

Background

Dual regression (DR) (Beckmann et al. (2009). Neuroimage.) is the main strategy to model group-level brain networks (priors) back onto individual scans, but presents 2 important limitations:

1. group-level priors do not account for individual variability in artefact shapes and numbers
2. the linear regression (used for modeling) does conduct source decomposition through ICA

Hypothesis: Dual ICA, which addresses these two issues is more robust to data quality biases than DR.

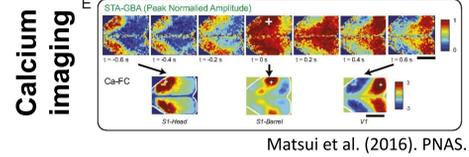
Dataset and processing software

- Mouse groups: anesthetized (N=59) and awake (N=25)
- Scan: GE-EPI at 11.7T (Dr. Joanes Grandjean)
- Processing: RABIES (<https://github.com/CoBrALab/RABIES>)
- Confound regression (CR): 6 motion parameters + WM/CSF signal

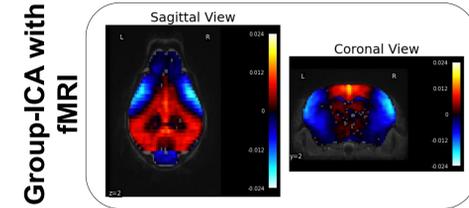
Methods

1) Neurally-grounded network detected from hemodynamics

- Cortex-wide calcium imaging finds neural dynamics reflected by hemodynamics.

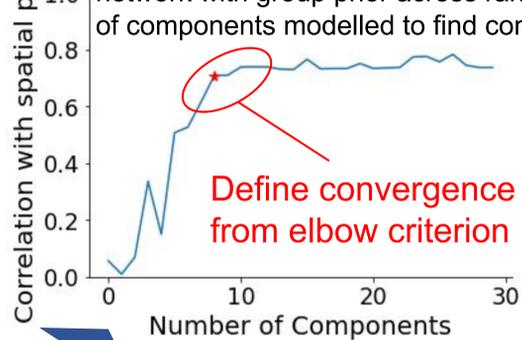


Matsui et al. (2016). PNAS.



3) Select individual-specific number of artefacts

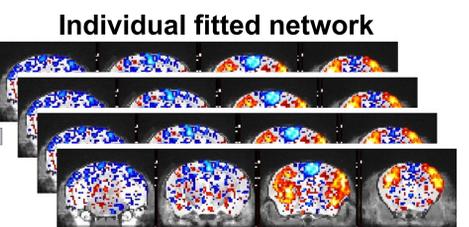
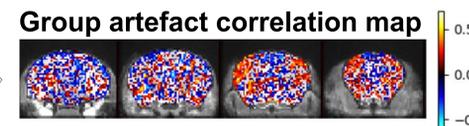
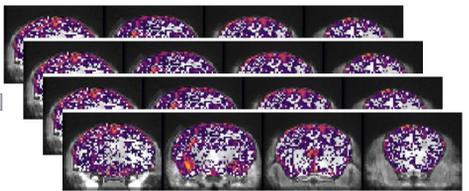
- For each scan, evaluate correlation of fitted network with group prior across ranging numbers of components modelled to find convergence



Define convergence from elbow criterion

4) Evaluate residual artefact effects at the group level

- Validation of algorithm is evaluated from residual artefact correlations
- Artefact effect if modelled voxelwise from the CR variance explained map

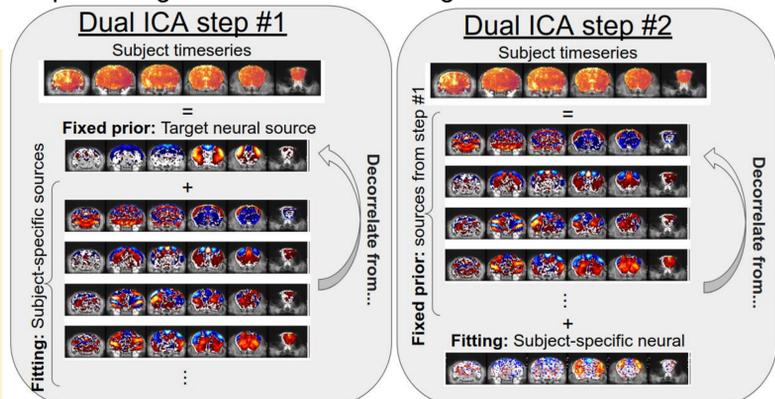


2) Network modeling in individuals: Dual ICA

- Conceptual diagram of the Dual ICA algorithm

Dual ICA algorithm

Modified ICA
(modified deflation ICA code from sklearn.decomposition.FastICA)
X <- Subject timeseries
C <- Fixed spatial prior(s)
For N components:
c <- random initialization
While not converged:
c <- fitting(c,X)
Impose orthogonality relative to all prior components
c <- decorrelate c from C
C <- Append c to C
Return C



