## 1. Non-normalized UMI counts matrices

Cellranger Filtered .h5 Seurat Objects



or



#### 2. Sample information: "sample\_metadata.csv"

Sample	Condition	Code
Patient1	Control	Control_1
Patient2	Control	Control_2
Patient3	DrugA	DrugA_1
Patient4	DrugA	DrugA_2
Patient5	DrugB	DrugB_1
Patient6	DrugB	DrugB_2

### 3. Comparison information: "comps.csv"



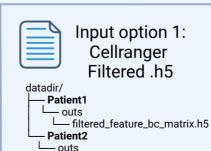
### 4. Optional: Label transfer references

SCT-normalized Seurat Objects



#### Harmonizing input gene expression matrices with sample metadata

# Sample | Condition | Code Patient1 | Control | Control\_1 Patient2 | Drug | Drug\_1 Example Comps C1 | C2 Drug | Control



filtered\_feature\_bc\_matrix.h5



Input option 2: Seurat Objects

datadir/
Patient1.rds
Patient2.rds