

# HCP Resting State Notes

## NO CORRECTION

Here are the results from performing PLM inference on the HCP resting state dataset provided to me by Hiro. In total this dataset contains:

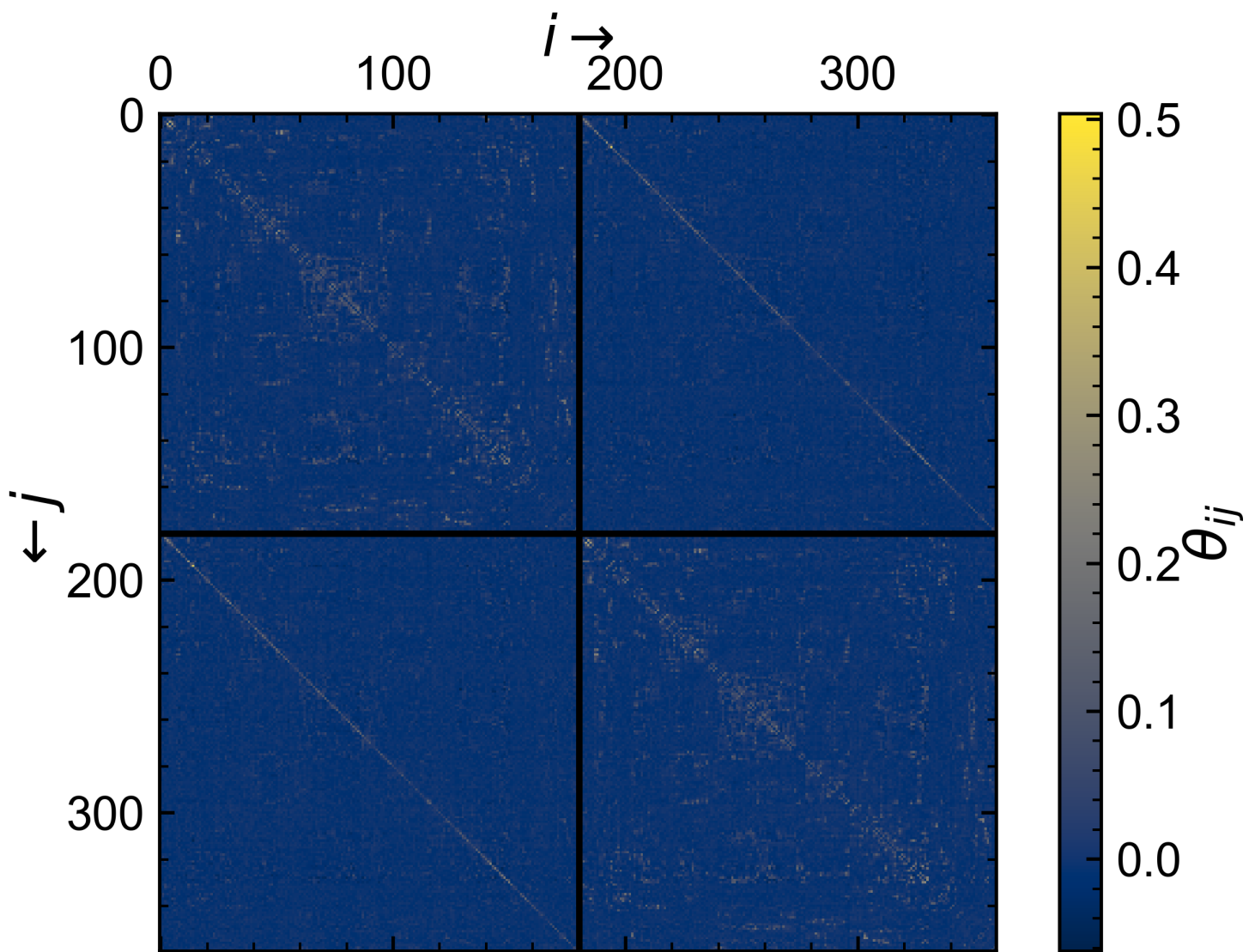
- 161 participants, for each of which I have 4724 samples and 360 ROIs (180 left, 180 right hemispheres)

I perform PLM on each individual, and on the grouped data (i.e. append all 161 x 4724 samples for each ROI). For the grouped data the number of samples,  $B$ , is 760,564. Comparing to only individual 0 at the moment, not averaging their distributions yet.

