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In [ ]: # Description:
        This script processes a single-nucleus RNA-seq dataset from afca, removes cells
        and filters cell types with fewer than 200 total cells or fewer than 100 cells p
        it filters out lowly expressed genes, while retaining those expressed in at least
        Each processed cell type is saved as a separate .h5ad file.
        # Import the libraries
        import os
        import matplotlib.pyplot as plt
        import pandas as pd
        import scanpy as sc
        import anndata as ad
In [3]: # Load the dataset data and get the metadata
        adata = ad.read h5ad("/hpc/shared/onco janssen/dhaynessimmons/data/ageing flies/
In [ ]: # Set the functions
        def split_by_batch_prefix(name):
            Splits the string into two parts:
            - Part before 'AFCA' or 'FCA'
            - The rest starting with 'AFCA' or 'FCA'
            match = re.search(r'(AFCA|FCA)', name)
            i = match.start()
            return name[i:]
In [4]: # print out the basics
        print([i for i in adata.obs.columns])
        print("shape of full data: ", adata.shape)
        #value couns for important columns
        print("\nAge value counts: ", adata.obs["age"].value_counts())
        print("\nSex value counts: ", adata.obs["sex"].value_counts())
        print("\nDataset value counts: ", adata.obs["dataset"].value_counts())
```

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['tissue', 'sex', 'age', 'sex_age', 'n_genes_by_counts', 'total_counts', 'total_c
       ounts_mt', 'pct_counts_mt', 'log1p_n_genes_by_counts', 'log1p_total_counts', 'log
       1p_total_counts_mt', 'dataset', 'fca_annotation', 'afca_annotation', 'afca_annotation'
       tion_broad']
       shape of full data: (276273, 15992)
      Age value counts: age
            96594
       30
          84496
       70
            49963
       50
            45220
       Name: count, dtype: int64
      Sex value counts: sex
       female 148049
      male
                123879
                 4345
       mix
      Name: count, dtype: int64
      Dataset value counts: dataset
       AFCA
            179679
       FCA
               96594
      Name: count, dtype: int64
In [ ]: # Get the unique afca cell types
        for cell_type in sorted(adata.obs['afca_annotation'].unique().tolist()):
            print(cell_type)
```

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16-cell germline cyst in germarium region 2a and 2b
CNS surface associated glial cell
adult Malpighian tubule principal cell
adult Malpighian tubule principal cell of initial segment
adult Malpighian tubule principal cell of lower segment
adult Malpighian tubule principal cell of lower ureter
adult Malpighian tubule stellate cell of main segment
adult alary muscle
adult differentiating enterocyte
adult fat body_body
adult glial cell
adult heart ventral longitudinal muscle
adult hindgut
adult midgut enterocyte
adult midgut-hindgut hybrid zone
adult oenocyte
adult peripheral nervous system
adult reticular neuropil associated glial cell_body
adult salivary gland
adult tracheal cell
adult ventral nervous system
anterior ejaculatory duct
antimicrobial peptide-producing cell
cardia (1)
cardia (2)
cardiomyocyte, working adult heart muscle (non-ostia)
cell body glial cell
copper cell
crop
cyst cell
ejaculatory bulb
ejaculatory bulb epithelium
enteroblast
enterocyte of anterior adult midgut epithelium
enterocyte of posterior adult midgut epithelium
enterocyte-like
enteroendocrine cell
eo support cell
epidermal cell that specialized in antimicrobial response
epithelial cell_body
escort cell
female reproductive system
follicle cell
follicle stem cell and prefollicle cell
germline cell
gustatory receptor neuron
hemocyte body
indirect flight muscle
intestinal stem cell
leg muscle motor neuron
male accessory gland main cell
male accessory gland secondary cell
mechanosensory neuron of haltere
midgut large flat cell
multidendritic neuron
muscle cell
oviduct
perineurial glial sheath
pheromone-sensing neuron
polar follicle cell
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posterior midgut*
       prefollicle cell/stalk follicle cell
       principal cell*
       scolopidial neuron
       seminal vesicle & testis epithelia
       spermatid
       spermatocyte
       stalk follicle cell
       subperineurial glial cell_body
       unannotated
       visceral muscle of the crop
       visceral muscle of the midgut
       young germ cell
       The Kernel crashed while executing code in the current cell or a previous cell.
       Please review the code in the cell(s) to identify a possible cause of the failur
       e.
