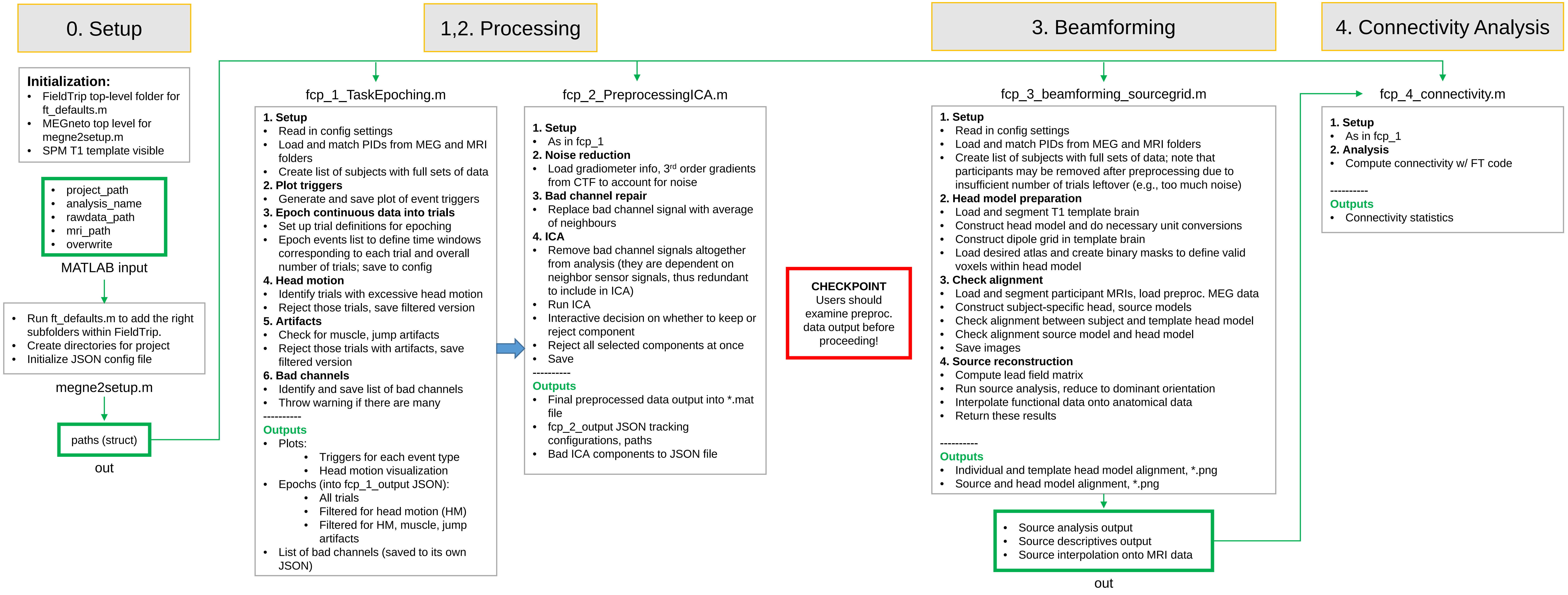

0. Setup

Initialization:
- FieldTrip top-level folder for ft_defaults.m
- MEGneto top level for megne2setup.m
- SPM T1 template visible

- project_path
- analysis_name
- rawdata_path
- mri_path
- overwrite

MATLAB input

- Run ft_defaults.m to add the right subfolders within FieldTrip.
- Create directories for project
- Initialize JSON config file

megne2setup.m

paths (struct)

out

1,2. Processing

fcp_1_TaskEpoching.m

1. Setup
- Read in config settings
- Load and match PIDs from MEG and MRI folders
- Create list of subjects with full sets of data

2. Plot triggers
- Generate and save plot of event triggers

3. Epoch continuous data into trials
- Set up trial definitions for epoching
- Epoch events list to define time windows corresponding to each trial and overall number of trials; save to config

4. Head motion
- Identify trials with excessive head motion
- Reject those trials, save filtered version

5. Artifacts
- Check for muscle, jump artifacts
- Reject those trials with artifacts, save filtered version

6. Bad channels
- Identify and save list of bad channels
- Throw warning if there are many

Outputs
- Plots:
  - Triggers for each event type
  - Head motion visualization
- Epochs (into fcp_1_output JSON):
  - All trials
  - Filtered for head motion (HM)
  - Filtered for HM, muscle, jump artifacts
- List of bad channels (saved to its own JSON)

fcp_2_PreprocessingICA.m

1. Setup
- As in fcp_1

2. Noise reduction
- Load gradiometer info, 3rd order gradients from CTF to account for noise

3. Bad channel repair
- Replace bad channel signal with average of neighbours

4. ICA
- Remove bad channel signals altogether from analysis (they are dependent on neighbor sensor signals, thus redundant to include in ICA)
- Run ICA
- Interactive decision on whether to keep or reject component
- Reject all selected components at once
- Save

Outputs
- Final preprocessed data output into *.mat file
- fcp_2_output JSON tracking configurations, paths
- Bad ICA components to JSON file

CHECKPOINT
Users should examine preproc. data output before proceeding!

3. Beamforming

fcp_3_beamforming_sourcegrid.m

1. Setup
- Read in config settings
- Load and match PIDs from MEG and MRI folders
- Create list of subjects with full sets of data; note that participants may be removed after preprocessing due to insufficient number of trials leftover (e.g., too much noise)

2. Head model preparation
- Load and segment T1 template brain
- Construct head model and do necessary unit conversions
- Construct dipole grid in template brain
- Load desired atlas and create binary masks to define valid voxels within head model

3. Check alignment
- Load and segment participant MRIs, load preproc. MEG data
- Construct subject-specific head, source models
- Check alignment between subject and template head model
- Check alignment source model and head model
- Save images

4. Source reconstruction
- Compute lead field matrix
- Run source analysis, reduce to dominant orientation
- Interpolate functional data onto anatomical data
- Return these results

Outputs
- Individual and template head model alignment, *.png
- Source and head model alignment, *.png

- Source analysis output
- Source descriptives output
- Source interpolation onto MRI data

out

4. Connectivity Analysis

fcp_4_connectivity.m

1. Setup
- As in fcp_1

2. Analysis
- Compute connectivity w/ FT code

Outputs
- Connectivity statistics

- ft_defaults
- path_generation
- save_to_json
- path_check

- load_config
- load_participants
- ds_pid_match
- write_match_if_not_empty
- ft_definetrial
- plotTriggers
- HeadMotionTool
- ft_artifact_muscle
- ft_artifact_jump
- ft_rejectartifact
- save_to_json
- detectBadChannels

- load_config
- load_participants
- ds_pid_match
- write_match_if_not_empty
- save_to_json