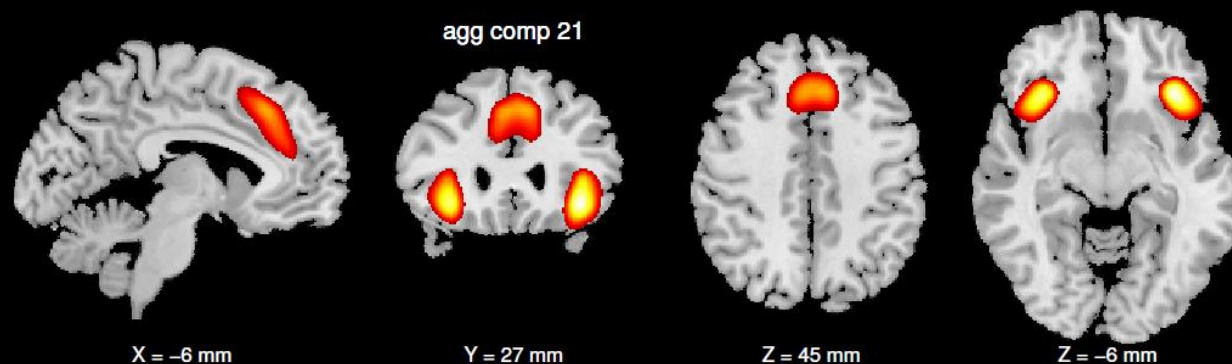


An Introduction to Independent Component Analysis (ICA)



Brain Connectivity Course 2013, Grenoble France

Elena A. Allen

Post-Doctoral Fellow

University of Bergen & The Mind Research Network

“Essentially, all models are wrong,
but some are useful.”

-George E.P. Box, statistician

In Empirical Model-Building and Response Surfaces, 1987

outline

- introduction to ICA
- a group ICA framework
- applications and examples
- practical challenges



*Your complimentary
use period has ended.
Thank you for using
PDF Complete.*

[Click Here to upgrade to
Unlimited Pages and Expanded Features](#)

ICA

ndent Component Analysis

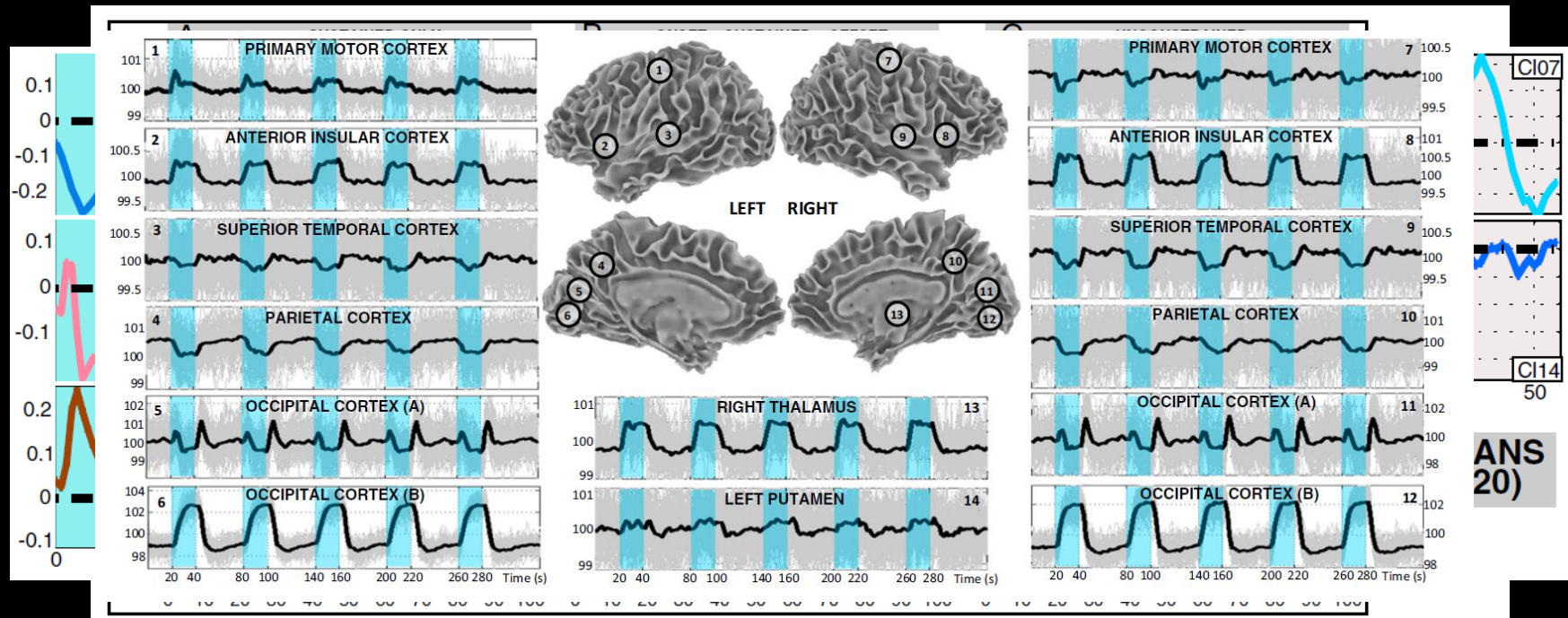
- A blind source separation (BSS) method
- Goal: separate sources from a linear mixture
- Model: $\mathbf{X}=\mathbf{A}\mathbf{S}$
 - \mathbf{X} : Mixture (observed data)
 - \mathbf{A} : Mixing coefficients (estimated)
 - \mathbf{S} : Sources (estimated)
- Estimate: $\hat{\mathbf{S}} = \mathbf{W}\mathbf{X}$, $\mathbf{W} = \mathbf{A}^{-1}$, based on maximizing statistical independence of $\hat{\mathbf{S}}$
- Assumptions
 - Linear mixing
 - Independence of sources
 - Non-Gaussian sources

Comparisons to other models

- With the general linear model (GLM) we can only study the **activation that we've modeled**.
 - ICA requires no explicit temporal model; temporal activations are data-driven.
- Seed-based connectivity uses only pair-wise (**bivariate**) relationships. It also requires **choice of a seed region**.
 - ICA is hugely multivariate. It considers the relationships between all voxels simultaneously. Component shapes and “centers” are data-driven.

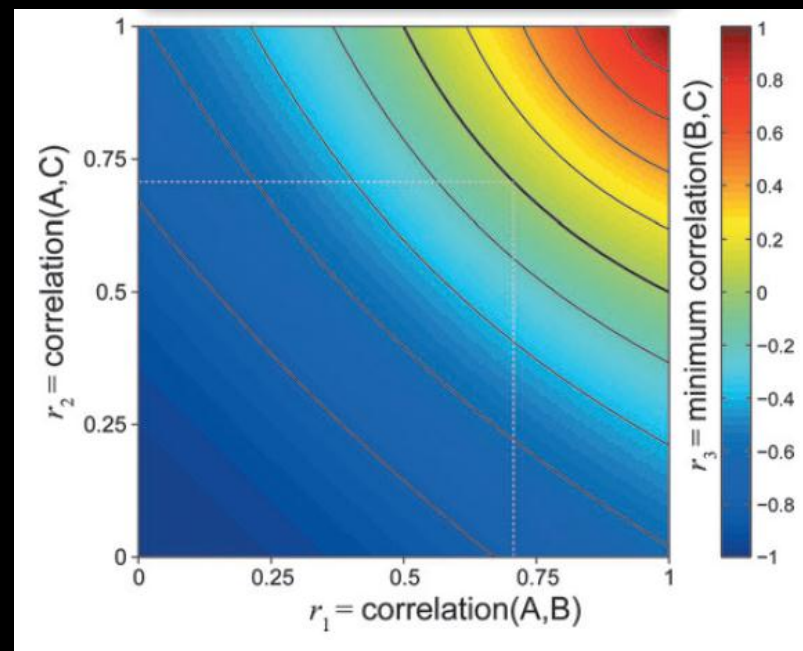
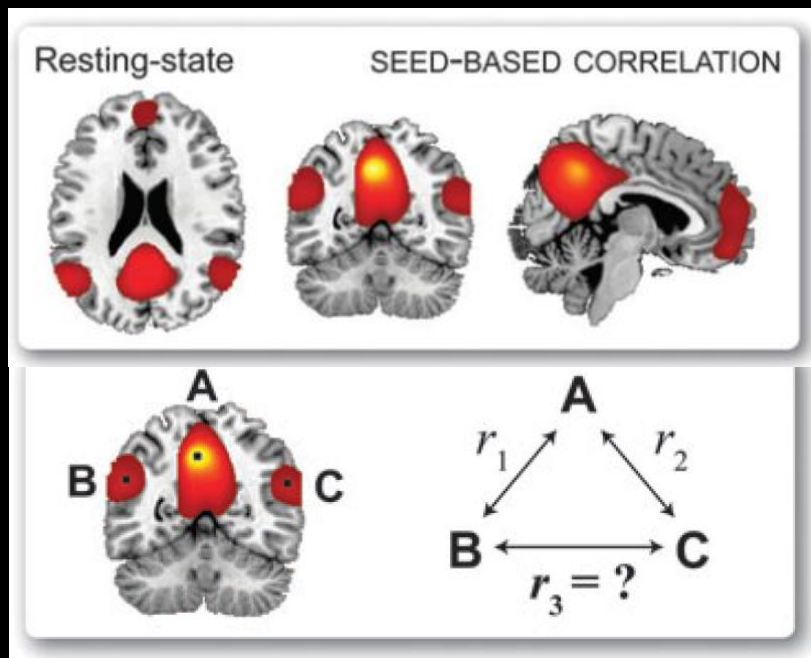
Comparisons to other models

- With the general linear model (GLM) we can only study the activation that we've modeled.
 - ICA requires no explicit temporal model; temporal activations are data-driven.



Gonzalez-Castillo et al., (2012). Whole-brain, time-locked activation with simple tasks revealed using massive averaging and model-free analysis. *PNAS*, 2012.

Comparisons to other models



- Seed-based connectivity uses only pair-wise (bivariate) relationships. It also requires choice of a seed region.
 - ICA is hugely multivariate. It considers the relationships between all voxels simultaneously. Component shapes and “centers” are data-driven.

(not so scary) example

Observations (X)



$$X=AS$$

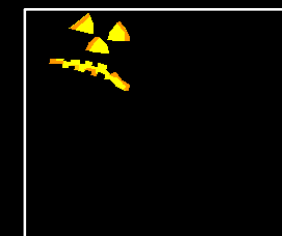
=

background

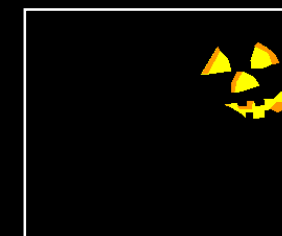
Mixing matrix (A)



