**Power analysis:**

**Segmentation:**

1. qlm573/melanoma-identification/images/scripts/img\_size.py

* Function: resize images to uniform size
* Input:
  + qlm573/melanoma-identification/images/ISIC-database /\*.JPG
* Output:
  + qlm573/melanoma-identification/images/resized/\*.JPG

1. qlm573/melanoma-identification/computer-vision/scripts/segmentation/image\_segmentation.py

* Function: segment resized images and save masks
* Input:
  + qlm573/melanoma-identification/images/resized/\*.JPG
* Output:
  + qlm573/melanoma-identification/images/segmented/masks/\*.png

**Metadata:**

1. qlm573/melanoma-identification/computer-vision/scripts/image\_selection/melanoma\_ids.py

* Function: save binary malignancy data
* Input:
  + qlm573/melanoma-identification/images/metadata/metadata.csv
* Output:
  + qlm573/melanoma-identification/computer-vision/scripts/image\_selection/melanoma\_ids.txt

1. qlm573/melanoma-identification/images/scripts/check-duplicates.sh

* Function: compare ISIC images for duplicates and return list of duplicated images.
* Input:
  + qlm573/melanoma-identification/images/ISIC-database/\*.JPG
* Output:
  + qlm573/melanoma-identification/images/duplicates/rm-list.txt
  + qlm573/melanoma-identification/images/duplicates/duplicate.txt

**Computer Vision Assessments:**

1. qlm573/melanoma-identification/computer-vision/scripts/feature-analysis/colour\_continuous.py

* Function: Generate and save color variance measures
* Input:
  + qlm573/melanoma-identification/images/resized/\*.JPG
  + qlm573/melanoma-identification/images/segmented/masks /\*.png
* Output:
  + qlm573/melanoma-identification/computer-vision/scripts/feature-analysis/colours\_continuous.txt

1. qlm573/melanoma-identification/computer-vision/scripts/feature-analysis/shape\_analysis.py

* Function: Generate and save shape measures – symmetry and border regularity
* Input:
  + qlm573/melanoma-identification/images/resized/\*.JPG
  + qlm573/melanoma-identification/images/segmented/masks /\*.png
* Output:
  + qlm573/melanoma-identification/computer-vision/scripts/feature-analysis/shape.txt

1. qlm573/melanoma-identification/feature-rating/cv-data/merge\_data.py

* Function: Merges the computer vision feature assessments and saves the combined file
* Input:
  + qlm573/melanoma-identification/feature-rating/cv-data/feature-rating-image-list.txt
  + qlm573/melanoma-identification/feature-rating/cv-data/malignant\_ids.txt
  + qlm573/melanoma-identification/feature-rating/cv-data/shape.txt
  + qlm573/melanoma-identification/feature-rating/cv-data/colour.txt
* Output:
  + qlm57/melanoma-identification/feature-rating/cv-data/cv-data.csv

**Experiment Images:**

1. qlm573/melanoma-identification/computer-vision/scripts/image\_selection/feature\_visualisations.py

* Function: select images for experiment
* Input:
  + qlm573/melanoma-identification/computer-vision/scripts/feature-analysis/shape.txt
  + qlm573/melanoma-identification/computer-vision/scripts/image\_selection/rm-list.txt
  + qlm573/melanoma-identification/computer-vision/scripts/image\_selection/malignant\_ids.txt
* Output:
  + qlm573/melanoma-identification/computer-vision/scripts/image\_selection/feature-rating-image-list.txt

1. qlm573/melanoma-identification/computer-vision/scripts/image\_selection/practice\_image\_selection.py

* Function: select images for experiment practice trials
* Input:
  + qlm573/melanoma-identification/computer-vision/scripts/image\_selection/feature-rating-image-list.txt
  + qlm573/melanoma-identification/computer-vision/scripts/image\_selection/malignant\_ids.txt
  + qlm573/melanoma-identification/computer-vision/scripts/feature-analysis/shape.txt
  + qlm573/melanoma-identification/computer-vision/scripts/feature-analysis/colours\_continuous.txt
* Output:
  + Print (*n*) images to console for you to painfully peruse.

**Human Judgments**

1. qlm573/melanoma-identification/feature-rating/scripts/read\_data.py

* Function: read individual experiment files and combine to save (i) raw response data, (ii) processed response data, and (iii) feature separated processed data
* Input:
  + qlm573/melanoma-identification/feature-rating/experiment/melanoma-2afc/data/\*.csv
* Output:
  + qlm573/melanoma-identification/feature-rating/btl-feature-data/data-raw.csv
  + qlm573/melanoma-identification/feature-rating/btl-feature-data/data-processed.csv
  + qlm573/melanoma-identification/feature-rating/btl-feature-data/btl-asymmetrycsv
  + qlm573/melanoma-identification/feature-rating/btl-feature-data/btl-border.csv
  + qlm573/melanoma-identification/feature-rating/btl-feature-data/btl-colour.csv

1. qlm573/melanoma-identification/feature-rating/scripts/applyBTL.py

* Function: Applies BTL algorithm (log regression) to the **processed** judgment data and saves the ‘abilities’ (r) as btl-scores-{feature}.csv
* Input:
  + qlm573/melanoma-identification/feature-rating/btl-feature-data/btl-asymmetry.csv
  + qlm573/melanoma-identification/feature-rating/btl-feature-data/btl--border.csv
  + qlm573/melanoma-identification/feature-rating/btl-feature-data/btl--colour.csv
* Output:
  + qlm573/melanoma-identification/feature-rating/btl-feature-data/btl-scores-symmetry.csv
  + qlm573/melanoma-identification/feature-rating/btl-feature-data/btl-scores-border.csv
  + qlm573/melanoma-identification/feature-rating/btl-feature-data/btl-scores-colour.csv

**Combine Human Judgments with Computer Vision**

1. qlm573/melanoma-identification/feature-rating/scripts/merge\_btl\_cv.py

* Function: merge the btl-score files with the already combined computer-vision scores and saves the merged data as
* Input:
  + qlm573/melanoma-identification/feature-rating/cv-data/cv-data.csv
  + qlm573/melanoma-identification/feature-rating/btl-feature-data/btl-scores-symmetry.csv
  + qlm573/melanoma-identification/feature-rating/btl-feature-data/btl-scores-border.csv
  + qlm573/melanoma-identification/feature-rating/btl-feature-data/btl-scores-colour.csv
* Output:
  + qlm573/melanoma-identification/feature-rating/btl-feature-data/btl-cv-data.csv