       Click <a href='https://aka.ms/vscodeJupyterKernelCrash'>here</a> for more info.
       View Jupyter <a href='command:jupyter.viewOutput'>log</a> for further details.
In [ ]: # get cells where sex is neither F nor M
        mix_adata = adata[(adata.obs.sex != "female")&(adata.obs.sex != "male")].copy()
        print(mix_adata.obs.shape)
        # Remove them from the dataset
        mf_adata = adata[~(adata.obs.index.isin(mix_adata.obs.index))&(adata.obs['afca_a
        # get the batch from the row name
        mf_adata.obs['batch'] = mf_adata.obs.index.map(lambda x: split_by_batch_prefix(x)
        print(mf adata.obs.shape)
       (4345, 15)
       (265979, 15)
In [ ]: # Get the observation dataframe as a pandas dataframe
        mf_adata_obs = mf_adata.obs.copy()
        print(type(mf adata obs))
        cell_list = []
        # Set the save path
        save_path = "/hpc/shared/onco_janssen/dhaynessimmons/data/ageing_flies/afca_data
        os.makedirs(save_path, exist_ok=True)
        # Gene list of interest
        gene_list = [
            "Su(var)205", "Su(var)3-9", "G9a", "HP1b", "HP1c", "HP4",
            "HP5", "HP6", "ADD1", "Su(var)2-HP2", "Su(var)3-7", "Lam",
            "LamC", "LBR", "Kdm4A", "Kdm4B", "His2Av", "His3.3A", "His3.3B"
        1
        \# Loop through the afca cell types and create a new adata object for each cell \mathsf{t}
        for cell_type in mf_adata_obs['afca_annotation'].unique():
            cell_type = cell_type.replace("/", "-")
            print("\n\nWorking on cell type: ", cell_type, "\n")
            # Get the indices of the cells that match the current cell type
            indices = mf adata obs[mf adata obs['afca annotation'] == cell type].index
            # Create new pandas dataframe with the indices
            cell_type_df = mf_adata_obs.loc[indices]
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# Evaluate the QC of the new adata object
cell_cnt = cell_type_df.shape[0]
print("number of cells: ", cell_cnt)
print("Min number of genes expressed : ", cell_type_df.n_genes_by_counts.min
if cell cnt < 200:</pre>
    print("Not enough cells to proceed with analysis")
    continue
else:
    print("Sufficient cells to proceed with analysis")
    # Check that each age group has at least 100 cells
    age_grouped = cell_type_df.groupby('age', observed=False).size()
    del cell_type_df
    min_value = age_grouped.min()
    del age_grouped
    print("Minimum number of cells in an age group: ", min_value)
    if min value < 100:</pre>
        print("Not enough cells in an age group to proceed with analysis")
        continue
    else:
        print("Sufficient cells in each age group to proceed with analysis")
        # Create a new adata object with the cell type data
        cell_list.append(cell_type)
# Create a new adata object for this cell type
cell_type_adata = mf_adata[indices].copy()
print("\nshape of cell type data: ", cell_type_adata.shape)
# ----- Custom gene filtering starts here ----- #
# Compute how many cells express each gene
gene_expression_counts = np.array((cell_type_adata.X > 0).sum(axis=0)).flatt
# Get gene names
gene_names = pd.Index(cell_type_adata.var_names)
# Genes expressed in >= 3 cells
genes_expressed_enough = gene_expression_counts >= 3
# Create a boolean mask to keep genes that are either:
# - expressed in enough cells
# - or present in the gene_list
gene_list_set = set(gene_list)
genes_in_list = gene_names.isin(gene_list_set)
# Combine masks
genes to keep = genes expressed enough | genes in list
cell_type_adata = cell_type_adata[:, genes_to_keep].copy()
print("\nshape of cell type data after filtering: ", cell type adata.shape)
# Save the new adata object
cell_type_adata.write_h5ad(f"{save_path}{cell_type}.h5ad")
print("\n\tSaved the new adata object to: ", f"{save_path}{cell_type}.h5ad\n
```

# Print list of successfully processed cell types
print(cell\_list)
del mf\_adata\_obs

<class 'pandas.core.frame.DataFrame'>

Working on cell type: follicle cell

number of cells: 25251

Min number of genes expressed : 226 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 5826

Sufficient cells in each age group to proceed with analysis

Working on cell type: adult fat body\_body

number of cells: 31311

Min number of genes expressed : 224 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 2703

Sufficient cells in each age group to proceed with analysis

Working on cell type: adult hindgut

number of cells: 683

Min number of genes expressed : 286
Sufficient cells to proceed with analysis
Minimum number of cells in an age group: 146
Sufficient cells in each age group to proceed with analysis

Working on cell type: adult oenocyte

number of cells: 5925

Min number of genes expressed : 233
Sufficient cells to proceed with analysis
Minimum number of cells in an age group: 1081

Sufficient cells in each age group to proceed with analysis

Working on cell type: hemocyte\_body

number of cells: 2962

