Custom Module: Export

Description: Export all files associated with current study: Seurat, TileDB array, and/or raw files.

For booleans: rawFiles, tiledbArray, & SeuratObject determine what type of data is exported.

* exportFOVImages, spotFiles, FullSeuratObject, & transcripts determine what is included in the data type export.
* To export spotFiles, rawFiles & spotFiles MUST be checked.

Setup:

|  |  |  |  |
| --- | --- | --- | --- |
| R version | CPU cores | RAM (GB) | Max run (h) |
| Any | 16 | 128+ | 4+ |

\* RAM and Max run time listed above are suggested minimums. Values may be increased (note that increasing RAM or Max run time may increase costs). If the module exceeds either value, it will immediately fail.

Variables:

Name must be spelled exactly as shown for script to work.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Type | Name | Display name | Range | Default | Required |
| STRING | studyName | Output Folder Name | 1-100 |  | Yes |
| STRING | outPath | Destination S3 file path | 5-300 |  | Yes |
| PRIVATE | access\_key | Destination AWS access key | 16-128 |  | Yes |
| PRIVATE | secret\_key | Destination AWS secret key | 1-300 |  | Yes |
| STRING | s3Region | Destination AWS region | 8-16 |  | Yes |
| PRIVATE | session\_token | Destination AWS session token, if configured | 1-1200 |  | No |
| BOOL | SeuratObject | Export a Seurat Object | 0-1 | 1 | No |
| BOOL | FullSeuratObject | Seurat object contains all previous module output | 0-1 | 1 | No |
| BOOL | transcripts | Export Seurat contains transcript coordinates (large data) | 0-1 | 1 | No |
| BOOL | tiledbArray | Export TileDB array | 0-1 | 1 | No |
| BOOL | rawFiles | Export Raw Files | 0-1 | 1 | No |
| BOOL | exportFOVImages | Export all FOV Images (large data) | 0-1 | 1 | No |
| BOOL | spotFiles | Export spot files to redo Target Decoding (large data) | 0-1 | 1 | No |

In AtoMx™ v1.3.2, PRIVATE parameters have been introduced. PRIVATE parameters are protected string variables and will not be displayed in the user interface (UI) or logged in any system logs.

If you do not see PRIVATE as a parameter type, it indicates that your AtoMx version has not yet been upgraded to v1.3.2. For older releases where PRIVATE parameters are unavailable as an option, please select STRING instead.

Packages: None

Outputs: 3 folders in user’s S3 bucket

1. TileDB array
2. Seurat RDS object
3. Raw files

Raw file structure shown on next page.

### RNA

Flowcell Folder/  
      Logs/  
              SpatialProfiling\_[sequence\_name].fovs  
                      - **FOV Coordinates for study, slide number matches SlideNum in next folder**  
      [sequence\_name]\_S[slot]/  
              plex\_[processing\_id].csv  
                      - **Target probes metadata**  
              CellStatsDir/  
                      CellComposite/  
                              CellComposite\_FOV[FOV].jpg (in the process of removing from pipeline, images might be blank)  
                                      - **Composite Colored Image for each FOV**   
                      CellOverlay/  
                              CellOverlay\_[FOV].jpg  
                                      - **B&W image with cell segmentation overlays for each FOV**  
                      FOV[FOV]/  
                              CellLabels\_F[FOV].TIF  
                                      - **cell segmentation labels**  
                                      - **pixel intensity values correspond with the unique cell\_id**  
                              CompartmentLabels\_F[FOV].TIF  
                                      - **cell subcellular compartment labels**  
                                      - **pixel intensity values correspond with the identified compartment label**  
                                      - **Nuclear = 1, Membrane = 2, Cytoplasmic = 3**  
                              [run\_name]\_[sequence\_name]\_S[slot]\_Cell\_Stats\_F[FOV].csv  
                                      - **cell info from image like area, centerX,Y coordinates and fluorescence values**  
                      Morphology2D/  
                              [sequence\_name]\_S[slot]\_C[cycle]\_P[pool]\_N[spot]\_F[FOV].TIF  
                                      - **OME-TIFF of fluorescence values**  
                      Morphology3D/ *(only for v1.1 studies)*  
                              FOV[FOV]  
                                      [sequence\_name]\_S[slot]\_C[cycle]\_P[pool]\_N[spot]\_F[FOV]\_Z[z].TIF  
                                              - **OME-TIFF of fluorescence values at each Z plane**  
                      RnD/  
                              Run\_[GUID]\_[sequence\_name]\_S[slot]\_Summary\_F[FOV].csv  
                                      - **FOV summary statistics**  
              RunSummary/  
                              Run\_[GUID]\_[date]\_S[slot]\_[instrument\_name]\_ExptConfig.txt  
                                      - **Instrument Config - includes the pixel to nm ratio**  
              AnalysisResults/[processing\_id]/  
                      FOV[FOV]/  
                              FOV[FOV]\_Analysis\_Summary.txt  
                                      - **Limits of Detection**  
                              Run\_[GUID]\_FOV[FOV]\_\_complete\_code\_cell\_target\_call\_coord.csv  
                                      - **Target coordinates and counts per cell**  
                                      - **other coord files are intermediate files**

