

# Extract trial-level bias metrics from eye-tracking/dot-probe data

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This provides documentation of the `bias.R` script, which calculates various trial-level metrics related to attention bias toward emotional vs. neutral stimuli. This script makes it possible to process multiple persons in parallel instead of one at a time. Note you will need the latest version of `itrak` from `github`.

## Expected Input Files

The script reads tab-separated `.txt` files that you will need to generate beforehand. Each file must correspond to the sample data for a single participant and contain each of the following columns:

- **RECORDING\_SESSION\_LABEL**
  - participant id associated with each file
- **SAMPLE\_INDEX**
  - consecutive integer sequence that restarts to 1 with each trial
- **SAMPLE\_MESSAGE**
  - contains the following strings which serve as event markers:
    - \* “FaceStimOnset”: marks the presentation of the face stimuli
    - \* “FaceStimOffset”: marks the presentation of the dot probe
    - \* “Ending Recording”: marks 500 ms following response to the dot probe
- **TIMESTAMP**
  - computer clock time in milliseconds
- **LEFT\_FIX\_INDEX**
  - fixation periods for the left eye are assigned integer values; saccades and blinks are assigned a “.” which is read in as a missing value
- **RIGHT\_FIX\_INDEX**
  - fixation periods for the right eye are assigned integer values; saccades and blinks are assigned a “.” which is read in as a missing value
- **LEFT\_INTEREST\_AREAS**
  - gaze direction of the left eye
    - \* “[ ]”: center of screen (neither face)
    - \* “[ 1 ]”: left face
    - \* “[ 2 ]”: right face
- **RIGHT\_INTEREST\_AREAS**
  - same as **LEFT\_INTEREST\_AREAS** but for the right eye
- **LFaceStim**
  - file name of the face presented on the left side
- **RFaceStim**
  - file name of the face presented on the right side
- **DotStim**
  - the dot probe and its location
    - \* “LeftO”
    - \* “LeftQ”
    - \* “RightO”
    - \* “RightQ”
- **ACC**

- Boolean value indicating accuracy of response
  - \* “0”: incorrect
  - \* “1”: correct

## Output Dictionary

For each file it reads, the script writes a trial-level `.csv` data file with the following columns:

- **id**
  - participant id associated with each file
- **trial**
  - trial number
- **left\_face**
  - file name for stimulus presented on the left side
- **right\_face**
  - file name for stimulus presented on the right side
- **emo\_valence**
  - valence of the emotional face (“Happy” or “Sad”)
- **dot\_location**
  - location of the dot probe (“Left” or “Right”)
- **emo\_location**
  - location of the emotional face (“Left” or “Right”)
- **congruent**
  - logical value indicating whether the location of the dot probe (`dot_location`) is congruent with the location of the emotional face (`emo_location`)
- **accurate**
  - logical value indicating whether dot-probe identification was accurate (`TRUE`) vs. inaccurate (`FALSE`)
- **RT**
  - reaction time in seconds; RTs for inaccurate trials and RT outliers ( $< 0.2$ ,  $> 1.5$  s, or more than 3 MADs from each participant’s median) have been changed to NAs
- **TLBS**
  - trial level bias score, using the weighted method from the `itrak` package
- **total\_fixation**
  - total seconds of fixation periods during which the eyes are fixated upon any point on the screen
- **emo\_fixation**
  - total seconds of fixation periods during which the eyes are fixated upon the emotional face
- **neu\_fixation**
  - total seconds of fixation periods during which the eyes are fixated upon the neutral face
- **initial\_bias**
  - index giving the initial direction toward which attention shifts after the faces are presented:
    - \* -1: away from the emotional face, toward the neutral face
    - \* 0: no shift in attention from the center of screen for the entire trial
    - \* 1: toward the emotional face, away from the neutral face
- **final\_bias**
  - index giving the final direction of gaze as the dot probe is presented:
    - \* -1: away from the emotional face, toward the neutral face
    - \* 0: toward the center of the screen, away from both faces
    - \* 1: toward the emotional face, away from the neutral face
- **total\_bias**
  - emotional - non-emotional fixations
    - \* the difference between fixations to the emotional face and fixations to the neutral face.
    - \* positive values indicate bias toward the emotional face; negative values indicate bias away from the emotional face; 0 indicates only fixations toward the center of screen for entire trial

Note that the units of RT bias are now in seconds instead of milliseconds. This is so that they resemble the scale of the dummy coding (-1, 0, 1) for initial and final bias.

## Lines of code you'll (occasionally) need to update

The first 6 lines of code are the only ones that you need to worry about changing, and only when you switch to a new project or new computer. Most of these lines specify the locations of where to read and write files.

1. **data\_path**: the full path to the `eye_tracking` folder in `MDL Projects/Projects/R33 ABM/Data` that contains 3 folders, the names of which are specified in the next 3 lines. Right now it specifies the path on my computer; you will need to change this so that it specifies the path on your computer.
2. **load\_folder**: the name of the folder that contains the files that you want processed. This is currently named “unprocessed\_reports”.
3. **archive\_folder**: the name of the folder where files in the `load_folder` should be moved once they have been processed. This is currently named “processed\_reports”. This supports a work flow in which you will place newly generated sample reports in the “unprocessed\_reports” folder, and the script will automatically move these files to the “processed\_reports” folder when it is done with each one. (If you have a bunch of files to process and want to monitor the script’s progress, you can open a Finder or Explorer window for each folder and watch the “unprocessed\_reports” folder empty and the “processed\_reports” folder fill up as the scripts run. It’s very satisfying!)
4. **save\_folder**: the name of the folder where the trial-level summary data should be written. This is currently named “tlbs”.
5. **n\_cores**: number of computer cores to be used for parallel processing. Right now it is set to 4, meaning 4 data files will be processed simultaneously. Note that this number should be set less than or equal to the number of available cores on your machine. This is only important if you are processing more than one file at the same time.
6. **n\_trial**: the expected number of trials. This is used as a “smoke alarm” to detect potential problems in the formatting of the data files. If the script ends up with a different number of trials than expected, it will throw an error.