Min number of genes expressed : 213 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 560

Sufficient cells in each age group to proceed with analysis

Working on cell type: adult tracheal cell

number of cells: 6939

Min number of genes expressed : 207 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 1154

Sufficient cells in each age group to proceed with analysis

Working on cell type: crop

number of cells: 6226

Min number of genes expressed : 261
Sufficient cells to proceed with analysis
Minimum number of cells in an age group: 1051

Sufficient cells in each age group to proceed with analysis

Working on cell type: adult ventral nervous system

number of cells: 22172

Min number of genes expressed : 271 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 3454

Sufficient cells in each age group to proceed with analysis

Working on cell type: enteroendocrine cell

number of cells: 529

Min number of genes expressed : 268 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 75

Not enough cells in an age group to proceed with analysis

Working on cell type: germline cell

number of cells: 3824

Min number of genes expressed : 208
Sufficient cells to proceed with analysis
Minimum number of cells in an age group: 435
Sufficient cells in each age group to proceed with analysis

Working on cell type: enterocyte of posterior adult midgut epithelium

number of cells: 751

Min number of genes expressed : 263 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 40

Not enough cells in an age group to proceed with analysis

Working on cell type: cardia (1)

number of cells: 1062

Min number of genes expressed : 298 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 42

Not enough cells in an age group to proceed with analysis

Working on cell type: antimicrobial peptide-producing cell

number of cells: 104

Min number of genes expressed : 390 Not enough cells to proceed with analysis

Working on cell type: female reproductive system

number of cells: 1219

Min number of genes expressed : 287 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 256

Sufficient cells in each age group to proceed with analysis

Working on cell type: scolopidial neuron

number of cells: 1295

Min number of genes expressed : 278 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 211

Sufficient cells in each age group to proceed with analysis

Working on cell type: adult salivary gland

number of cells: 583

Min number of genes expressed : 280 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 52

Not enough cells in an age group to proceed with analysis

Working on cell type: intestinal stem cell

number of cells: 2132

Min number of genes expressed : 282 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 254

Sufficient cells in each age group to proceed with analysis

Working on cell type: adult peripheral nervous system

number of cells: 5889

Min number of genes expressed : 255 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 737

Sufficient cells in each age group to proceed with analysis

Working on cell type: mechanosensory neuron of haltere

number of cells: 635

Min number of genes expressed : 259 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 136

Sufficient cells in each age group to proceed with analysis

Working on cell type: epithelial cell\_body

number of cells: 42978

Min number of genes expressed : 211 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 5034

Sufficient cells in each age group to proceed with analysis

Working on cell type: escort cell

number of cells: 756

Min number of genes expressed : 304 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 99

Not enough cells in an age group to proceed with analysis

Working on cell type: enterocyte of anterior adult midgut epithelium

number of cells: 182

Min number of genes expressed : 281 Not enough cells to proceed with analysis

Working on cell type: midgut large flat cell

number of cells: 73

Min number of genes expressed : 525 Not enough cells to proceed with analysis

Working on cell type: eo support cell

number of cells: 2449

Min number of genes expressed : 268
Sufficient cells to proceed with analysis
Minimum number of cells in an age group: 407
Sufficient cells in each age group to proceed with analysis

Working on cell type: pheromone-sensing neuron

number of cells: 672

Min number of genes expressed : 303 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 101

Sufficient cells in each age group to proceed with analysis

Working on cell type: polar follicle cell

number of cells: 304

Min number of genes expressed : 318 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 48

Not enough cells in an age group to proceed with analysis

Working on cell type: enteroblast

number of cells: 2404

Min number of genes expressed : 270 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 247

Sufficient cells in each age group to proceed with analysis

Working on cell type: oviduct

number of cells: 1517