candle 1



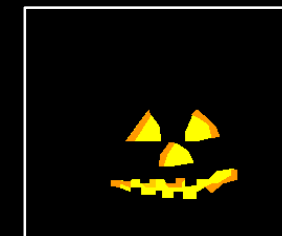
candle 2



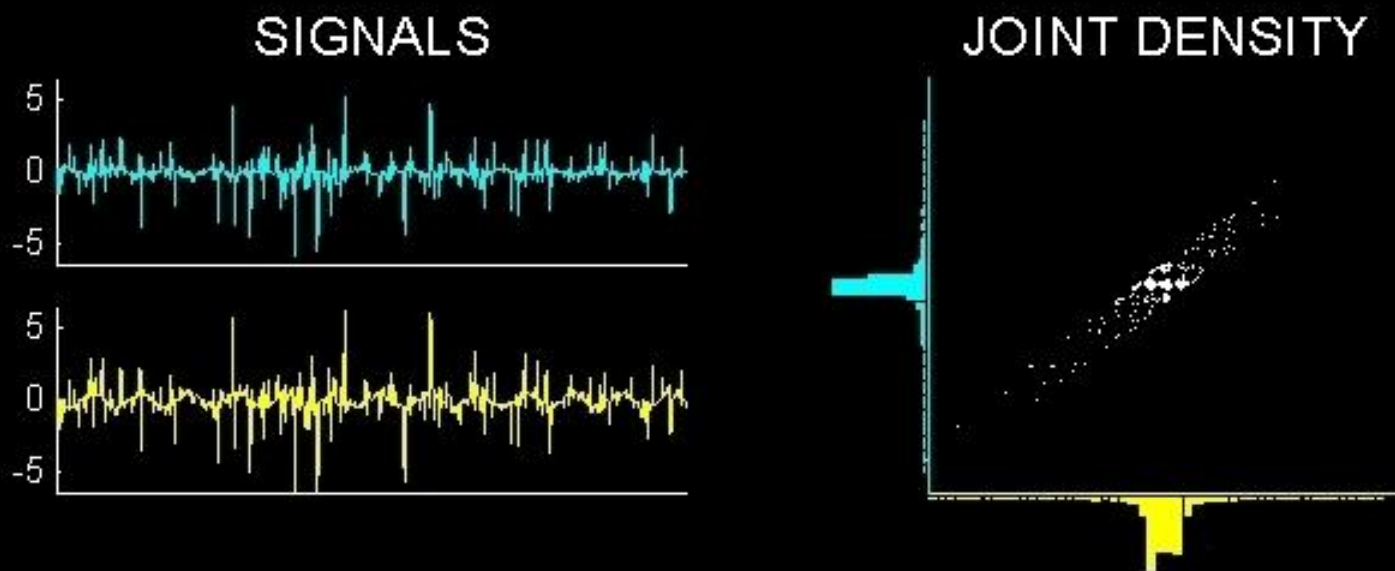
candle 3



time candle out



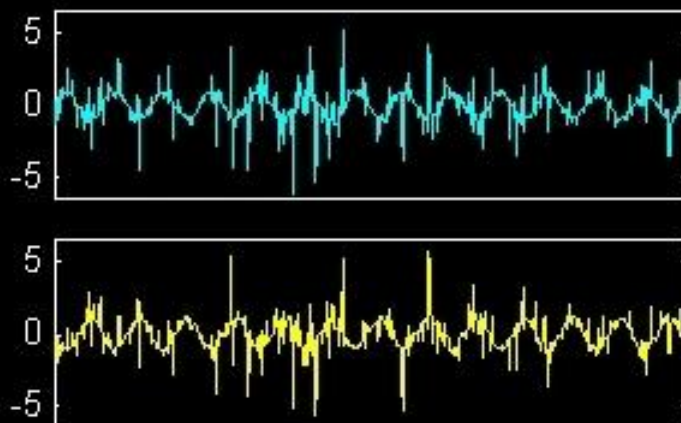
stICA demo: mixtures



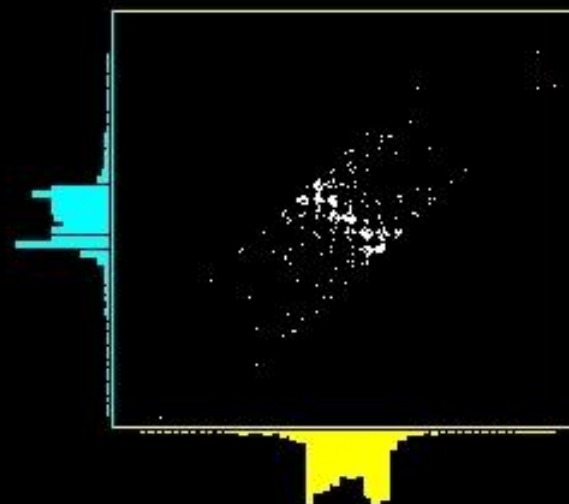
Input signals and density

stICA demo: whitened

SIGNALS

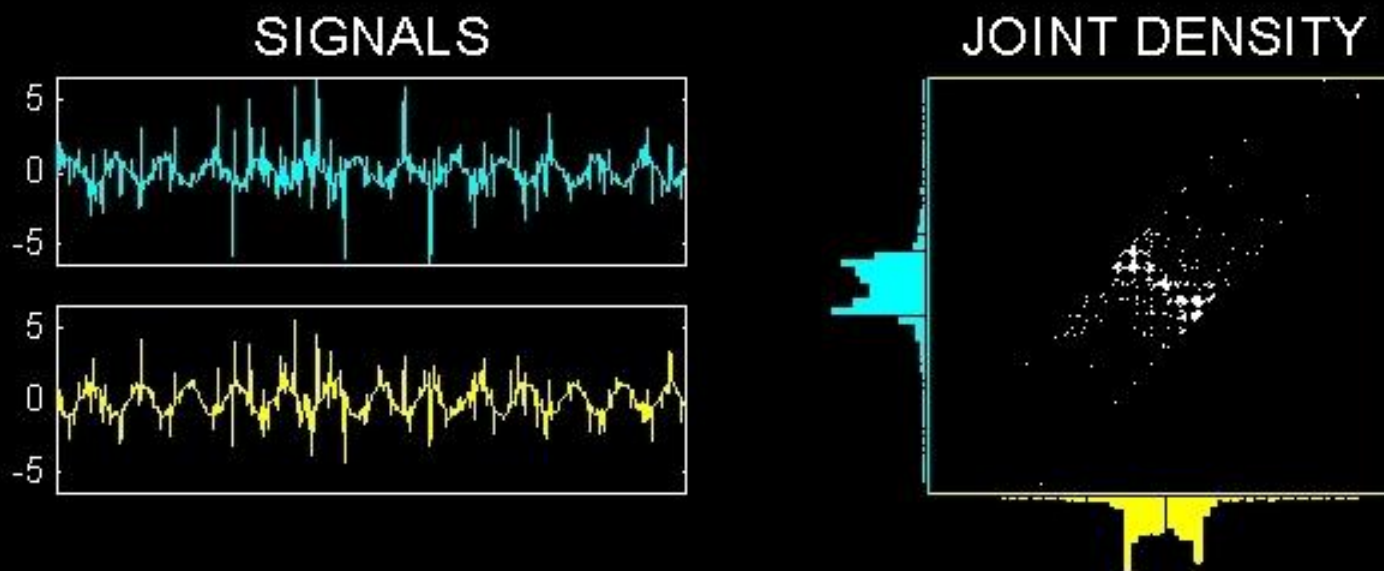


JOINT DENSITY



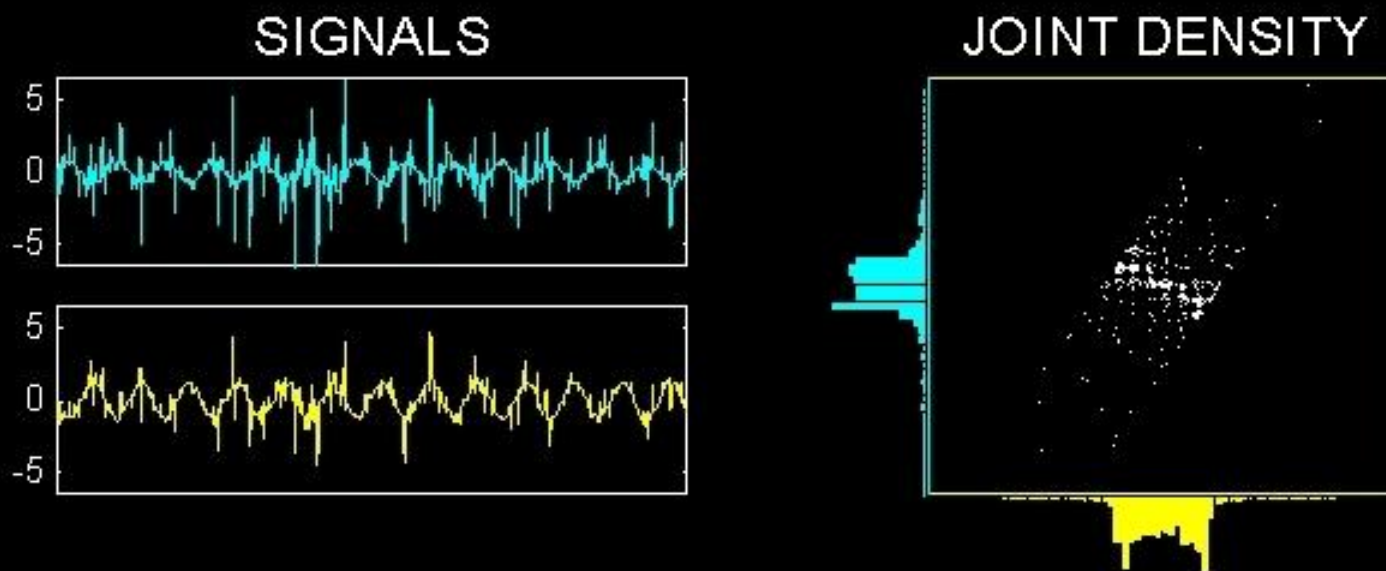
Whitened signals and density

FastICA demo (step 1)



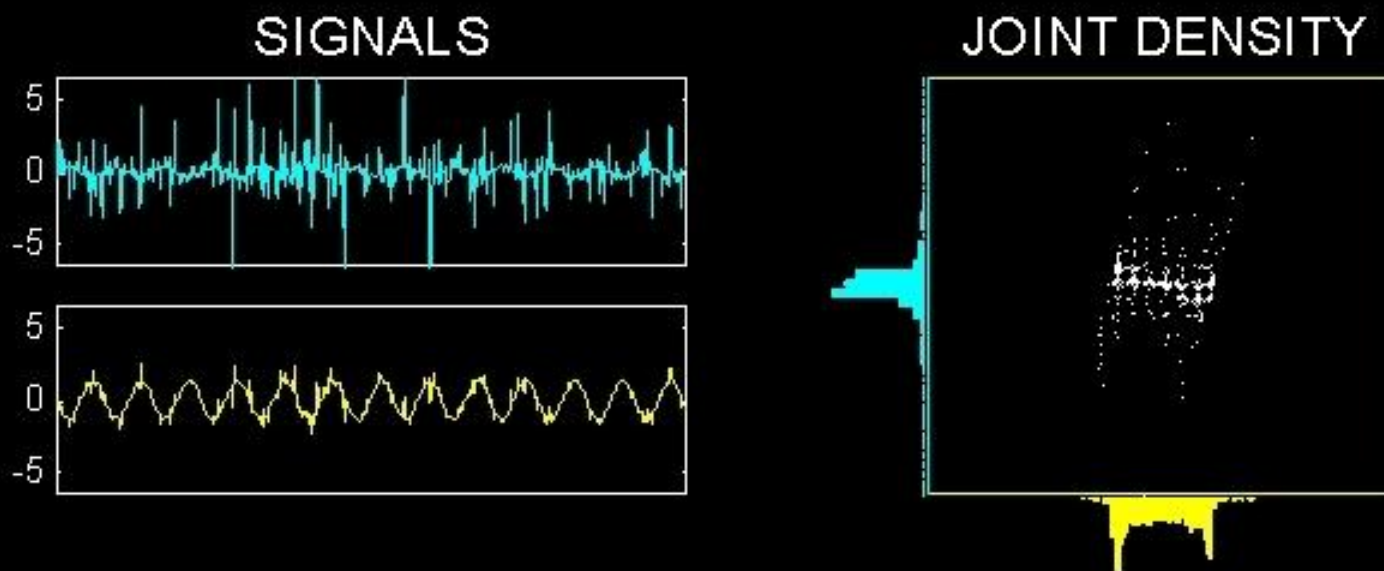
Separated signals after 1 step of FastICA

FastICA demo (step 2)



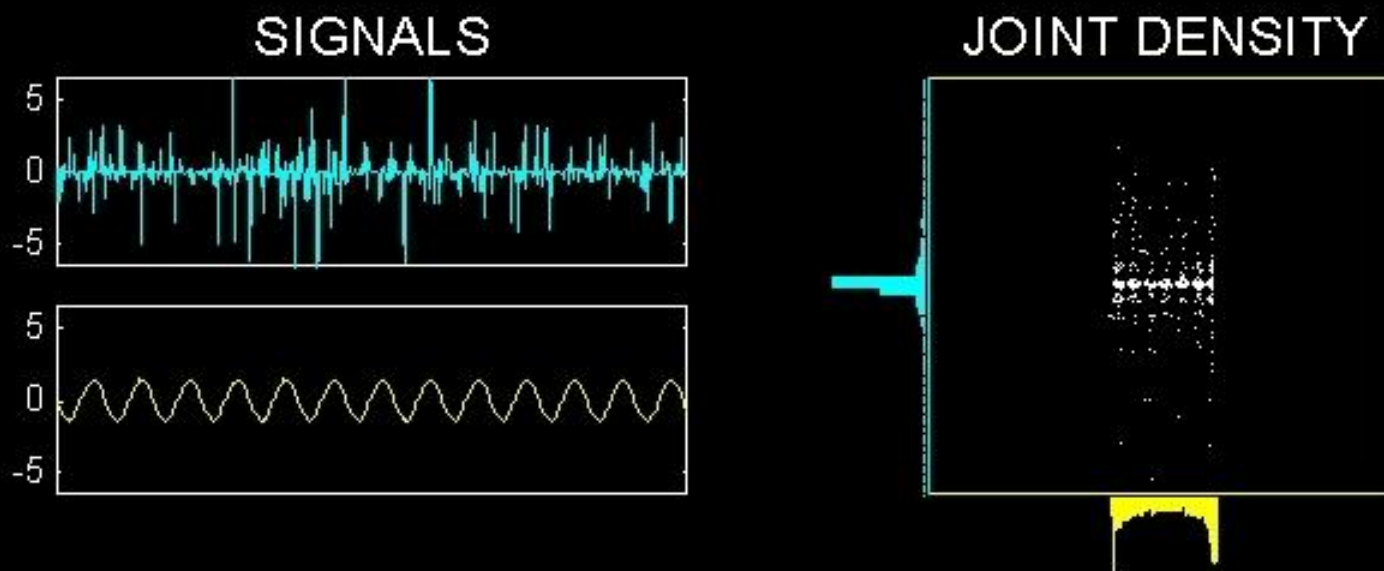
Separated signals after 2 steps of FastICA

FastICA demo (step 3)



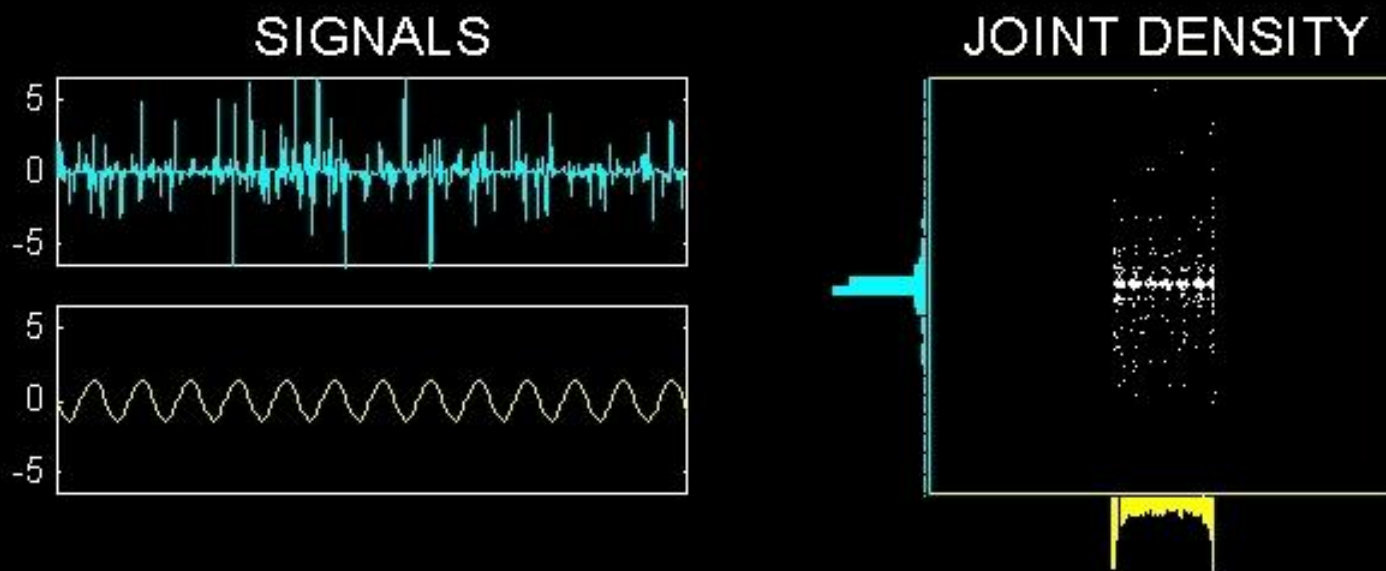
Separated signals after 3 steps of FastICA

