```
(***Input identifying information***)

projType = ToString[
    Evaluate[Input["Input the projection type (i.e V1toPM, LMtoPM, or LPtoPM)"]]];

mouse = ToString[Evaluate[Input["Input the mouse identity (e.g. Mouse123)"]]];

firstSection = ToString[
    Evaluate[Input["Input the number of the first histological section in the series"]]];

lastSection = ToString[
    Evaluate[Input["Input the number of the last histological section in the series"]]];

sectRange = Range[firstSection, lastSection];

(*******************************************)
```

```
In[ ]:= laminarFluorPerSection = Table[Join[Drop[Flatten[
            Import[StringJoin["S:/Imaging/Garrett/BCMM_EpifluorConfocScope/Other/
                LaminarAxonFluorescenceHistology/",
              projType, "/", mouse, "/LaminarFluorData/", mouse, "_Section",
            ToString[sectRange[[n]]], "_Upper.xlsx"]], 1], 2],
        Partition[Riffle[(Drop[Flatten[Import[StringJoin[
                    "S:/Imaging/Garrett/BCMM_EpifluorConfocScope/Other/
                      LaminarAxonFluorescenceHistology/",
                  projType, "/", mouse, "/LaminarFluorData/", mouse,
                  "_Section", ToString[sectRange[[n]]], "_Lower.xlsx"]], 1],
              2][[All, 1]] + Last[Drop[Flatten[Import[StringJoin[
                    "S:/Imaging/Garrett/BCMM_EpifluorConfocScope/Other/
                      LaminarAxonFluorescenceHistology/",
                  projType, "/", mouse, "/LaminarFluorData/", mouse, "_Section",
                  ToString[sectRange[[n]]], "_Upper.xlsx"]], 1],
                2][[All, 1]]]), (Drop[Flatten[Import[StringJoin[
                  "S:/Imaging/Garrett/BCMM_EpifluorConfocScope/Other/
                    LaminarAxonFluorescenceHistology/",
                projType, "/", mouse, "/LaminarFluorData/", mouse,
                "_Section", ToString[sectRange[[n]]], "_Lower.xlsx"]], 1],
              2][[All, 2]])], 2]], {n, 1, Length[sectRange]}];
```

```
In[ ]:= resol = (Last[laminarFluorPerSection[[1]][[All, 1]]] -
        First[laminarFluorPerSection[[1]][[All, 1]]]) /
      Length[laminarFluorPerSection[[1]][[All, 1]]];
```

```
In[ ]:= (***Median-smooth at 10 um***)
```

```
In[ ]:= window = Round[10 / resol];
```

```
In[ ]:= medianSmoothedPerSection =
    Table[Partition[Riffle[(laminarFluorPerSection[[n]])[[All, 1]],
        MovingMap[Quantile[#, 1 / 2] &, (laminarFluorPerSection[[n]])[[All, 2]],
         window, "Reflected"]], 2], {n, 1, Length[sectRange]}];
```

```
(***Check that all sections go up to at least 800 um***)
```

```
In[ ]:= Manipulate[ListLinePlot[medianSmoothedPerSection[[n]], PlotRange → All],
        {n, 1, Length[sectRange], 1}]
```

```
In[ ]:= Table[Last[medianSmoothedPerSection[[n]][[All, 1]]], {n, 1, Length[sectRange]}]
```

```
In[ ]:= (****Truncate all lists at 800 um***)
```

```
In[ ]:= truncPoint = Round[800 / resol];
```

```
In[ ]:= medianSmoothedPerSectionTrunc =
        Table[Take[medianSmoothedPerSection[[n]], truncPoint], {n, 1, Length[sectRange]}];
```

```
In[ ]:= (***Normalize all lists to max fluorescence***)
```

```
In[ ]:= maxFluor = Max[Flatten[
        Table[medianSmoothedPerSectionTrunc[[n]][[All, 2]], {n, 1, Length[sectRange]}]]];
```

```
In[ ]:= medianSmoothedPerSectionTruncNorm =
        Table[Partition[Riffle[medianSmoothedPerSectionTrunc[[n]][[All, 1]],
          medianSmoothedPerSectionTrunc[[n]][[All, 2]] / maxFluor],
         2], {n, 1, Length[sectRange]}];
```

```
In[ ]:= (***Calculate the mean laminar fluorescence profile for this animal and export data***)
```

```
In[ ]:= meanFluorProfile =
        Mean[Table[medianSmoothedPerSectionTruncNorm[[n]], {n, 1, Length[sectRange]}]];

        (***Export laminar profile of the mean
         normalized axonal fluorescence from this animal***)
```

```
In[ ]:= Export[StringJoin[
        "S:/Imaging/Garrett/BCMM_EpifluorConfocScope/Other/LaminarAxonFluorescenceHistology/"
         , projType, "/", mouse, "/", mouse, "_meanLaminarFluor.txt"],
        meanFluorProfile];
```