Min number of genes expressed : 256 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 257

Sufficient cells in each age group to proceed with analysis

Working on cell type: muscle cell

number of cells: 53895

Min number of genes expressed : 201 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 5675

Sufficient cells in each age group to proceed with analysis

Working on cell type: copper cell

number of cells: 149

Min number of genes expressed : 265 Not enough cells to proceed with analysis

Working on cell type: enterocyte-like

number of cells: 259

Min number of genes expressed : 301 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 38

Not enough cells in an age group to proceed with analysis

Working on cell type: follicle stem cell and prefollicle cell

number of cells: 430

Min number of genes expressed : 278 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 5

Not enough cells in an age group to proceed with analysis

Working on cell type: leg muscle motor neuron

number of cells: 355

Min number of genes expressed : 384 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 64

Not enough cells in an age group to proceed with analysis

Working on cell type: adult midgut-hindgut hybrid zone

number of cells: 576

Min number of genes expressed : 279 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 51

Not enough cells in an age group to proceed with analysis

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Working on cell type: adult midgut enterocyte
number of cells: 97
Min number of genes expressed: 367
Not enough cells to proceed with analysis
Working on cell type: gustatory receptor neuron
number of cells: 695
Min number of genes expressed: 298
Sufficient cells to proceed with analysis
Minimum number of cells in an age group: 100
Sufficient cells in each age group to proceed with analysis
Working on cell type: adult Malpighian tubule principal cell of lower segment
number of cells: 50
Min number of genes expressed: 317
Not enough cells to proceed with analysis
Working on cell type: cardia (2)
number of cells: 60
Min number of genes expressed: 332
Not enough cells to proceed with analysis
Working on cell type: adult Malpighian tubule principal cell
number of cells: 47
Min number of genes expressed: 238
Not enough cells to proceed with analysis
Working on cell type: young germ cell
number of cells: 224
Min number of genes expressed: 216
Sufficient cells to proceed with analysis
Minimum number of cells in an age group: 24
Not enough cells in an age group to proceed with analysis
Working on cell type: 16-cell germline cyst in germarium region 2a and 2b
number of cells: 532
Min number of genes expressed: 366
Sufficient cells to proceed with analysis
Minimum number of cells in an age group: 82
Not enough cells in an age group to proceed with analysis
Working on cell type: adult Malpighian tubule principal cell of lower ureter
number of cells: 35
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file:///D:/projects/ageing\_flies/Scripts/afca\_analysis/preprocessing/afca\_analysis\_dgea\_set\_data\_prep\_280425.html

Min number of genes expressed: 582

Not enough cells to proceed with analysis

Working on cell type: stalk follicle cell

number of cells: 293

Min number of genes expressed : 276 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 33

Not enough cells in an age group to proceed with analysis

Working on cell type: multidendritic neuron

number of cells: 210

Min number of genes expressed : 263 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 27

Not enough cells in an age group to proceed with analysis

Working on cell type: posterior midgut\*

number of cells: 114

Min number of genes expressed : 343 Not enough cells to proceed with analysis

Working on cell type: prefollicle cell-stalk follicle cell

number of cells: 0

Min number of genes expressed : nan Not enough cells to proceed with analysis

Working on cell type: epidermal cell that specialized in antimicrobial response

number of cells: 91

Min number of genes expressed : 268
Not enough cells to proceed with analysis

Working on cell type: indirect flight muscle

number of cells: 17625

Min number of genes expressed : 211 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 773

Sufficient cells in each age group to proceed with analysis

Working on cell type: cell body glial cell

number of cells: 2306

Min number of genes expressed : 223 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 357

Sufficient cells in each age group to proceed with analysis

Working on cell type: visceral muscle of the midgut

number of cells: 1253

Min number of genes expressed : 275 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 227

Sufficient cells in each age group to proceed with analysis

Working on cell type: adult alary muscle

number of cells: 2706

Min number of genes expressed : 226 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 362

Sufficient cells in each age group to proceed with analysis

Working on cell type: visceral muscle of the crop

number of cells: 760

Min number of genes expressed : 274 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 67

Not enough cells in an age group to proceed with analysis

Working on cell type: adult glial cell

number of cells: 2153

Min number of genes expressed: 252 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 282

Sufficient cells in each age group to proceed with analysis

Working on cell type: cardiomyocyte, working adult heart muscle (non-ostia)

number of cells: 34

Min number of genes expressed : 465 Not enough cells to proceed with analysis

Working on cell type: principal cell\*

number of cells: 121

Min number of genes expressed : 223 Not enough cells to proceed with analysis

Working on cell type: adult heart ventral longitudinal muscle

number of cells: 112

Min number of genes expressed : 280 Not enough cells to proceed with analysis

Working on cell type: adult differentiating enterocyte

number of cells: 72

Min number of genes expressed : 460 Not enough cells to proceed with analysis

Working on cell type: perineurial glial sheath

number of cells: 2181

Min number of genes expressed : 260 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 334

Sufficient cells in each age group to proceed with analysis

Working on cell type: subperineurial glial cell\_body

number of cells: 1431

Min number of genes expressed : 280 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 279

Sufficient cells in each age group to proceed with analysis

Working on cell type: adult Malpighian tubule principal cell of initial segment

number of cells: 70

Min number of genes expressed : 295 Not enough cells to proceed with analysis

Working on cell type: CNS surface associated glial cell

number of cells: 208

Min number of genes expressed : 271 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 31

Not enough cells in an age group to proceed with analysis

Working on cell type: adult reticular neuropil associated glial cell\_body

number of cells: 521

Min number of genes expressed : 255 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 29

Not enough cells in an age group to proceed with analysis

Working on cell type: adult Malpighian tubule stellate cell of main segment

number of cells: 10

Min number of genes expressed : 675 Not enough cells to proceed with analysis

Working on cell type: seminal vesicle & testis epithelia

number of cells: 635

Min number of genes expressed : 253 Sufficient cells to proceed with analysis Minimum number of cells in an age group: 121 Sufficient cells in each age group to proceed with analysis

Working on cell type: ejaculatory bulb

number of cells: 1401

Min number of genes expressed : 285
Sufficient cells to proceed with analysis
Minimum number of cells in an age group: 125

Sufficient cells in each age group to proceed with analysis

Working on cell type: ejaculatory bulb epithelium

number of cells: 549

Min number of genes expressed : 334
Sufficient cells to proceed with analysis
Minimum number of cells in an age group: 56

Not enough cells in an age group to proceed with analysis

Working on cell type: anterior ejaculatory duct

number of cells: 189

Min number of genes expressed : 280 Not enough cells to proceed with analysis

Working on cell type: male accessory gland main cell

number of cells: 2015

Min number of genes expressed : 265
Sufficient cells to proceed with analysis
Minimum number of cells in an age group: 225
Sufficient cells in each age group to proceed with

Sufficient cells in each age group to proceed with analysis

Working on cell type: spermatid

number of cells: 131

Min number of genes expressed : 203 Not enough cells to proceed with analysis

Working on cell type: cyst cell

number of cells: 201

Min number of genes expressed: 207
Sufficient cells to proceed with analysis
Minimum number of cells in an age group: 26

Not enough cells in an age group to proceed with analysis

Working on cell type: male accessory gland secondary cell

number of cells: 20

Min number of genes expressed : 336 Not enough cells to proceed with analysis Working on cell type: spermatocyte

number of cells: 90

Min number of genes expressed : 224

Not enough cells to proceed with analysis

['follicle cell', 'adult fat body\_body', 'adult hindgut', 'adult oenocyte', 'hemo cyte\_body', 'adult tracheal cell', 'crop', 'adult ventral nervous system', 'germl ine cell', 'female reproductive system', 'scolopidial neuron', 'intestinal stem cell', 'adult peripheral nervous system', 'mechanosensory neuron of haltere', 'epi thelial cell\_body', 'eo support cell', 'pheromone-sensing neuron', 'enteroblast', 'oviduct', 'muscle cell', 'gustatory receptor neuron', 'indirect flight muscle', 'cell body glial cell', 'visceral muscle of the midgut', 'adult alary muscle', 'adult glial cell', 'perineurial glial sheath', 'subperineurial glial cell\_body', 'seminal vesicle & testis epithelia', 'ejaculatory bulb', 'male accessory gland main cell']