FastICA demo (step 4)



Separated signals after 4 steps of FastICA

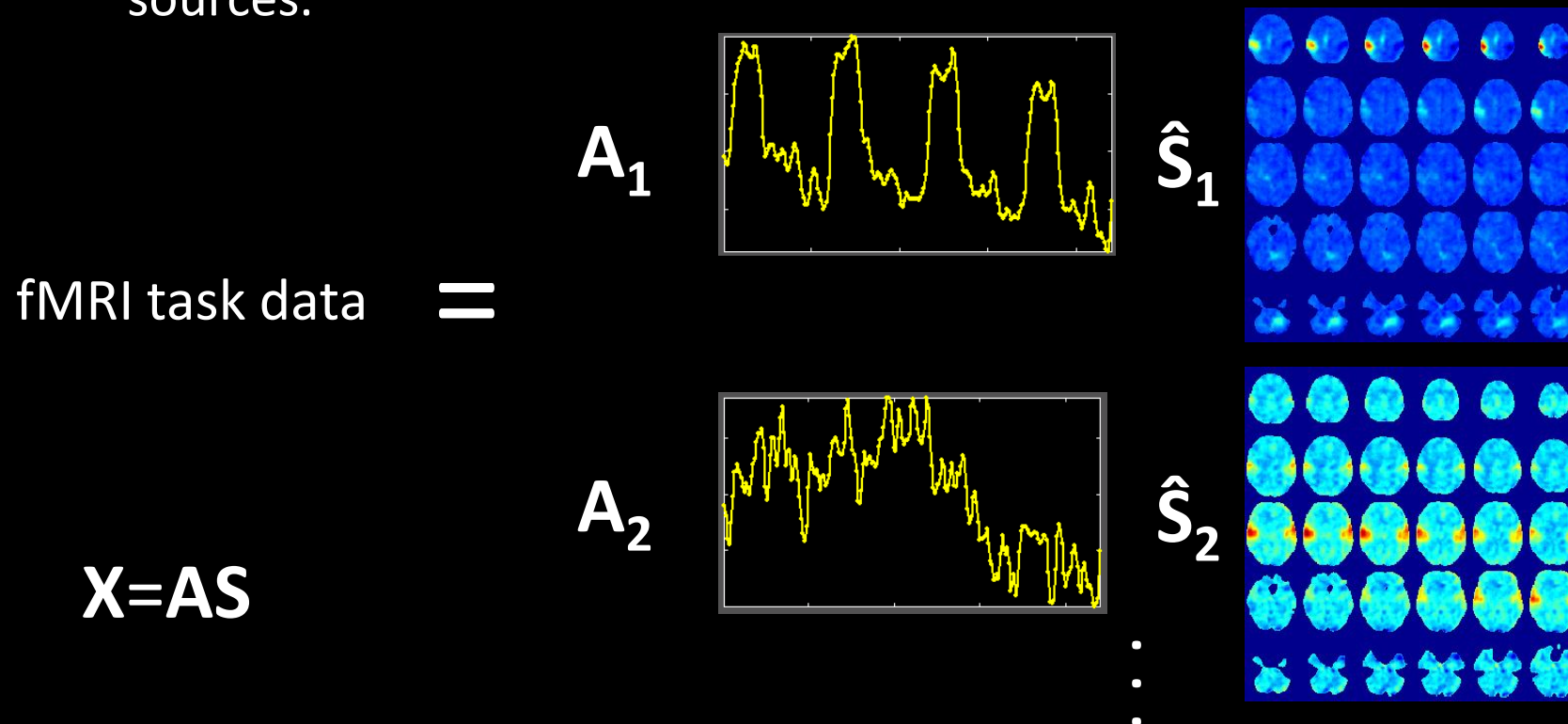
FastICA demo (step 5)



Separated signals after 5 steps of FastICA

ICA applied to fMRI

- We typically perform spatial ICA:
 - the sources are maps that are **maximally spatially independent** (i.e., non-overlapping)
 - the mixing matrix represents **activation time courses** of the sources.





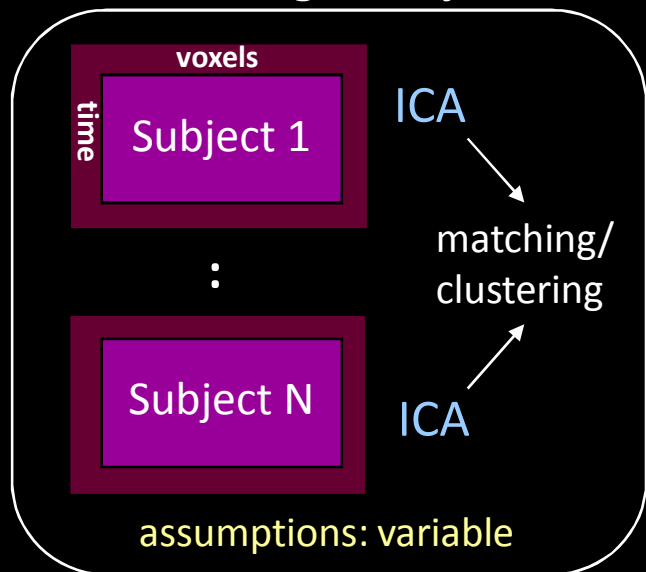
*Your complimentary
use period has ended.
Thank you for using
PDF Complete.*

[Click Here to upgrade to
Unlimited Pages and Expanded Features](#)

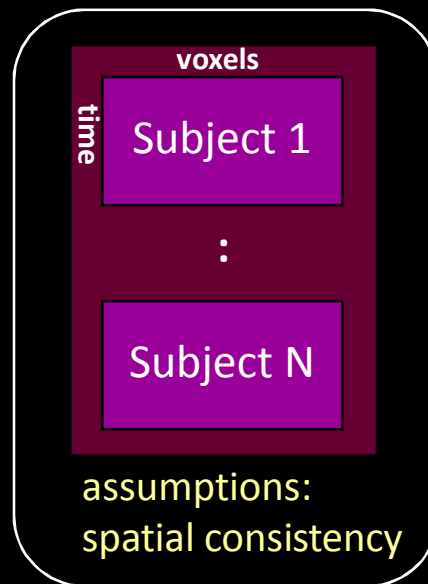
group ICA

-subject ICA frameworks

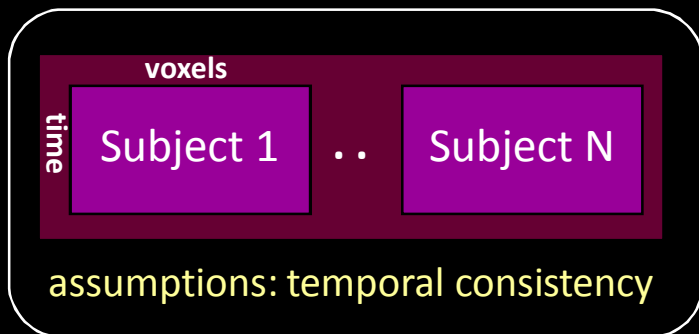
combine single subject ICAs



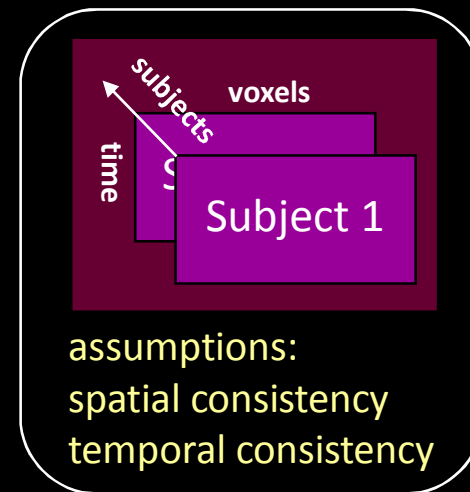
group ICA with temporal concatenation



group ICA with spatial concatenation



tensor ICA

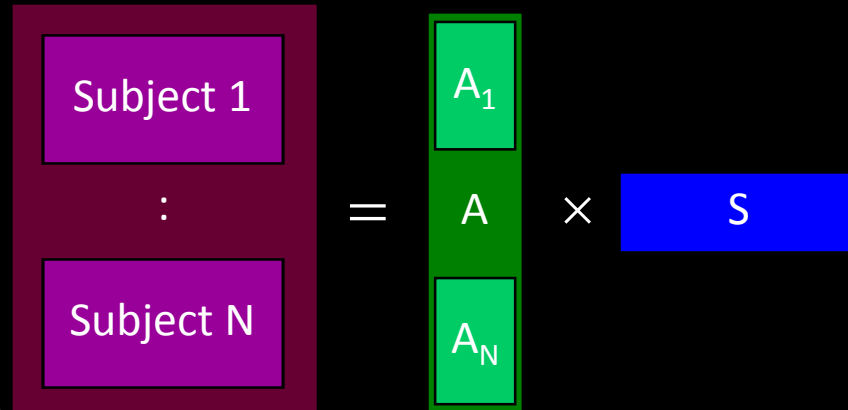


A with single subject estimation

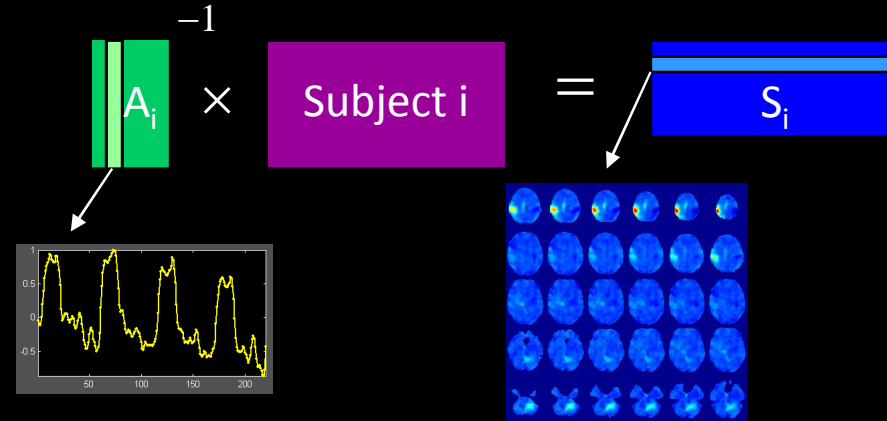
ICA (Forward Estimation)

