:///C:/ci/jedi\_1592833832328/work  
Jinja2==2.11.2  
joblib @ file:///tmp/build/80754af9/joblib\_1594236160679/work  
json5==0.9.5  
jsonschema @ file:///C:/ci/jsonschema\_1594363671836/work  
jupyter==1.0.0  
jupyter-client @ file:///tmp/build/80754af9/jupyter\_client\_1594826976318/work  
jupyter-console==6.1.0  
jupyter-core==4.6.3  
jupyterlab==2.1.5  
jupyterlab-server @ file:///tmp/build/80754af9/jupyterlab\_server\_1594164409481/work  
keyring @ file:///C:/ci/keyring\_1593109817825/work  
kiwisolver==1.2.0  
lazy-object-proxy==1.4.3  
legacy-api-wrap==1.2  
leidenalg==0.7.0  
libarchive-c==2.9  
llvmlite==0.33.0+1.g022ab0f  
locket==0.2.0  
lxml @ file:///C:/ci/lxml\_1594826938446/work  
MarkupSafe @ file:///C:/ci/markupsafe\_1594405949945/work

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matplotlib==3.3.0
matplotlib-venn==0.11.5
mccabe==0.6.1
menuinst==1.4.16
mistune @ file:///C:/ci/mistune_1594373272338/work
mizani==0.7.1
mkl-fft==1.1.0
mkl-random==1.1.1
mkl-service==2.3.0
mock==4.0.2
more-itertools==8.4.0
mpmath==1.1.0
msgpack==1.0.0
multipledispatch==0.6.0
natsort==6.2.0
navigator-updater==0.2.1
nbconvert @ file:///C:/ci/nbconvert_1594372737468/work
nbformat==5.0.7
networkx @ file:///tmp/build/80754af9/networkx_1594377231366/work
nlTK @ file:///tmp/build/80754af9/nltk_1592496090529/work
nose @ file:///C:/ci/nose_1594377973236/work
notebook==6.0.3
numba==0.50.1
numexpr==2.7.1
numpy==1.18.5
numpydoc @ file:///tmp/build/80754af9/numpydoc_1594166760263/work
olefile==0.46
openpyxl @ file:///tmp/build/80754af9/openpyxl_1594167385094/work
packaging==20.4
palettable==3.3.0
pandas @ file:///C:/ci/pandas_1592841747005/work
pandocfilters==1.4.2
paramiko==2.7.1
parasail==1.2
parsel==1.5.2
parso==0.7.0
partd==1.1.0
path==14.0.1
path.py==12.0.2
pathlib2 @ file:///C:/ci/pathlib2_1594381094851/work
pathtools==0.1.2
patsy==0.5.1
pep8==1.7.1
pexpect @ file:///C:/ci/pexpect_1594383465186/work
pickleshare @ file:///C:/ci/pickleshare_1594374056827/work
Pillow @ file:///C:/ci/pillow_1594298234712/work
pkginfo==1.5.0.1
plotnine==0.5.1
pluggy==0.13.1
ply==3.11
presto==0.6.1
prometheus-client==0.8.0
prompt-toolkit==3.0.5
Protego==0.1.16
psutil==5.7.0
py @ file:///tmp/build/80754af9/py_1593446248552/work
pyasn1==0.4.8
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pycairo==1.20.0  
pycodestyle==2.6.0  
pycosat==0.6.3  
pycparser @ file:///tmp/build/80754af9/pycparser\_1594388511720/work  
pycrypto==2.6.1  
pycurl==7.43.0.5  
PyDispatcher==2.0.5  
pydocstyle @ file:///tmp/build/80754af9/pydocstyle\_1592848020240/work  
pyflakes==2.2.0  
Pygments==2.6.1  
PyHamcrest @ file:///tmp/build/80754af9/pyhamcrest\_1594390921726/work  
pylint @ file:///C:/ci/pylint\_1592487534522/work  
PyNaCl @ file:///C:/ci/pynacl\_1595009241355/work  
pyodbc===4.0.0-unsupported  
pyOpenSSL @ file:///tmp/build/80754af9/pyopenssl\_1594392929924/work  
pyparsing==2.4.7  
pyreadline==2.1  
pysistent==0.16.0  
PySocks @ file:///C:/ci/pysocks\_1594394709107/work  
pytest==5.4.3  
pytest-runner==5.2  
python-dateutil==2.8.1  
python-igraph==0.7.1.post7  
python-jsonrpc-server @ file:///tmp/build/80754af9/python-jsonrpc-server\_1594397536060/work  
python-language-server @ file:///C:/ci/python-language-server\_1594152769556/work  
python-Levenshtein==0.12.0  
python-louvain==0.13  
pytoml==0.1.21  
pytz==2020.1  
pyvdj @ git+https://github.com/veghep/pyVDJ.git@31cec7d6123853fb9307458a205677101983d845  
PyWavelets==1.1.1  
pywin32==227  
pywin32-ctypes @ file:///C:/ci/pywin32-ctypes\_1594392691209/work  
pywinpty==0.5.7  
PyYAML==5.3.1  
pyzmq==19.0.1  
QDarkStyle==2.8.1  
QtAwesome==0.7.2  
qtconsole @ file:///tmp/build/80754af9/qtconsole\_1592848611704/work  
QtPy==1.9.0  
queuelib==1.5.0  
regex @ file:///C:/ci/regex\_1593435644645/work  
requests @ file:///tmp/build/80754af9/requests\_1592841827918/work  
rope==0.17.0  
Rtree==0.9.4  
ruamel-yaml==0.15.87  
scanpy==1.6.0  
scikit-image==0.16.2  
scikit-learn==0.23.1  
scipy @ file:///C:/ci/scipy\_1592916958183/work  
scirpy==0.5.0  
Scrapy @ file:///D:/bld/scrapy\_1593704860927/work  
seaborn==0.10.1