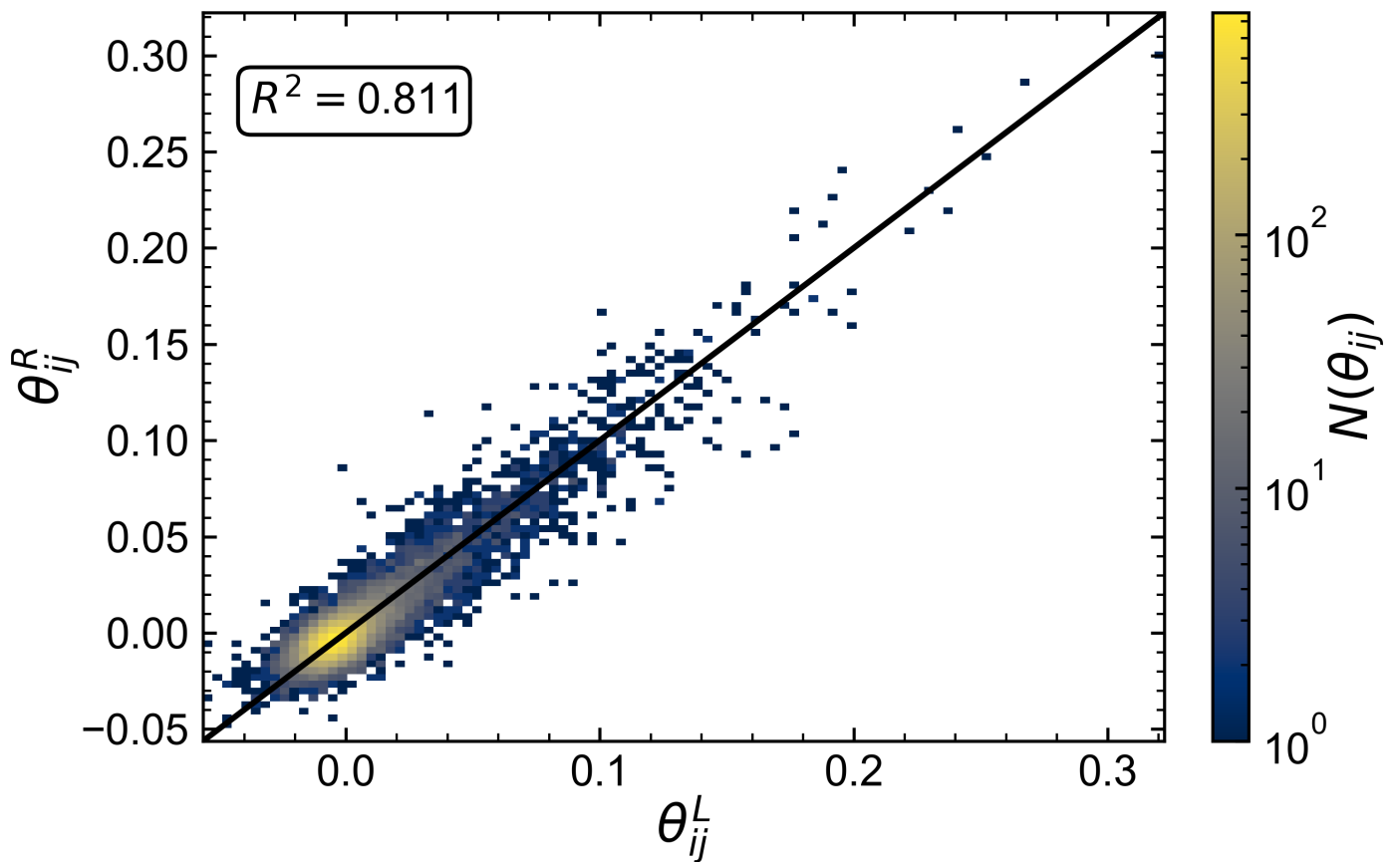
- Grouped data  $\leftrightarrow$  GRP
- Individuals data  $\leftrightarrow$  IND