Data

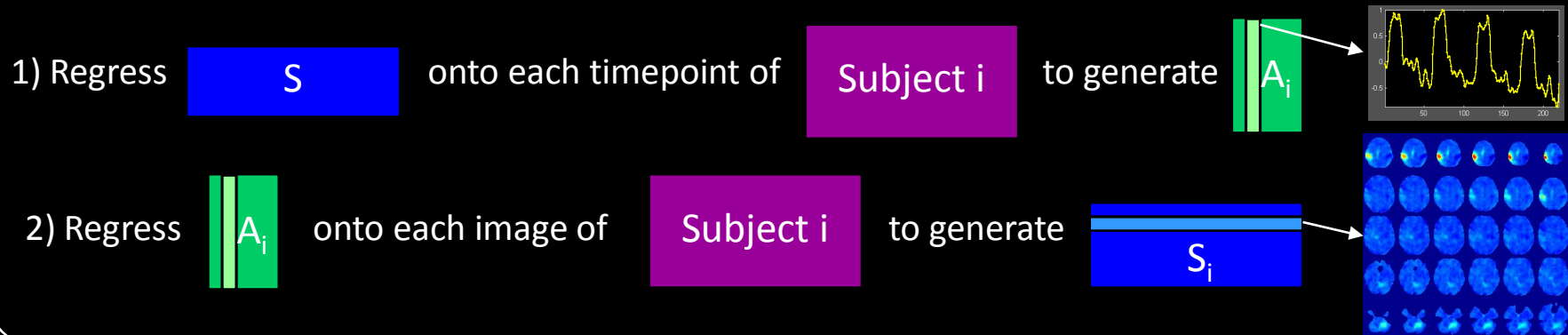
PCA reductions



Back-reconstruction through inversion

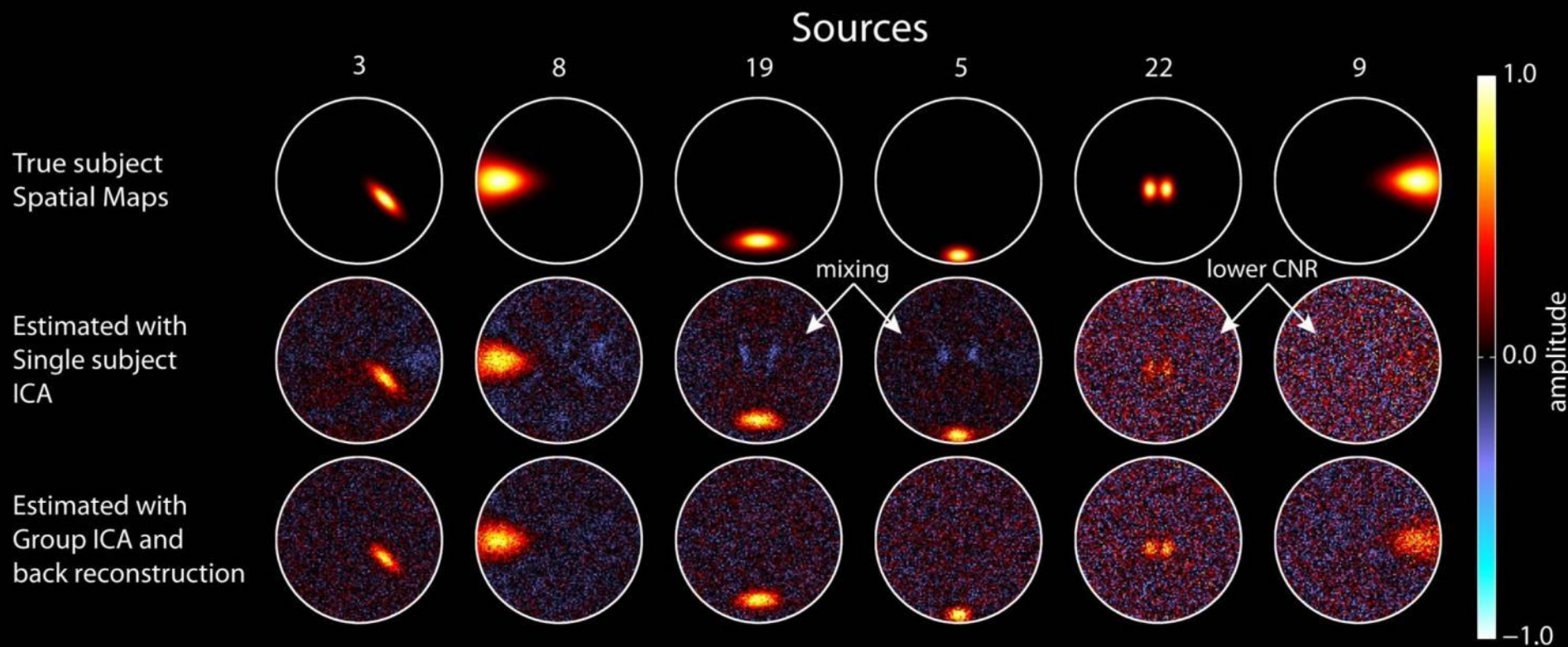


Back-reconstruction through spatial-temporal (dual) regression

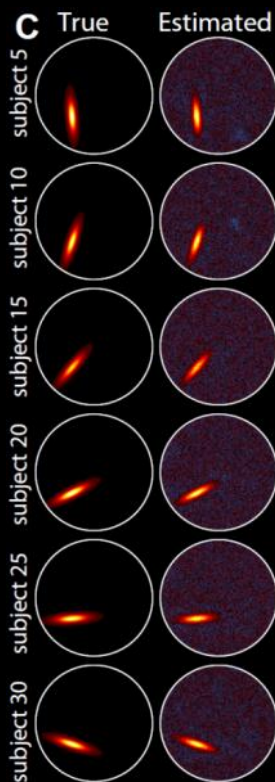
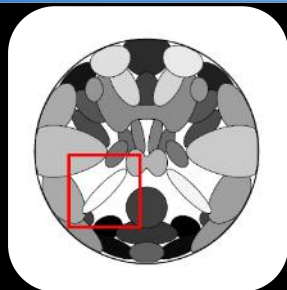


Benefits of group ICA

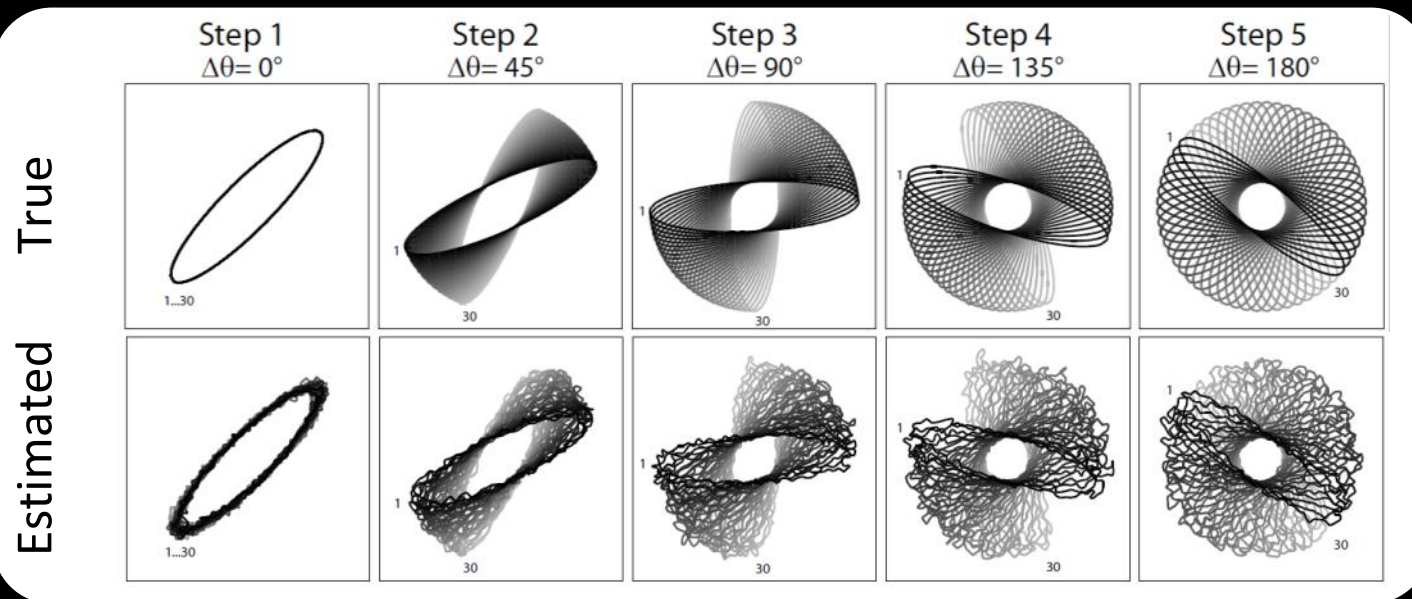
Compare single subject ICA with group ICA (5 subjects) and subsequent back-reconstruction



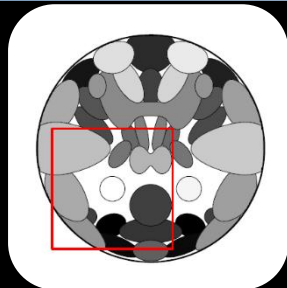
inter-subject variability



simulations



Inter-subject variability



simulations

Step 1
 $\sigma_{x,y} = 0$

Step 2
 $\sigma_{x,y} = 2$

Step 3
 $\sigma_{x,y} = 4$

Step 4
 $\sigma_{x,y} = 6$

Step 5
 $\sigma_{x,y} = 8$

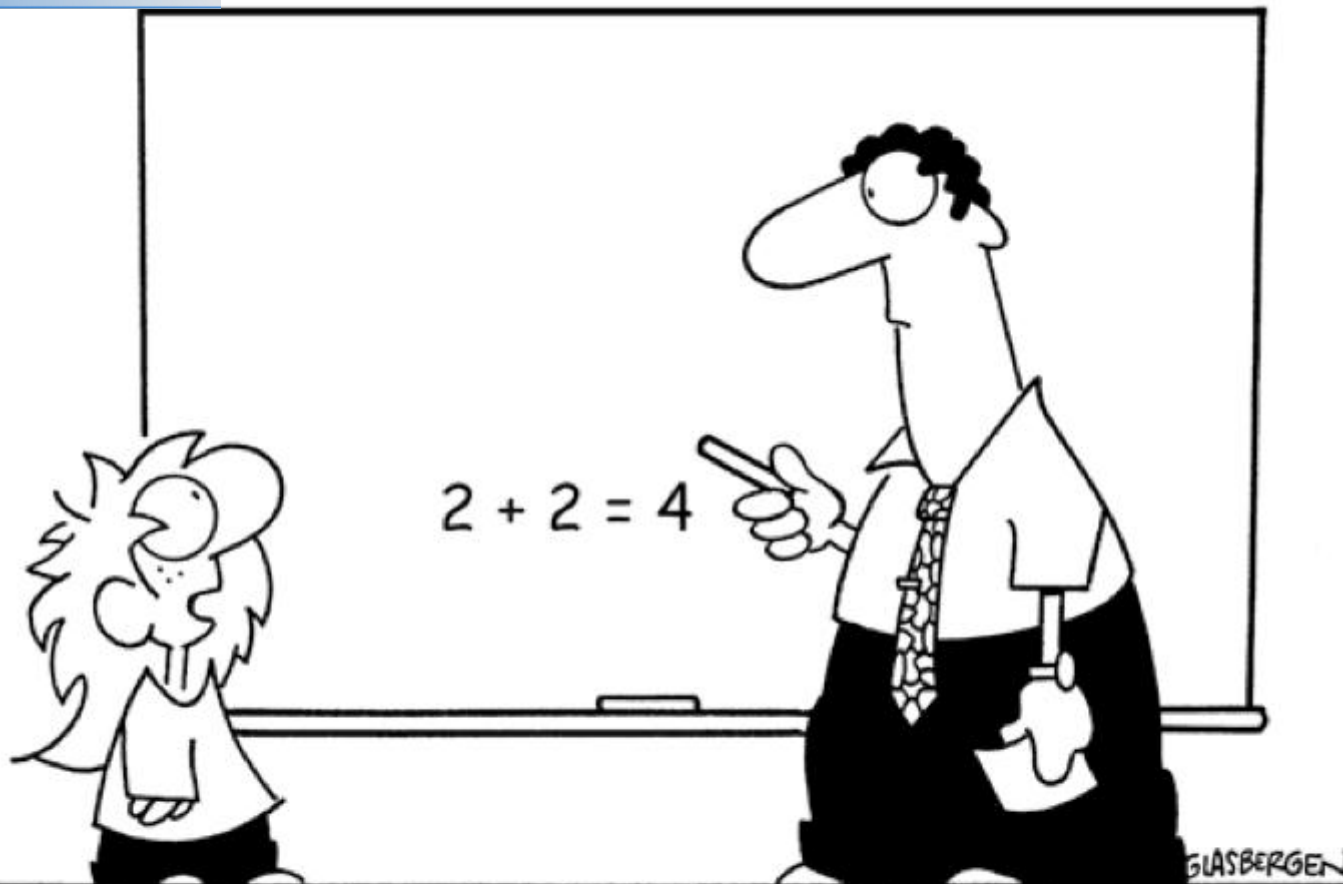
True
subject 23 $d = 2.0$
subject 24 $d = 4.8$
subject 10 $d = 10.3$
subject 20 $d = 12.7$
subject 12 $d = 15.7$
subject 30 $d = 17.7$

Table 2

Inter-subject spatial variability reported for functional areas. In all studies subject datasets were spatially normalized prior to group analysis. VOTC = ventral occipito-temporal cortex; LOTC = lateral occipito-temporal cortex; IFJ = inferior-frontal junction; BA = Brodmann area; SMA = supplementary motor area; ACC = anterior cingulate cortex; STG = superior temporal gyrus; IFG = inferior temporal gyrus.

Study	Method	<i>n</i>	Region	Group peak (MNI)	Average distance ± SD
Wilms et al. (2005)	fMRI	14	Right V5/MT+	51, -72, 10	9.5 ± 7.6 mm
Wilms et al. (2005)	fMRI	14	Left V5/MT+	-45, -76, 14	8.7 ± 3.9 mm
Duncan et al. (2009)	fMRI	45	Left VOTC	-42, -50, -20	15.0 ± 5.0 mm
Duncan et al. (2009)	fMRI	45	Left LOTC	-40, -58, -20	9.0 ± 3.0 mm
Derrfuss et al. (2009)	fMRI	14	Left IFJ	-39, 2, 32	8.2 ± 3.8 mm
Xiong et al. (2000)	PET	20	SMA, BA 6	0, 15, 51	9.4 ± 3.4 mm
Xiong et al. (2000)	PET	20	ACC, BA 32/24	3, 26, 28	9.7 ± 4.4 mm
Xiong et al. (2000)	PET	20	Left M1, BA 4/6	-44, -7, 38	13.4 ± 5.6 mm
Xiong et al. (2000)	PET	20	Left STG, BA 22	-54, -35, 10	11.9 ± 5.1 mm
Xiong et al. (2000)	PET	20	Left IFG, BA 44	-46, 21, 7	11.7 ± 4.7 mm
Xiong et al. (2000)	PET	20	Left IFG, BA 47	-38, 32, -19	13.1 ± 5.4 mm

- Group ICA **facilitates** the estimation of components in single subjects
- Estimation is **robust** to considerable variability
- Temporal and spatial patterns can be captured at the level of the **individual**



**“How can I trust your information when
you’re using such outdated technology?”**



*Your complimentary
use period has ended.
Thank you for using
PDF Complete.*

[Click Here to upgrade to
Unlimited Pages and Expanded Features](#)

examples

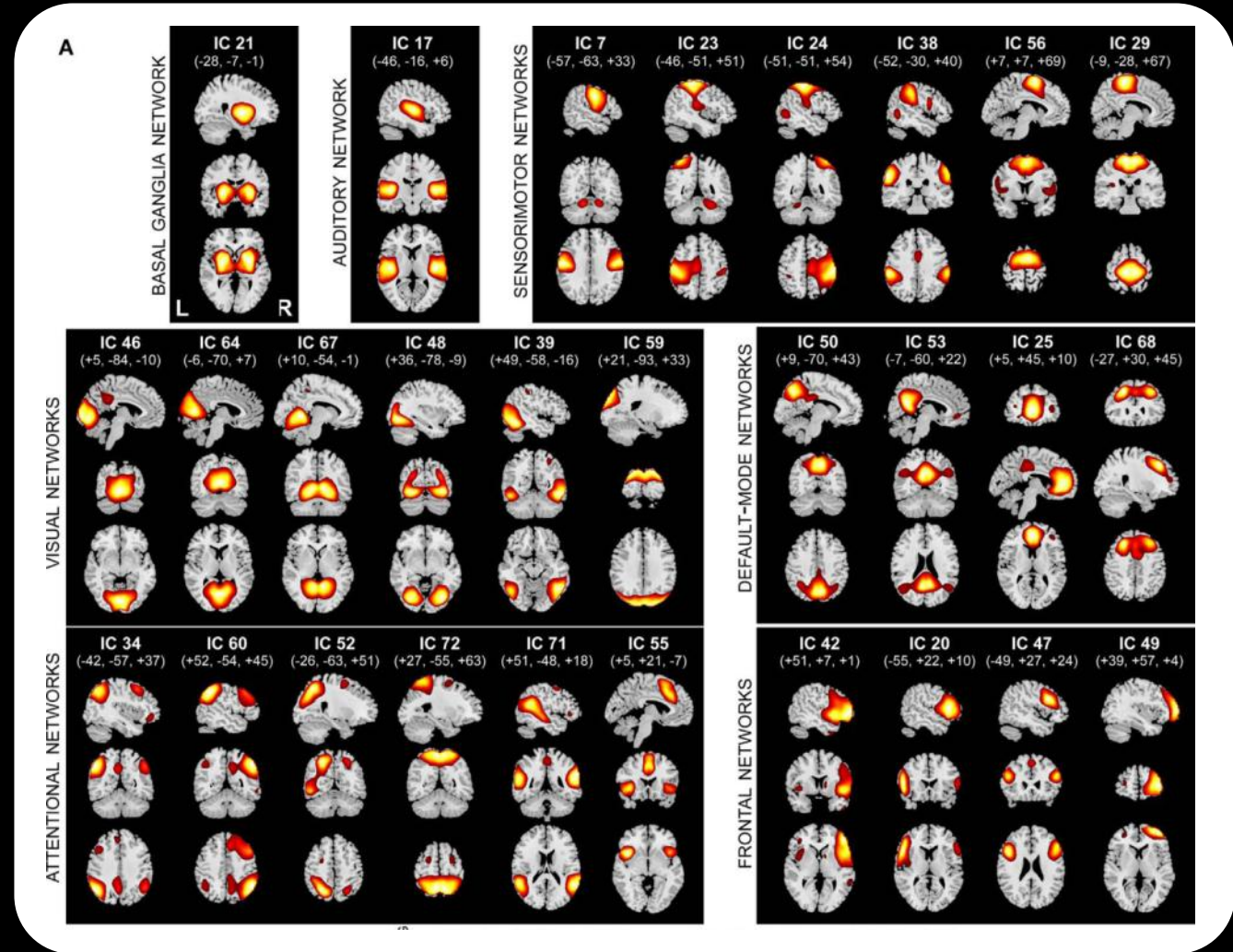
ity in a healthy sample (n=603)

