**Applicant**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Name | |  | Date | | | |  |
| Email |  | | UW Department |  | | | |
| ID |  | | New  Extension | |  |  | |

**Project overview**

Brief 3-4 sentences detailing the project, data types, and goals.

**Data**

List data types and access instructions

**Research questions**

* Provide 1 or more specific questions to be addressed by this project

**Deliverables (may change upon PI request, template contains common outputs)**

1. Data cleaning and quality control
   1. Report: Data processing, normalization, and scaling following the Seurat pipeline
2. Definition of cell types
   1. Report: Clustering, biomarker identification, and annotation of cells
   2. Table(s): Cell identity to clusters
   3. Table(s): Gene association to clusters including log fold change and p-values
   4. Tables(s): Annotation of clusters to cell types based on marker genes
3. Differential gene expression (DEG) analysis
   1. Report: Comparison of models to determine a best fit model including simple linear and linear mixed effects models with co-variates as appropriate
   2. Table(s): Estimates, fit, and significance of best fit model(s)
   3. Table(s): List of significant DEGs variables of interest
4. Attendance at monthly research group meetings throughout project. Present associated results to group as needed.
5. Limited continued work for manuscript preparation included. Additional analyses and/or substantial changes for publication to be assessed at such a time as they are needed.

**Authorship**

It is expected that INSERT BIOINFORMATICIAN HERE will be co-author(s) on publications associated with this work.

**Budget**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Month** | **Objective** | **Personnel** | **% FTE** | **Salary** | **Benefits** | **Total** |
|  |  |  |  |  |  |  |
|  |  |  |  |  |  | **TOTAL** |