Cross-subject correlation

Figure 1: Fitting quality outcomes with and without confound regression (CR)

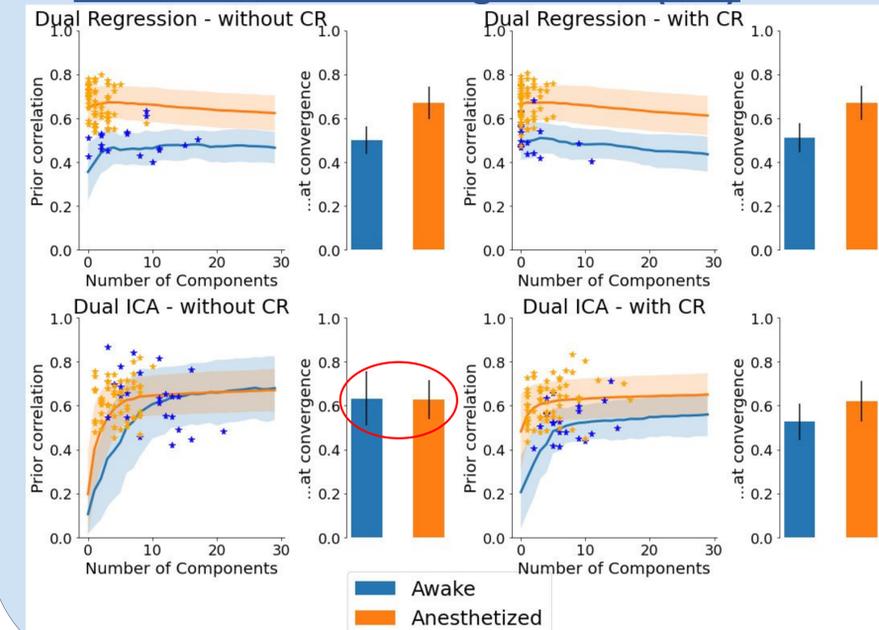


Figure 1: For each scan, network modeling was conducted over a range of number of confound sources and a subject specific number is selected (as shown in methods 3). Points represent individual scans at convergence, and bar graphs represent group averages at convergence. **Take-away: Only Dual ICA without CR avoids fitting quality bias**

Figure 2: Compare artefact effects (without CR)

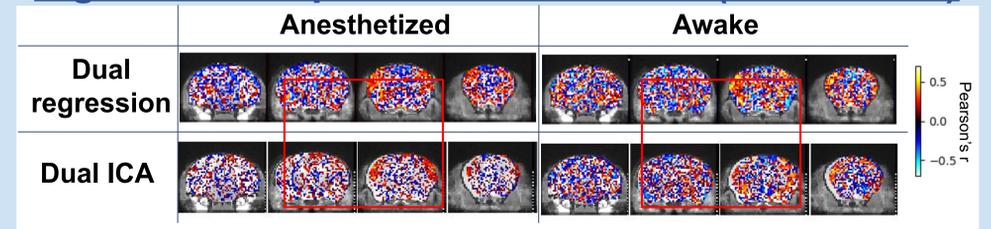


Figure 2: Group-level artefact correlation maps (as in method 2). Confound regression wasn't applied for this figure.

Take-away: Dual ICA clearly outperforms DR (lower CR correlations)

Figure 3: Compare resulting group contrasts (blue = ↑anesthetized)

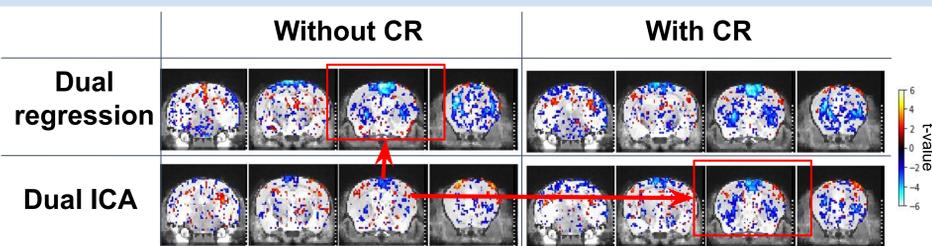


Figure 3: Network connectivity is modelled as a function of group and CR-VE using a linear mixed effect model voxelwise (Connectivity ~ group + CR-VE). The group effect t-values between anesthetized and awake groups is shown.

Take-away:

- Dual ICA -> DR (without CR): a "network-like" effect appears with increasing artefacts in DR (figure 2)
- Without CR -> with CR (dual ICA): the same false positive is introduced by CR

Implications

- We introduce a novel algorithm for network modeling, i.e. Dual ICA, which we demonstrate to be more robust to data quality biases than standard methods
- Confound regression can introduce network-like false positives driven by data quality
- Network fitting quality indices (figure 1) and artefact effects (figure 2) are complementary in attributing the proper interpretation to group analysis
- Open source code implemented in RABIES <https://github.com/CoBrALab/RABIES>