5 minutes of resting-state data from ~600 healthy subjects combined across studies

Datasets decomposed in a single group ICA

28 components (RSNs) selected for analysis

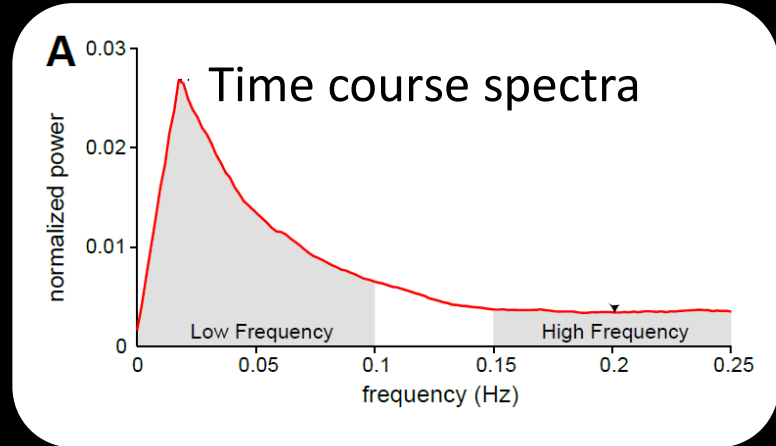
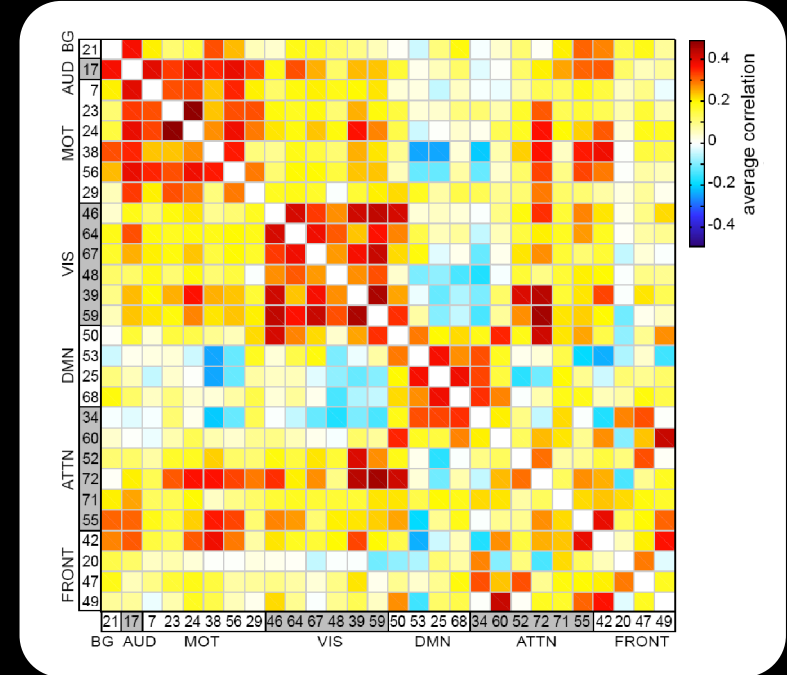
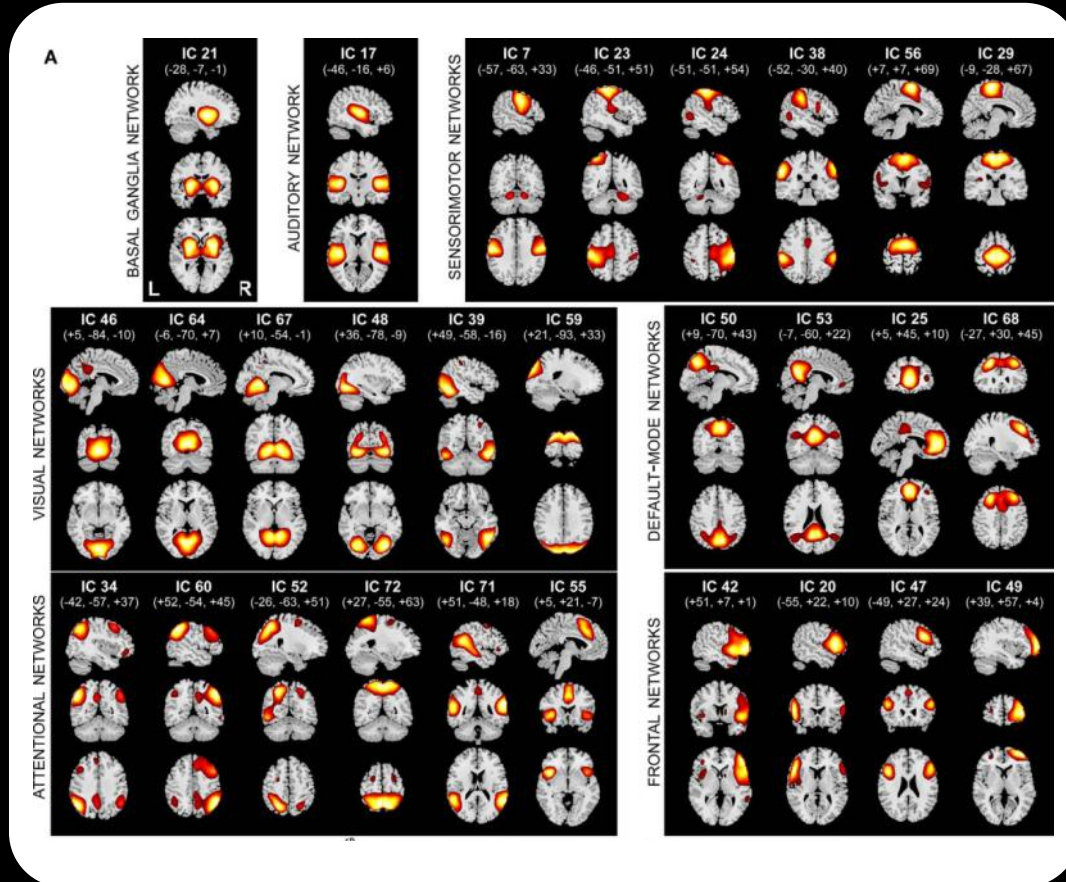
Examined how baseline factors such as age and gender affect functional connectivity



Functional connectivity features

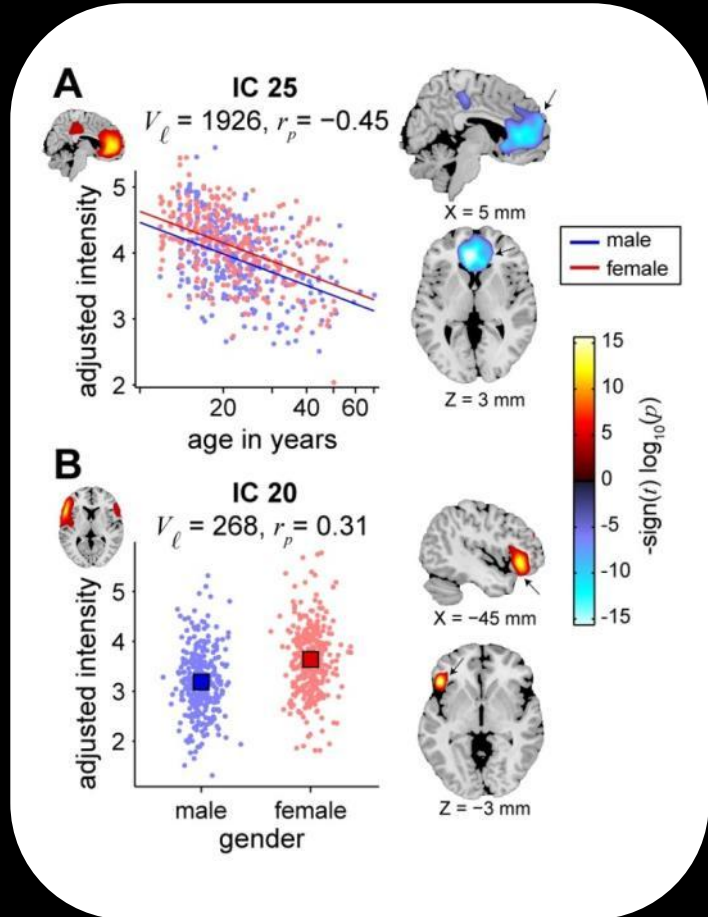
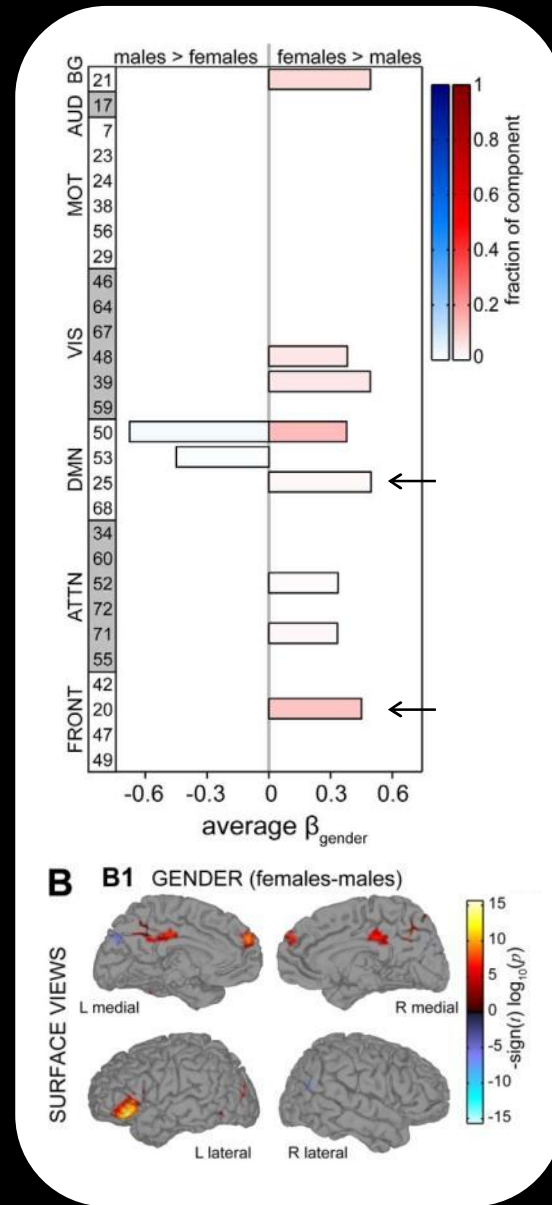
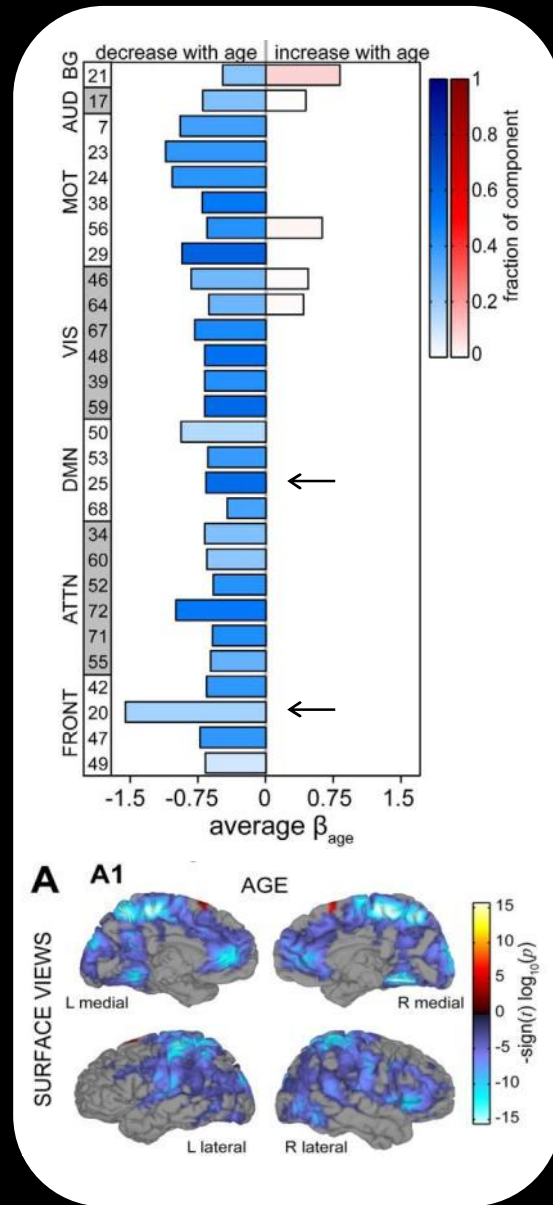
Functional network connectivity (FNC)

