

This document contains notes regarding the data from the following paper:

Keshvari S, Van den Berg R, Ma WJ (2013) **No evidence for an item limit in change detection** *PLoS Computational Biology* 9(2): e1002927. DOI: [10.1371/journal.pcbi.1002927](https://doi.org/10.1371/journal.pcbi.1002927)

The data was originally in a format that was difficult to understand, so it has been reformatted to be intuitive. The data for each experiment is stored in a cell, which each element being a struct that stores the data from a single subject. The struct has the following fields and datatypes, and each is a vector that has the data from all trials from a subject:

data.change

- *logical*, 1 if the trial had a change, 0 if no change

data.response

- *logical*, 1 if the subject responded change, 0 if no change

data.delta

- *double*, magnitude of change in radians, computed with `circ_dist()`

data.RT

- *double*, response time in milliseconds

data.setsize

- *double*, number of ellipses displayed in a trial

data.ort_first

- *double 2D array*, orientations (or colors) of the ellipses in radians in the first display on a trial, the elements in unused positions (because the array has 8 columns and set size varies from 2 to 8) are set to zero

data.ort_second

- *double 2D array*, orientations (or colors) of the ellipses in radians in the second display on a trial, the elements in unused positions are set to zero

The code to convert from the old data format to the new data format is called `convert_data()`, and the code to revert back to the old format (to avoid rewriting the analysis software) is called `revert_data()`. There should be no reason to use these functions, since they are already integrated with the code and saved data format. The original old-format data is saved in a subfolder of data called `old_data`.