## Inference overview (GRP)

### The Inferred Network

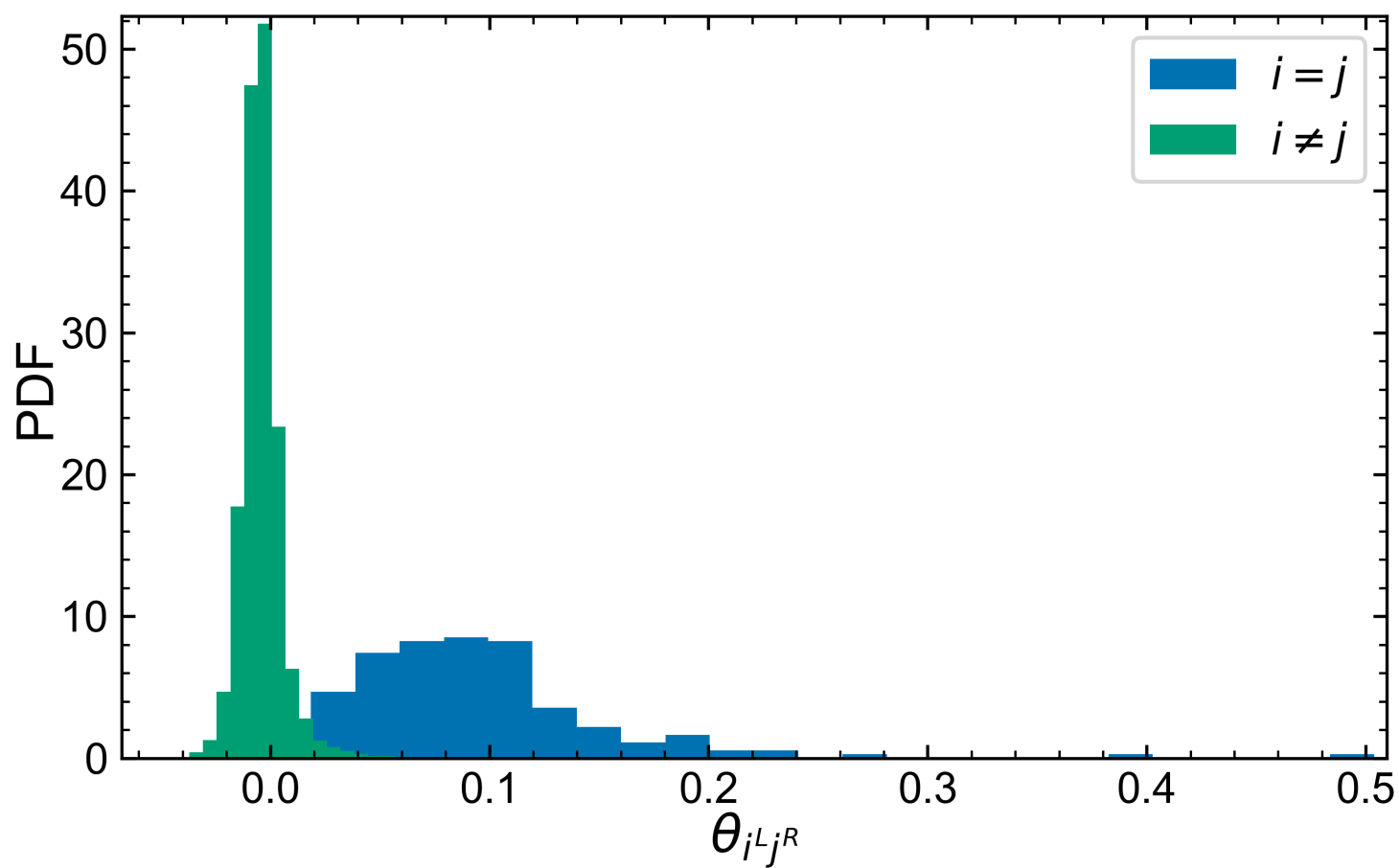


- Look at the inference output for GRP (i.e. for the typical human resting state network)
- Find interesting property; there is a high degree of symmetry between the two hemispheres
- the inter-hemisphere network (i.e. top-right) shows how left couples to right
- Symmetry is shown here by high values of  $\theta_{ij}$  on the diagonal, i.e. same ROIs in different hemispheres are strongly functionally coupled, implying if one is active the other will also be
- **BY LOOKING AT THIS DIAGONAL I CAN IDENTIFY REGIONS WHERE THIS IS NOT TRUE!**