Component spatial maps



univariate followup

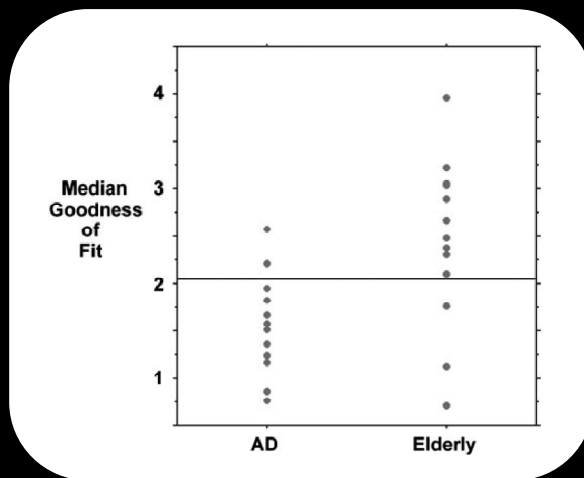
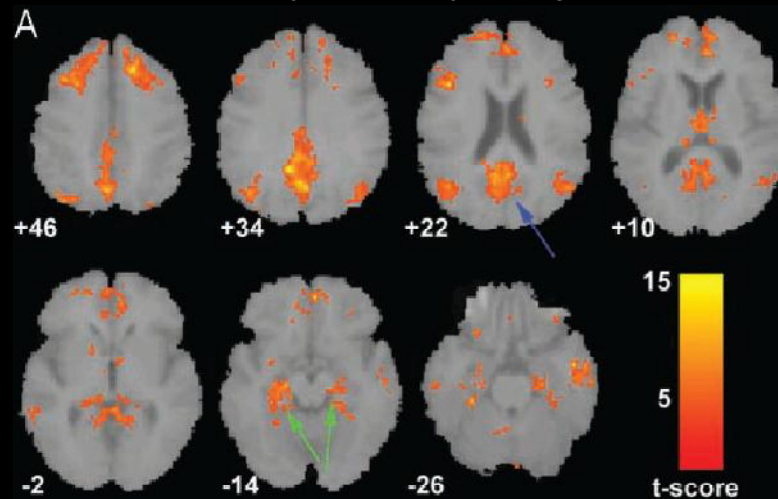
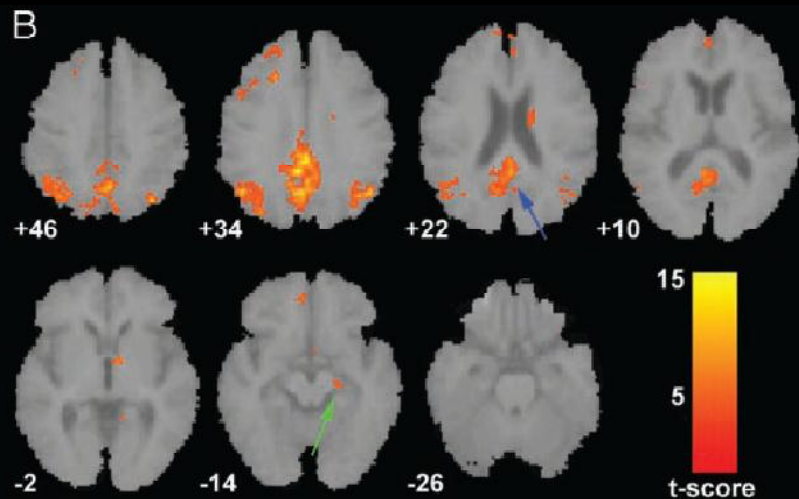
examples



ons in disease: spatial maps

subjects with Alzheimer's disease

healthy elderly subjects



Greicius MD, Srivastava S, Reiss AL, Menon V: Default-mode network activity distinguishes Alzheimer's disease from healthy aging: Evidence from fMRI. *Proc Natl Acad Sci* 101:4637-42 (2004).

ICA is not the end point: it's just the beginning!

- ICA provides you with a linear “functional parcellation” of the brain.
- Use time courses for
 - task-based models (GLM)
 - functional connectivity
 - graph construction
 - PPI
 - DCM
 - ...
- Use components for
 - ROI definitions/data-driven seeds
 - artifact removal



*Your complimentary
use period has ended.
Thank you for using
PDF Complete.*

[Click Here to upgrade to
Unlimited Pages and Expanded Features](#)

challenges

Some practical challenges

- How many components should be estimated?
- Which components should be used in feature analysis?
- Should I remove artifacts from the data before performing ICA?

Which model order is correct?

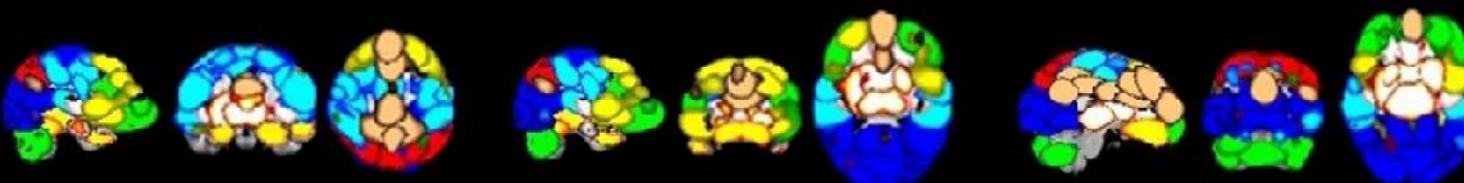
11 RSNs identified at low model order of 20 ICs



47 RSNs identified at high model order of 70 ICs



70 RSNs identified at high model order of 100 ICs



-42

-14

44

-44

24

10

8

-66

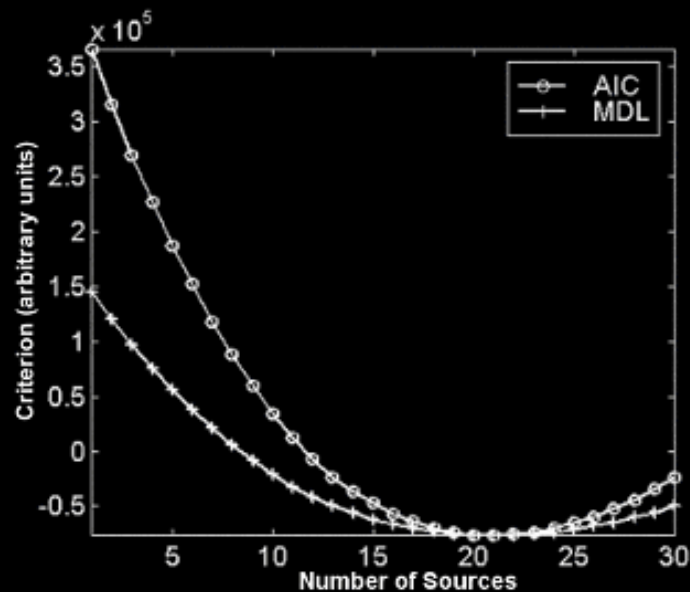
2

Abou Elseoud A, Littow H, Remes J, Starck T, Nikkinen J, Nissilä J, Timonen M, Tervonen O and Kiviniemi V (2011) Group-ICA model order highlights patterns of functional brain connectivity. *Front. Syst. Neurosci.* 5:37.

Methods to select model order

theoretical

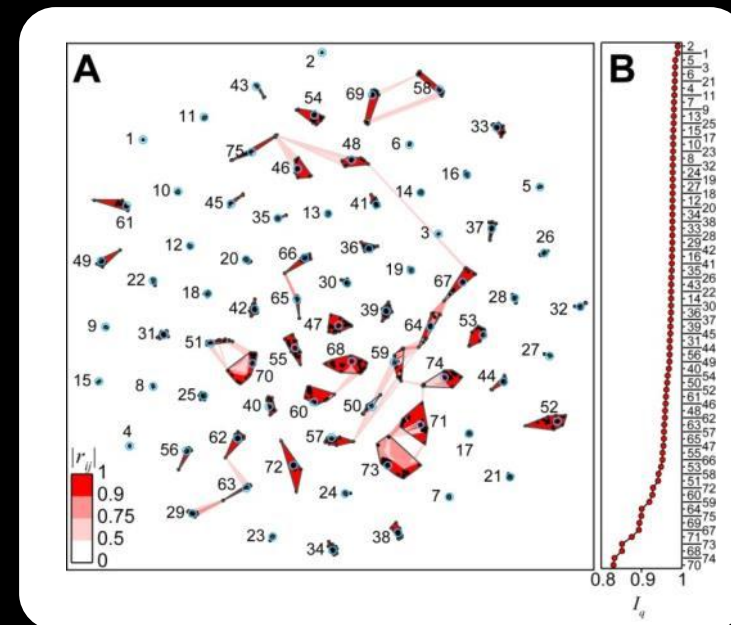
Information theoretic criteria reward goodness of fit, and penalize the number of estimated parameters



Real imaging data may not match theoretic assumptions...

empirical

Empirical methods consider the stability of components over randomized initial conditions of the ICA algorithm and/or bootstrap resamples of subjects



Under- or over-split components may still be stable...

How much does it matter?

of model order



x=40

Striatum

M1

M2

S1 / S2

PCUN

10

z=65 y=50
R L

20

z=32
R L

30

40

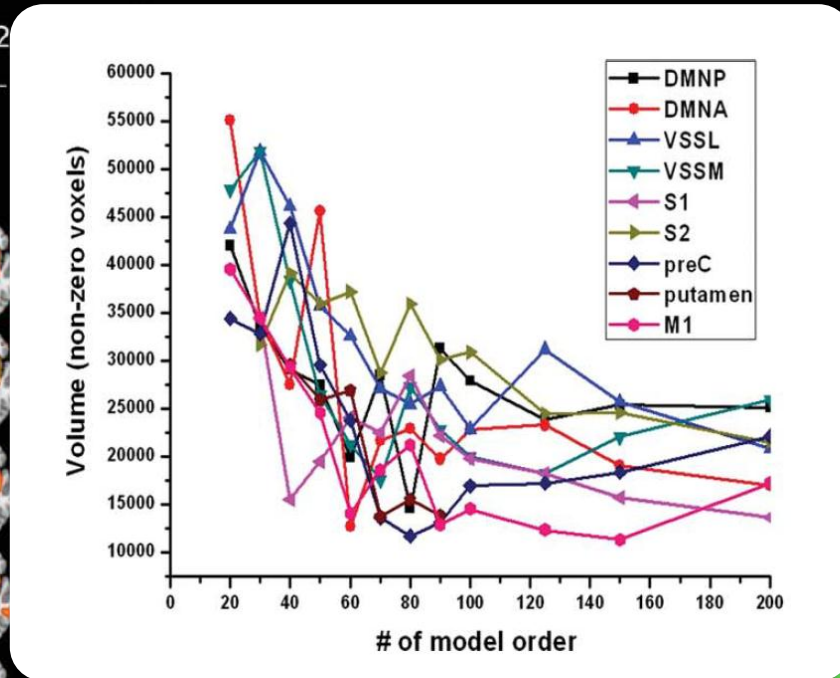
50

60

70

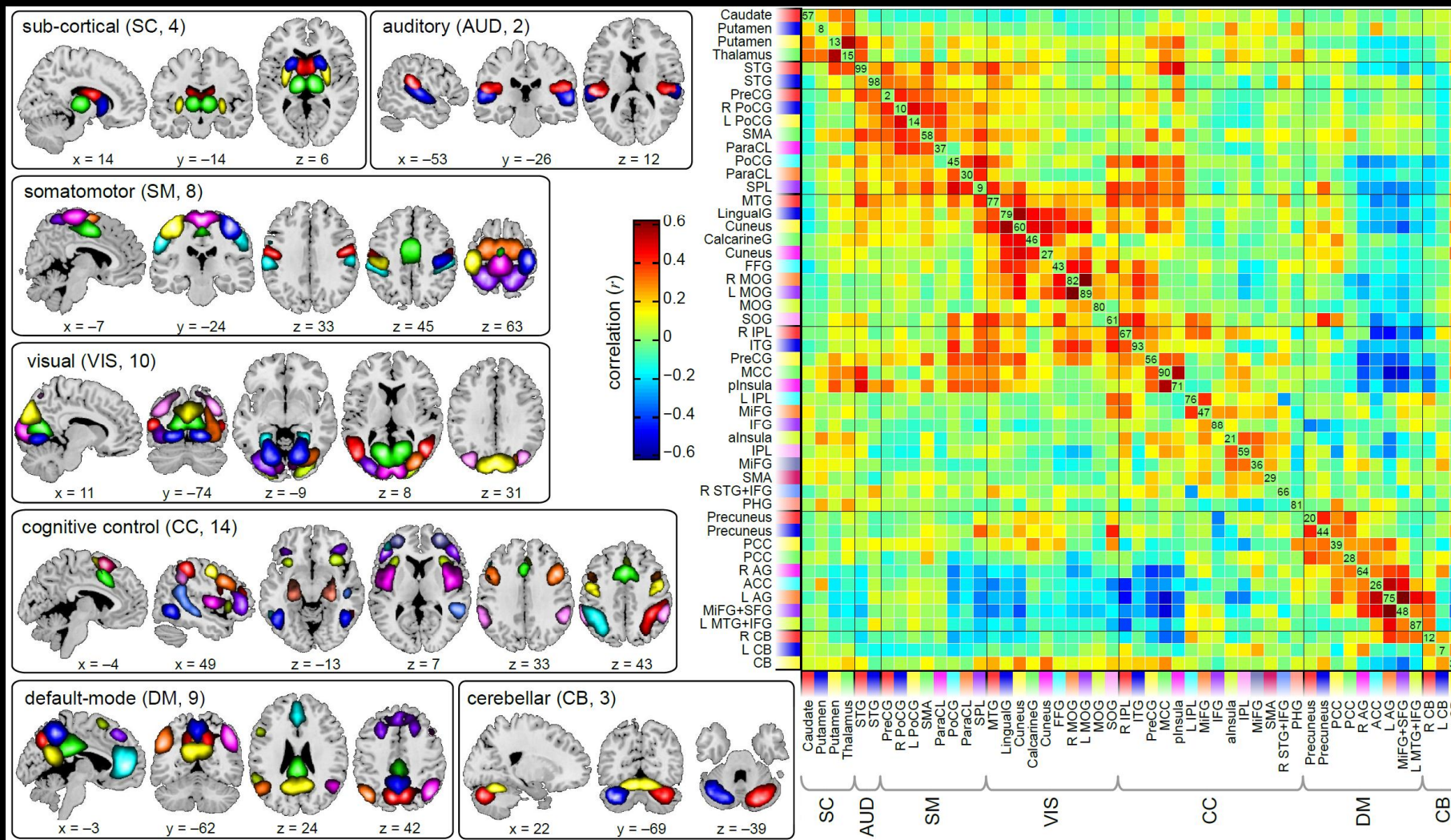
80

90



About Elseoud A, Littow H, Remes J, Starck T, Nikkinen J, Nissilä J, Timonen M, Tervonen O and Kiviniemi V (2010). The Effect of Model Order Selection in GroupPICA. *Human Brain Mapping*.

