**Deep Learning qBRM Analyzer — MATLAB App Documentation**

**Purpose**

This MATLAB App is designed to perform and visualize deep learning-based analysis of myelin pathology using quantitative Birefringence Microscopy (qBRM) images. It supports:

* Object detection using a trained network
* Multi-channel image augmentation
* Stitched image reconstruction
* ROI-based quantification of myelin damage
* Visualization and export of results

**App Flow Overview**

**1. Load Deep Learning Model (Main Tab)**

* **Browse** button allows user to load a .mat file containing training\_struct.detector.
* Updates:
  + Model path field
  + Network input size (auto-filled)
  + System log entry

**2. Select Folders for Analysis (Main Tab)**

* **Select Folders** prompts user to choose a parent directory.
* Recursively finds subfolders with \_qBRM\_ (customizable via input field).
* Extracts:
  + all\_folders: folder paths per sample
  + sampleNames: formatted as MonkeyID\_SampleID
* ListBoxes display folders and sample names.

**3. Run Deep Learning Analysis**

* **Run Deep Learning** button initiates processing:
  + For each sample folder:
    - Runs solve\_widefield\_qBRM\_folder() if needed
    - Loads RGB\_norm images
    - Applies object detection on RGB, BRG, GBR channel orders
    - Applies NMS to merge detections
    - Saves bounding box annotations
    - Stitches images (RGB and retardance)
    - Applies spatial correction to bounding boxes
    - Saves stitched images and combined annotations
* **Stop Analysis** button allows safe early exit
* Progress is shown in the progress bar and system log

**Analysis Tab Functions**

**4. Select Processed Folder**

* **Select Folders** button loads a folder containing \_Fused\_RGB.tif, \_retardance.tif, and \_annotations\_128.mat files.
* Extracts sample names into the filenameStructure\_2 list.

**5. Run ROI-Based Defect Quantification**

* **Run Analysis** loops over samples in filenameStructure\_2:
  + Loads image, retardance, and annotation files
  + Computes defect density and mean retardance
  + Optionally saves .mat file per sample
  + Compiles results into a summary .xlsx file

**6. Visualize Myelin Defects**

* **Visualize Myelin Defects** button:
  + Requires a sample selected in the list
  + Displays either Fused\_RGB.tif or retardance.tif image
  + Overlays bounding boxes from the annotation file

**Key Components**

| **Feature** | **UI Component** | **Notes** |
| --- | --- | --- |
| Model loader | DeeplearningmodelpathEditField | Set when loading .mat model file |
| Folder selection | SelectFoldersButton | Used in both Main and Analysis tabs |
| Sample name display | filenameStructure, \_2 | Populated from folder/file name parsing |
| Cancel running analysis | StopAnalysisButton | Acts as a soft interrupt flag |
| System feedback | SystemLogTextArea | Shows recent logs (up to 9 entries) |
| Progress bar | ProgressAxes | Visually tracks current task progress |

**User Workflow Summary**

1. **Main Tab**:
   * Load trained detector
   * Select folders matching qBRM format
   * Run deep learning analysis
2. **Analysis Tab**:
   * Select folder containing processed .tif and .mat files
   * Run analysis to quantify myelin damage
   * Visualize results and export summary

**Advanced Features**

* Multi-channel object detection (RGB, BRG, GBR)
* Grid-aware image stitching with overlap correction
* Real-time logging and UI responsiveness
* Defect quantification tied to myelin structure metrics

**Future Improvements**

* Add export button for .mat and .xlsx
* Implement full GUI-based annotation review
* Allow custom channel combinations for detection
* Support drag-and-drop folder selection
* Add Help or Documentation tab with this guide