Beads-task EEG preprocessing/analysis pipeline:

- Conversion to spm object
- Define channels (EEG + EOG)
- Look for bad channels – this is an important step and needs to be done for each subject before creating the montage. If a subject has a bad channel during recording, we need to specify it at the next step and exclude it from re-referencing.
- Create montage (EEG + vertical, horizontal EOG) & re-reference (average for now) – use modified montage.m function
- High pass filtering: cutoff 0.5 (or 0.1)
- Downsampling: 256Hz
- Low pass filtering: cutoff 30
- Epoching (with baseline correction) – use modified trialdef.m function
    - Probability: easy/diff
    - Choices: draw/urn
- Merging (concatenating) blocks
- Preparing – Channel coordinates for fiducials: will use the default spm Biosemi64 montage
- Artefact detection/removal
- **Evoked analysis (ERPs):**
    - Average epochs/trials
    - Compute Contrast conditions (use the average – contrast method)
        - Urn vs Draw [-1 1 -1 1]
        - Difficult vs Easy [1 1 -1 -1]
        - Interaction [-1 1 1 -1]
        - Only urns [0 1 0 1]
        - Only draws [1 0 1 0]
    - Convert to 3D images
    - Smooth 3D images
- 2nd level Mass Univariate analysis using the contrasts [urn vs draw, diff vs easy, interaction] and the entire peristimulus time [-500 800]
- Individual differences analysis:
    - 2nd-level Massive Univariate analysis – Use urn choices contrasts and array of number of draws as covariate
- Association of evoked responses and action values
    - Compute grand average (over subjects). Using the grand average file, select a specific time-range and sensors that show larger response to urn choices and draw choices
    - For each participant, crop the urn choice trials around the time-range and for sensors specified at the above step and extract the data from the meeg object as a new dataset.
    - Compute the difference between action values (dAQ) for drawing again and choosing urns
    - Linear Regression (draw-by draw/ 1st level/ within subjects) – using the diff in (dAQ) as regressor

    - Use the 1st level beta weights to model a 2nd level (one sample) t-test
    - Optional: draw-by-draw (epochs) correlation with dAQ → get one r value per participant → convert r values to z (Fisher's r-to-z transformation) and run (one sample t-test at group level (to test if overall r values differ from 0).
- **Time-Frequency Representation Analysis (TFRs):**
    - Wavelet estimation (factor 7) for power 1-55Hz – output is 2 files (phase and power)
    - Baseline rescaling (-500ms to -50ms) – only power file
    - Average epochs/trials:
        - Over beta range [13 to 30 Hz]
        - Over time using the entire peristimulus time
    - Traditional robust average of conditions
    - Compute Contrast conditions (use the average – contrast method)
        - Urn vs Draw [-1 1 -1 1]
        - Difficult vs Easy [1 1 -1 -1]
        - Interaction [-1 1 1 -1]
        - Only urns [0 1 0 1]
        - Only draws [1 0 1 0]
    - Convert to 3D images
    - Smooth 3D images
- 2nd level Mass Univariate analysis using the contrasts [urn vs draw, diff vs easy, interaction] and the entire peristimulus time [-500 800] and all frequencies
- Individual differences analysis:
    - 2nd-level Massive Univariate analysis – Use urn choices contrasts and number of draws as covariate
- Association of beta power and action values:
    - Average TFR-rescaled object over specific time and frequency range:
        - Compute grand average (over subjects). Using the grand average file, select a specific time-range, frequency (beta range) and sensors that show larger response to urn choices and draw choices
        - Average subject meeg object over frequency (beta range – slow [13-20Hz] and fast [21-30Hz])
        - Average subject meeg object over time selected using the GrandMean object
    - Compute the difference between action values (dAQ) for drawing again and choosing urns
    - Linear Regression (draw-by draw/ 1st level/ within subjects) with beta range data as dependent variable – using the diff in (dAQ) as regressor
    - Use the 1st level beta weights to model a 2nd level (one sample) t-test
    - Optional: draw-by-draw (epochs in beta range) correlation with dAQ → get one r value per participant → convert r values to z (Fisher's r-to-z transformation) and run (one sample t-test at group level (to test if overall r values differ from 0).