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More independent linear EEG decompositions include more near-dipolar components

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Independent component analysis

Mixture of Brain source activity













Weight matrix W

ICA activity U





ICA and PCA

While PCA simply decorrelates the outputs (using an orthogonal matrix W), ICA attempts to make the outputs statistically independent, while placing no constraints on the matrix W.



Central limit theorem





ICA/EEG Assumptions

OK

- Mixing is linear at electrodes **OK**
- Propagation delays are negligible
- Component time courses are ~ independent
- Number of components less than the number of channels.



Number of independent components



Characteristics of Independent Component of the EEG

Component properties

- Concurrent Activity
- Maximally Temporally Independent
- Overlapping Maps and Spectra
- Dipolar Scalp Maps
- Functionally Independent
- Between-Subject Regularity

Component types

- Artifacts
- Stimulus-locked activity
- Response-locked activity
- Non-phase locked activity
- Event-modulated oscillatory activity



ICA Decomposition into Independent Components



Selective Projection onto Scalp Channels





ICA-based Artifact Removal

Coriginal



Artifact removal using ICA





Some Independent EMG Components



















Localization



Patch of Cortex Acting as a Dipole





Dipolar Scalp Projections

ICA creates a spatial filter for each temporally independent source





Computing residual variance (%)



$$\mathbf{r} = \Sigma (\mathbf{x}_i - \mathbf{x}_i)^2 / \Sigma \mathbf{x}_i^2$$

Validation of the ICA algorithm for EEG

Data

- 13 subjects performing a memory task
- 71 electrodes including EOGs
- more than 300,000 data points/subject

Decomposition

• 23 ICA algorithms plus PCA and Promax

Analysis

• Localization of all components with a single dipole (4-shell spherical model)

Algorithm (Matlab func.)	D%	LL	Origin
Extended Infomax (runica)	29.9	178	EEGLAB 4.515
Pearson	29.1	169	ICAcentral (6)
Infomax (runica)	28.2	160	EEGLAB 4.515
ERICA	26.9	184	ICALAB 1.5.2
SONS	25.4	183	ICALAB 1.5.2
SHIBBS	23.7	169	ICAcentral (5)
FastICA*	23.5	169	ICAcentral (2)
JADE (jader)	23.4	169	EEGLAB 4.515
TICA	23.4	169	ICALAB 1.5.2
JADE optimized (jade_op)	21.4	169	ICALAB 1.5.2
JADE w/ time delay (jade_td)	20.2	169	ICALAB 1.5.2
eeA	19.0	305	ICAcentral (8)
Infomax (icaML) †	18.8	212	ICA DTU Tbox
FOBI	18.6	169	ICALAB 1.5.2
SOBIRO (acsobiro)	17.9	167	EEGLAB 4.515
EVD 24	17.7	169	ICALAB 1.5.2
EVD	17.0	169	ICALAB 1.5.2
SOBI	16.1	583	EEGLAB 4.515
icaMS†	10.6	169	ICA DTU Tbox
AMUSE	8.5	169	ICALAB 1.5.2
PCA	3.1	583	EEGLAB 4.515
Promax	33.7	467	EEGLAB 4.515
Whitening/Sphering	57.6	164	EEGLAB 4.515

Component examples





Mutual information reduction (MIR)

For the linear transformation y = Wx, the entropy of the vector y is given by,

 $h(y) = h(y_1, y_2, y_3, y_4, ...)$ = log |det W| + h(x)

 $I(y_1, y_2) = h(y_1) + h(y_2) - h(y_1, y_2)$

The mutual information I(y) is then,

$$(y) = h(y_1) + ... + h(y_n) - h(y)$$

= h(y_1) + ... + h(y_n) - log |det W| - h(x)

mutual information reduction (MIR), i.e. the amount of mutual information removed from set of channels, is given by,

$$MIR = I(x) - I(y)$$

= $[h(x_1) + ... + h(x_n)] - [h(y_1) + ... + h(y_n)] - h(x) + \log |det W| + h(x)$
= $\log |det W| + [h(x_1) + ... + h(x_n)] - [h(y_1) + ... + h(y_n)]$
univariate

More independence -> more biological components







Alpha Scalp map corr. (r) fMθ 1 Blink 0.9 left μ 0.8 right μ 0.7 lat. EOG 0.6 EMG 0.5 Alpha Raw data corr. fMθ Blink left μ $\text{right}\,\mu$ lat. EOG EMG 0 ÷ -İ-Information reduction difference (bits) -16 JADE opt Amica Infomax SHIBBS JADE FastICA TICA SOBIRO Sphering EVD24 icaMS AMUSE ERICA EVD PCA SONS eeA SOBI Ext. Infomax Pearson JADE-TD FOBI

Correlations between decompositions

PMI – pairwise mutual information

 $I(y_1, y_2) = H(y_1) + H(y_2) - H(y_1, y_2)$



Left μ cluster









S7 IC35

S5 IC48



S14 IC45















Occipital α cluster



Frontal Midline θ cluster





More independence -> more biological components



Take home message

 Different ICA algorithms return similar solutions

• The ICA algorithms that return the most biologically plausible solutiosn are also the one that return the most independent decompositions







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