### Protein

Flowcell Folder/  
      Logs/  
              SpatialProfiling\_[sequence\_name].fovs  
                      - **FOV Coordinates for study, slide number matches SlideNum in next folder**  
      [Flowcell]\_[SlideNum]/  
              plex\_[processing\_id].csv  
                      - **Target probes metadata**  
              CellStatsDir/  
                      CellComposite/  
                              CellComposite\_FOV[FOV].jpg  
                                      - **Composite Colored Image for each FOV**   
                      CellOverlay/  
                              CellOverlay\_[FOV].jpg  
                                      - **B&W image with cell segmentation overlays for each FOV**  
                      FOV[FOV]/  
                              CellLabels\_F[FOV].TIF  
                                      - **cell segmentation labels**  
                                      - **pixel intensity values correspond with the unique cell\_id**  
                              CompartmentLabels\_F[FOV].TIF  
                                      - **cell subcellular compartment labels**  
                                      - **pixel intensity values correspond with the identified compartment label**  
                                      - **Nuclear = 1, Membrane = 2, Cytoplasmic = 3**  
                              [run\_name]\_[sequence\_name]\_S[slot]\_Cell\_Stats\_F[FOV].csv  
                                      - **cell info from image like area, centerX,Y coordinates and fluorescence values**  
                      Morphology2D/  
                              [sequence\_name]\_S[slot]\_C[cycle]\_P[pool]\_N[spot]\_F[FOV].TIF  
                                      - **OME-TIFF of fluorescence values**  
                      Morphology3D/ *(only for v1.1 studies)*  
                              FOV[FOV]  
                                      [sequence\_name]\_S[slot]\_C[cycle]\_P[pool]\_N[spot]\_F[FOV]\_Z[z].TIF  
                                              - **OME-TIFF of fluorescence values at each Z plane**  
                      RnD/  
                              Run\_[GUID]\_[sequence\_name]\_S[slot]\_Summary\_F[FOV].csv  
                                      - **FOV summary statistics**  
              RunSummary/  
                              Run\_[GUID]\_[date]\_S[slot]\_[instrument\_name]\_ExptConfig.txt  
                                      - **Instrument Config - includes the pixel to nm ratio**  
              ProteinDir/  
                      FOV[FOV]/  
                              - **Files are used to generate ProteinImages, ProteinMasks, & Protein Stats in AnalysisResults/ folder**  
              AnalysisResults/[processing\_id]/  
                      FOV[FOV]/  
                              PerCellStats/  
                                      [sequence\_name]\_S[slot]*C001\_F[FOV]*[probe\_id]\_perCell\_1ChStats.csv  
                                              - **Counts per probe\_id per cell**  
                                              - **1 file per protein in panel**  
                                              - **Avg Fluorescence is considered count**  
                              ProteinImages/  
                                      [sequence\_name]\_S[slot]*C001\_F[FOV]*[probe\_id].TIF  
                                              - **OME-TIFF with decoded fluorescence intensity of protein target across FOV**  
                              ProteinMasks/  
                                      [sequence\_name]\_S[slot]*C001\_F[FOV]*[probe\_id]\_Mask.TIF  
                                              - **OME-TIFF displaying area of target**  
                                              - **255 = present, 0 = absent**