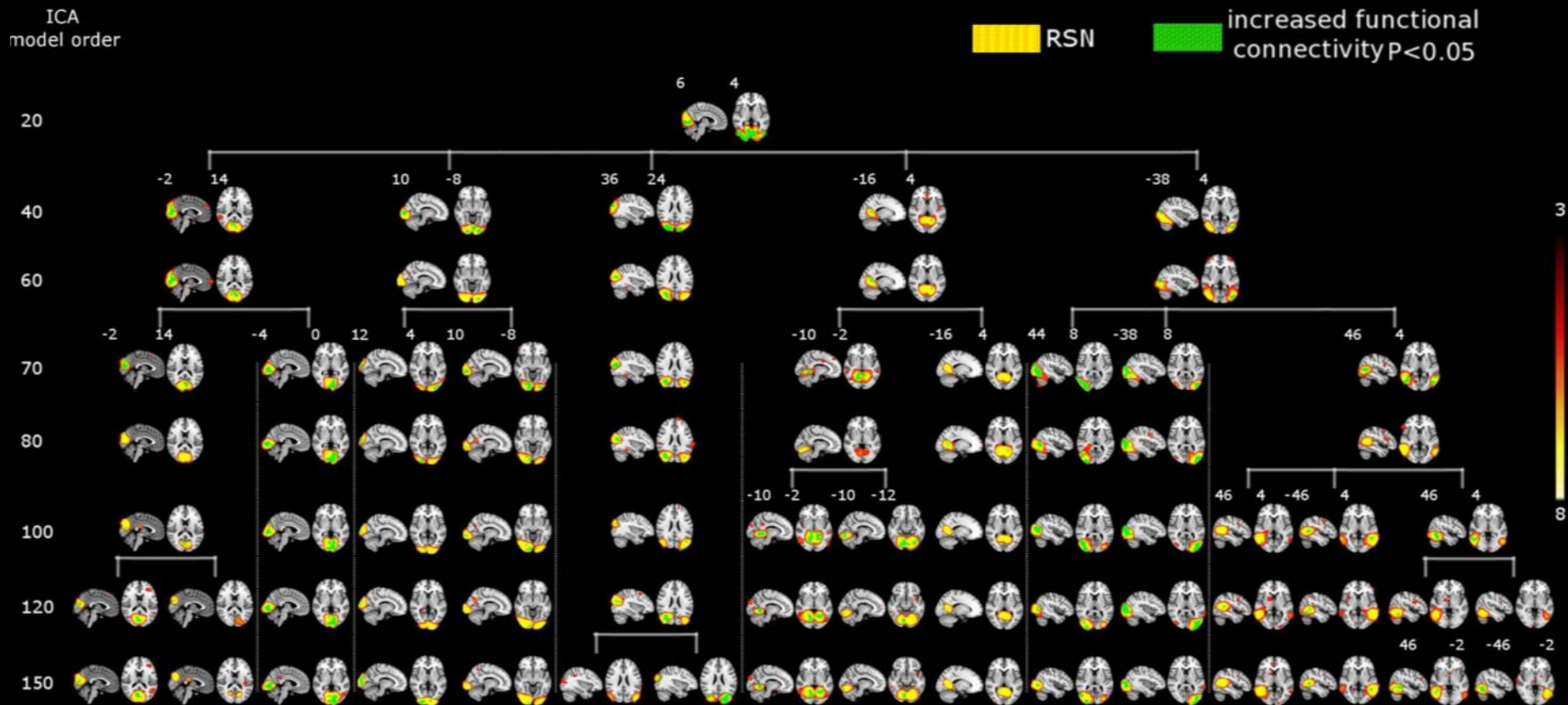
How much does it matter?



Allen, et al. (2012) Tracking Whole-Brain Connectivity Dynamics in the Resting State. *Cerebral Cortex*.

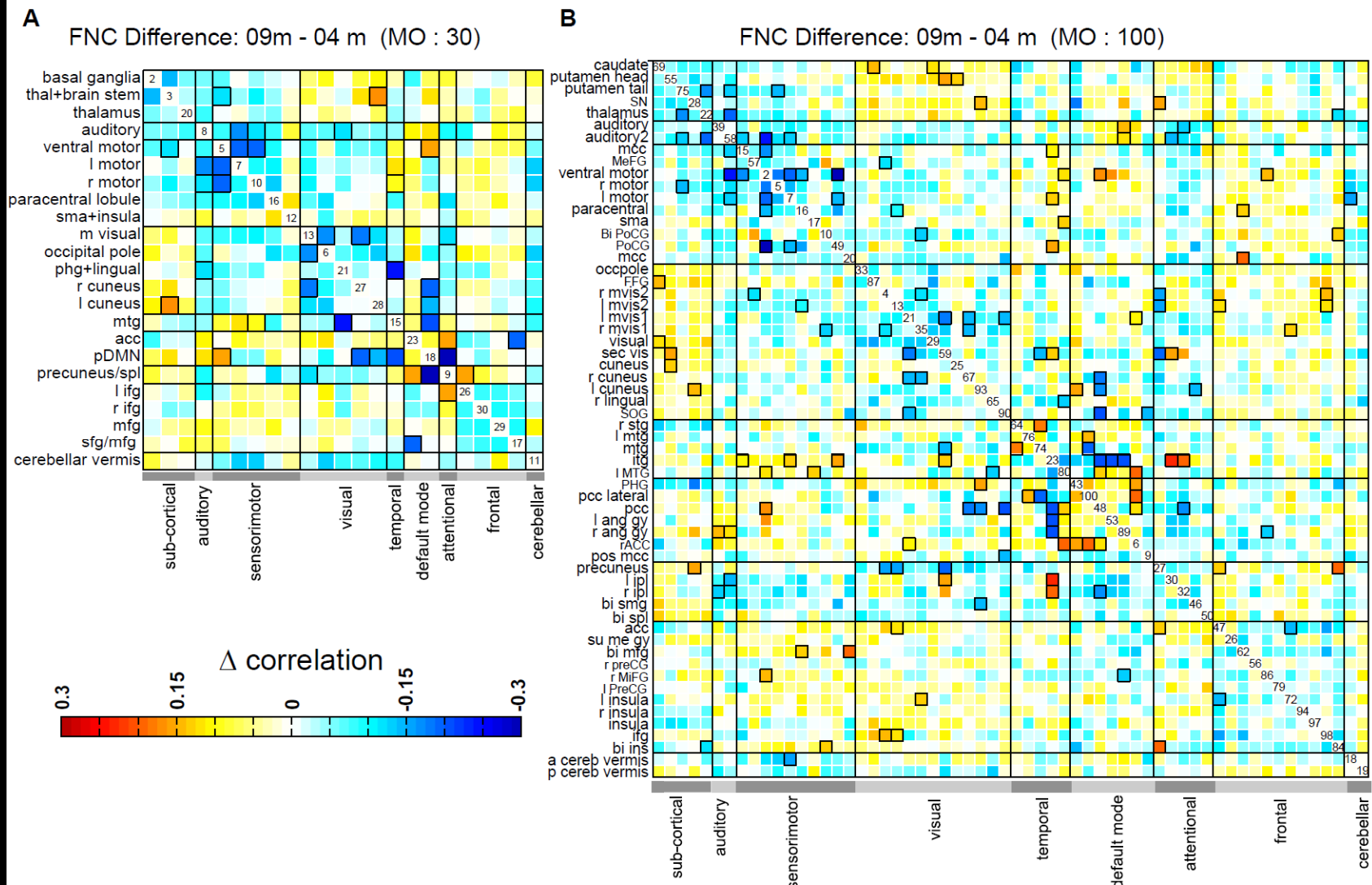
How much does it matter?

seasonal affective disorder (SAD) > healthy controls



Abou Elseoud A, Littow H, Remes J, Starck T, Nikkinen J, Nissilä J, Timonen M, Tervonen O and Kiviniemi V (2011) Group-ICA model order highlights patterns of functional brain connectivity. *Front. Syst. Neurosci.* 5:37.

How much does it matter?

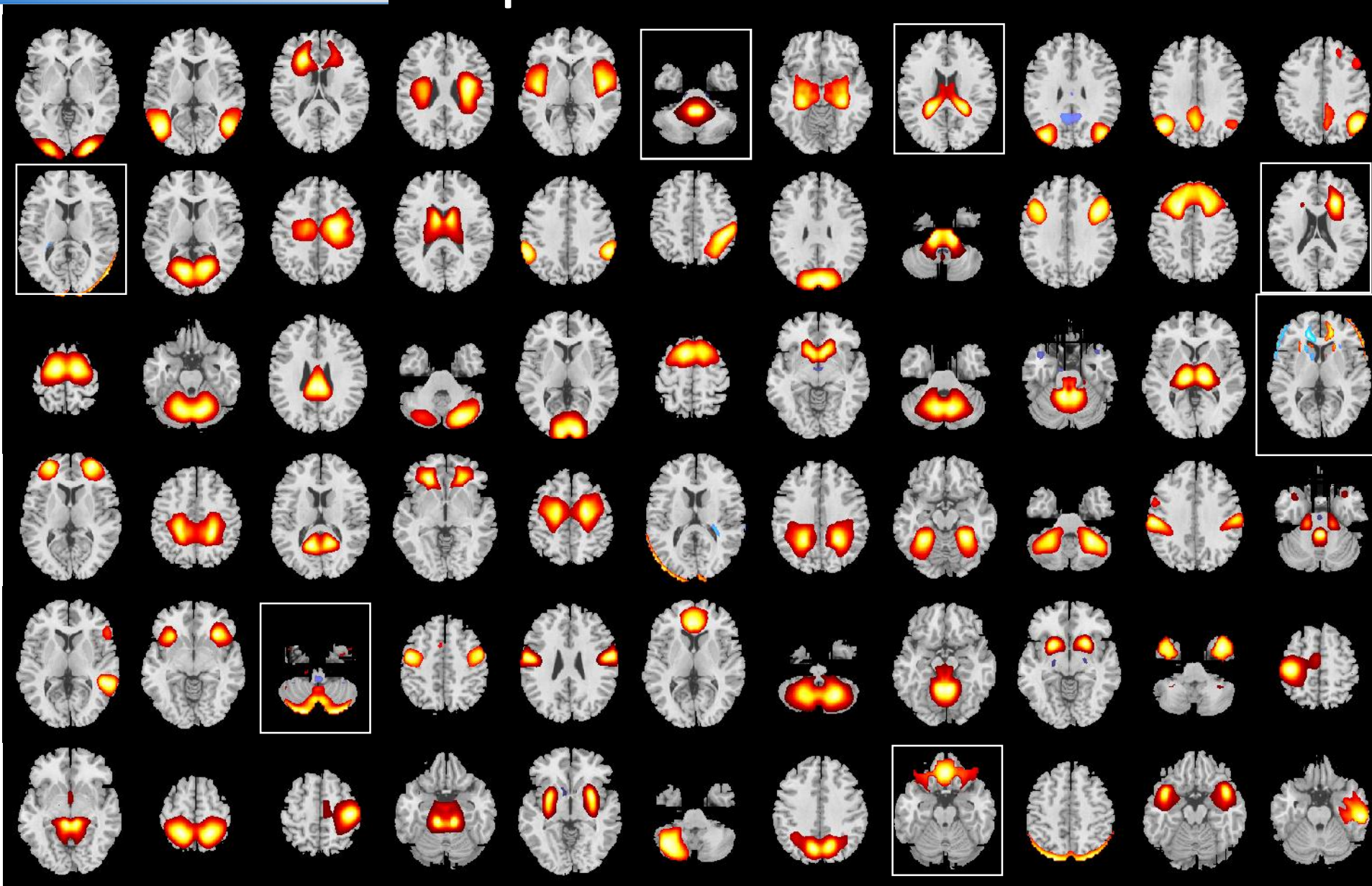


Damaraju et al., (In Press). Functional connectivity in the developing brain: A longitudinal study from 4 to 9 months of age. *NeuroImage*.

choosing a model order...