Send2Trash==1.5.0  
service-identity==18.1.0  
setuptools-scm==4.1.2  
simplegeneric==0.8.1  
sinfo==0.3.1  
singledispatch==3.4.0.3  
six==1.15.0  
snowballstemmer==2.0.0  
sortedcollections==1.2.1  
sortedcontainers==2.2.2  
soupsieve==2.0.1  
Sphinx @ file:///tmp/build/80754af9/sphinx\_1594223420021/work  
sphinxcontrib-applehelp==1.0.2  
sphinxcontrib-devhelp==1.0.2  
sphinxcontrib-htmlhelp==1.0.3  
sphinxcontrib-jsmath==1.0.1  
sphinxcontrib-qthelp==1.0.3  
sphinxcontrib-serializinghtml==1.1.4  
sphinxcontrib-websupport @ file:///tmp/build/80754af9/sphinxcontrib-websupport\_1593446360927/work  
spyder @ file:///C:/ci/spyder\_1594826266791/work  
spyder-kernels @ file:///C:/ci/spyder-kernels\_1594751701920/work  
SQLAlchemy @ file:///C:/ci/sqlalchemy\_1593445585180/work  
squarify==0.4.3  
statsmodels==0.11.1  
stdlib-list==0.7.0  
sympy @ file:///C:/ci/sympy\_1594234541241/work  
tables==3.5.1  
tbb==2019.0  
tblib==1.6.0  
terminado==0.8.3  
testpath==0.4.4  
threadpoolctl @ file:///tmp/tmp9twdgx9k/threadpoolctl-2.1.0-py3-none-any.whl  
toml @ file:///tmp/build/80754af9/toml\_1592853716807/work  
toolz==0.10.0  
tornado==6.0.4  
tqdm @ file:///tmp/build/80754af9/tqdm\_1593446365756/work  
traitlets==4.3.3  
Twisted==20.3.0  
typed-ast==1.4.1  
typing-extensions @ file:///tmp/build/80754af9/typing\_extensions\_1592847887441/work  
ujson==1.35  
umap-learn @ file:///D:/bld/umap-learn\_1593739921313/work  
unicodcsv==0.14.1  
UpSetPlot==0.3.0.post3  
urllib3==1.25.9  
w3lib==1.21.0  
watchdog @ file:///C:/ci/watchdog\_1593446515400/work  
wcwidth @ file:///tmp/build/80754af9/wcwidth\_1593447189090/work  
webencodings==0.5.1  
Werkzeug==1.0.1  
widgetsnextension==3.5.1  
win-inet-pton==1.1.0  
win-unicode-console==0.5  
wincertstore==0.2  
wrapt==1.11.2

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xlrd==1.2.0
XlsxWriter==1.2.9
xlwings==0.19.5
xlwt==1.3.0
xmldict==0.12.0
yamllordereddictloader==0.4.0
yapf @ file:///tmp/build/80754af9/yapf_1593528177422/work
zict==2.0.0
zipp==3.1.0
zope.event==4.4
zope.interface==4.7.1
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In [ ]: