scRNAseq analysis

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import numpy as np  
import pandas as pd  
import scanpy as sc  
import scipy  
import os  
import scipy.io as sio

# Adjusting scanpy default settings

Scanpy allows you to customize various aspects of the default package behavior.

sc.settings.verbosity = 1 # verbosity: errors (0), warnings (1), info (2), hints (3)  
sc.settings.set\_figure\_params(dpi=100, fontsize=10, dpi\_save=300, figsize=(5,4), format='png')  
sc.settings.figdir = 'Z:/ResearchHome/Groups/sapkogrp/projects/RNAseq/common/scRNAseq\_Paul\_cardiomyopathy/newvolume/analysis/combined\_figures/'

# Reading in data

After reading in the data we’ll perform basic filtering on our expression matrix to remove low-quality cells and uninformative genes. The parameter “min\_genes” will keep cells that have at least 300 genes, and similarly, “min\_cells” will keep genes that are expressed in at least 5 cells.