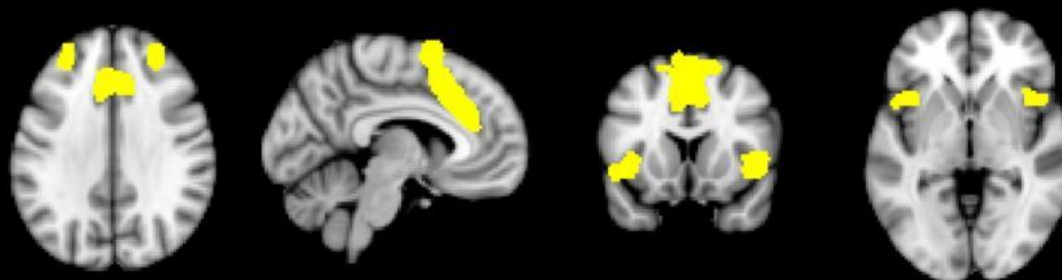
- let theoretical estimates guide you
- let empirical estimates inform you
- consider the needs and goals of your study
- consider the quality of your data
- don't worry too much

component selection



Methods to select components

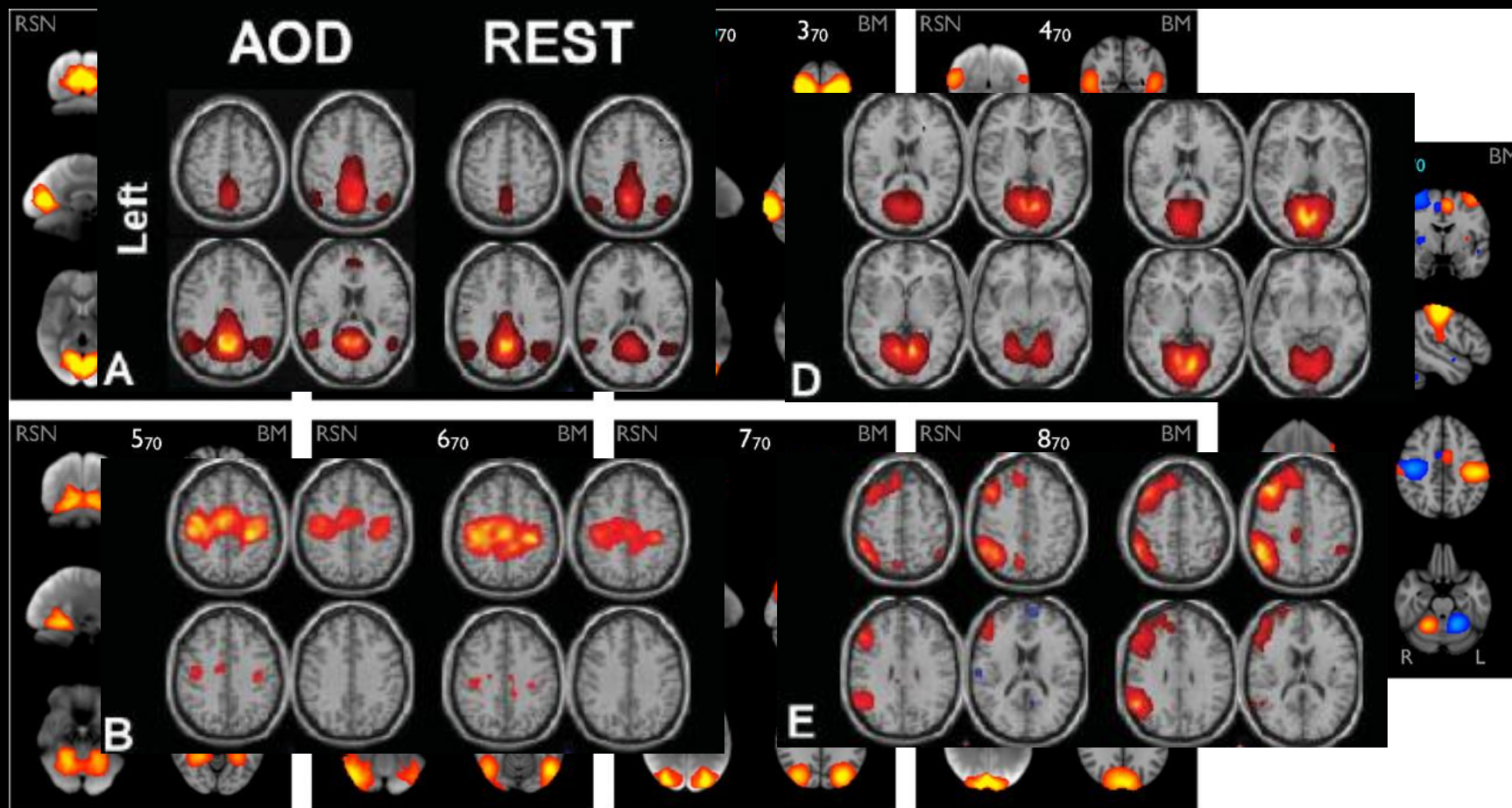
- Spatial characteristics
 - Overlap with gray matter
 - Similarity with previously defined intrinsic networks
 - MRN: mialab.mrn.org/data
 - Oxford/San Antonio: fsl.fmrib.ox.ac.uk/analysis/brainmap+rsns
 - Stanford: findlab.stanford.edu/functional_ROIs.html



Anterior Insula / Dorsal ACC (Anterior Salience Network)

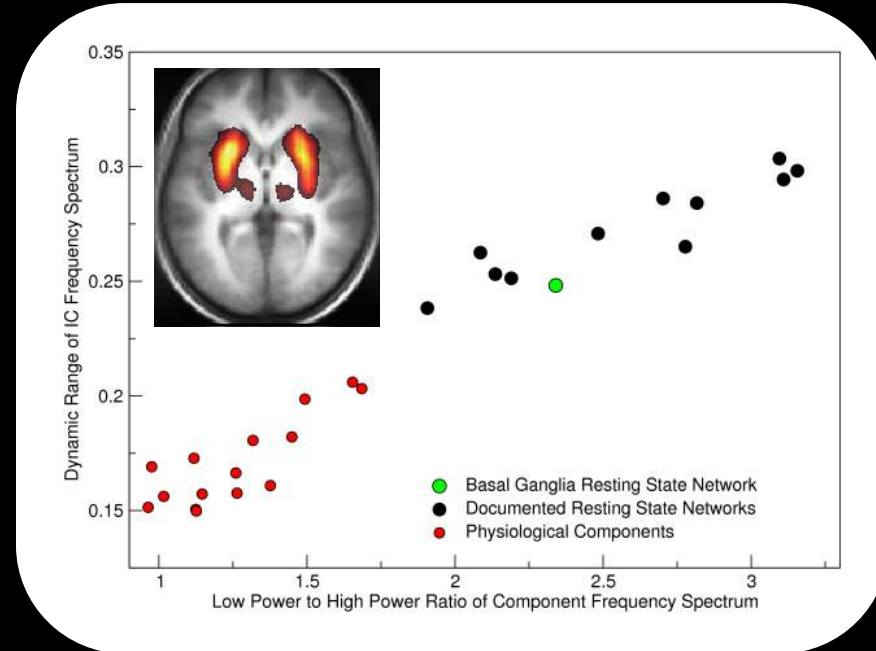
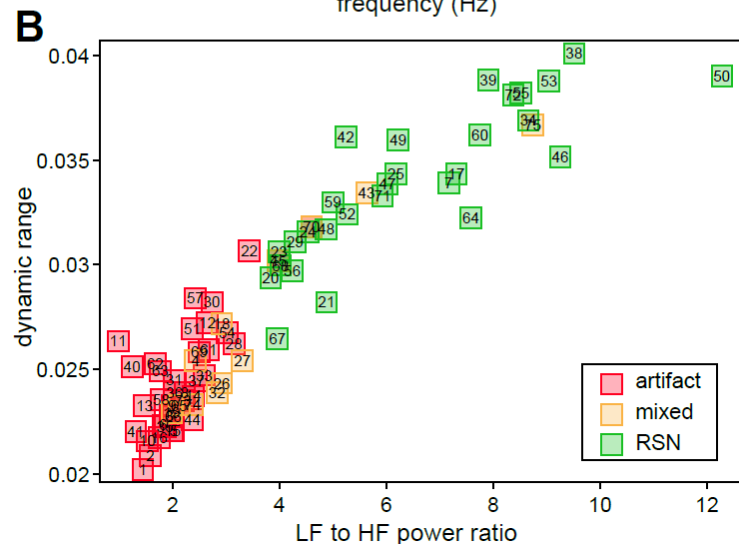
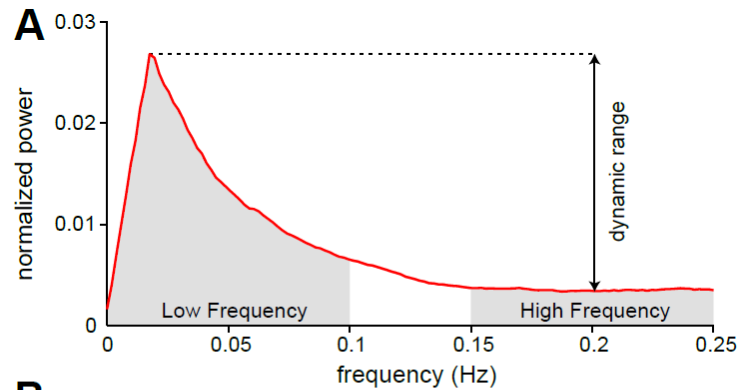
Methods to select components

How similar will components be in rest and different tasks?



Methods to select components

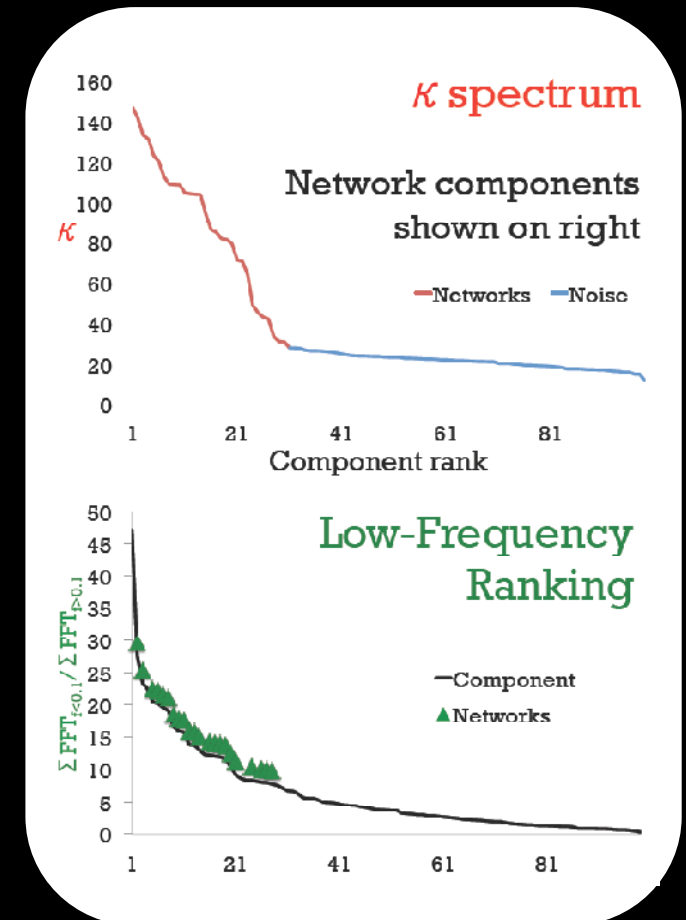
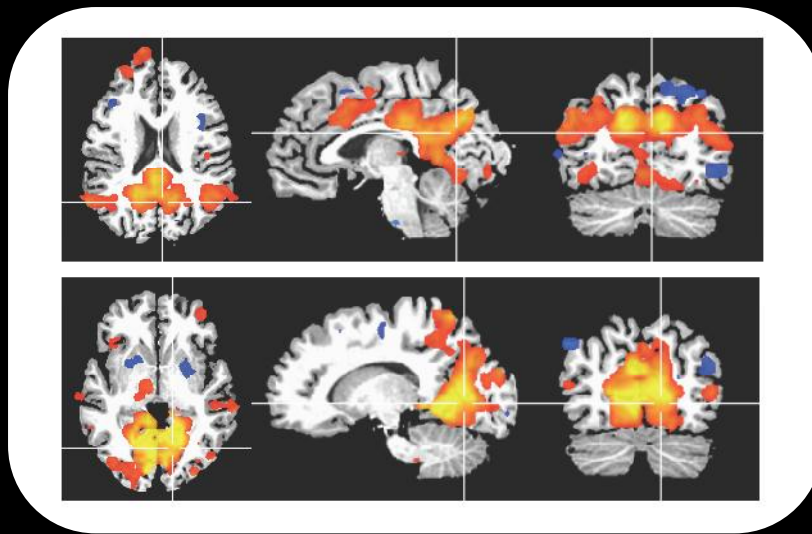
- Spectral characteristics
 - Intrinsic networks should have very slow oscillations



Robinson, S., Basso, G., Soldati, N., Sailer, U., Jovicich, J., Bruzzone, L., Kryspin-Exner, I., Bauer, H., and Moser, E. (2009). A resting state network in the motor control circuit of the basal ganglia. *BMC Neurosci.* 10, 137

Methods to select components

- Temporal characteristics
 - Time course correlation with nuisance variables (motion, CSF, respiration)
- TE-dependence of components
 - Requires multi-echo pulse sequence



Prantik Kundu, Souheil Inati, Jennifer W. Evans, Wen-Ming Luh, Peter Bandettini (2012). Differentiating BOLD and Non-BOLD Signals in fMRI Time Series Using Multi-Echo EPI, *Neuroimage*, 60(3).

Artifact removal prior to ICA?

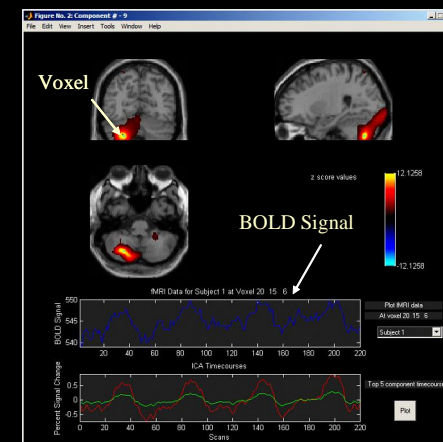
- In general we recommend to leave the data “as is”,
- ICA separates artifact sources well, especially at high model order.
- Filtering or regression of artifacts is always imperfect; residual variance will remain and ICA will have greater difficulty separating the remaining noise.
- One exception might be large movements (which violates spatial stationarity), though this is debated. Note that you will still find motion artifact components even if you have “removed” this variance with regression.
- Other exceptions might be sources of noise that are spatially heterogeneous across subjects.

to summarize

- ICA is not model free (assumes independence & consistency), but may be more flexible and have fewer assumptions than other approaches
- Can provide an alternative to voxel-wise analyses, with interpretable results
- Though a group framework, identifies the features or projection space that can be used to characterize a new subject.

software

- mialab.mrn.org/software
- Group ICA of fMRI Toolbox (GIFT)
 - Single subject/Group ICA
 - Model order estimation
 - ICASSO (clustering/stability)
 - MANCOVA testing framework
 - Dynamic FNC
- Simulation Toolbox (SimTB)
 - Flexible generation of fMRI-like data





*Your complimentary
use period has ended.
Thank you for using
PDF Complete.*

[Click Here to upgrade to
Unlimited Pages and Expanded Features](#)

ATIONS

EXTENSIONS

CHALLENGES

SUMMARY

fin