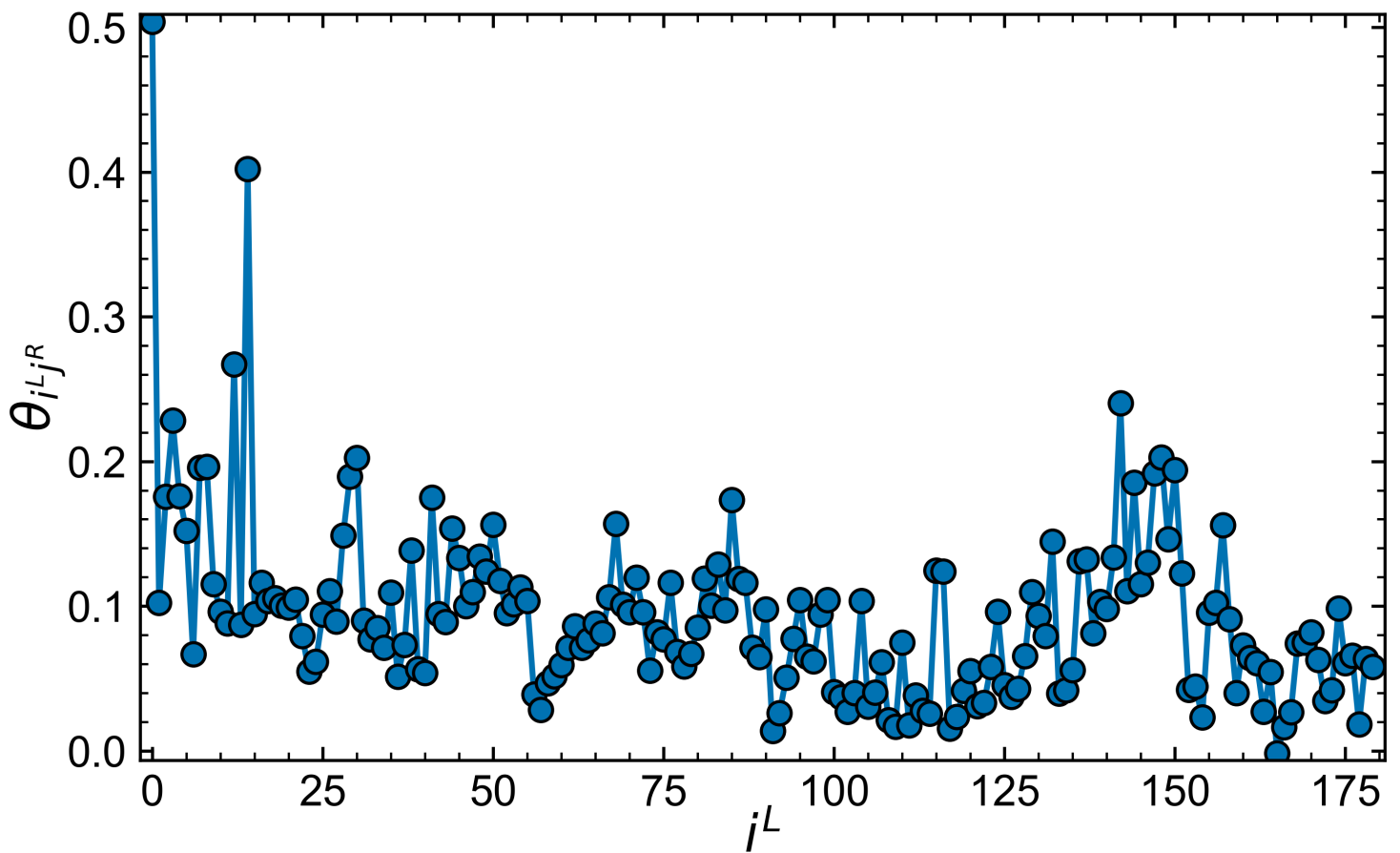
- Correlation between left and right parameter sets is high
- Because of this structuring I analyze left and right networks separately for remainder of analysis, although outliers exist
- Analyze distribution of parameters next, in order to gain more understanding of network structure (and introduce a threshold)

## Inter-hemisphere network (L-R network)



Diagonal:  $\mu_{i=j} = 0.09 \pm 0.06$

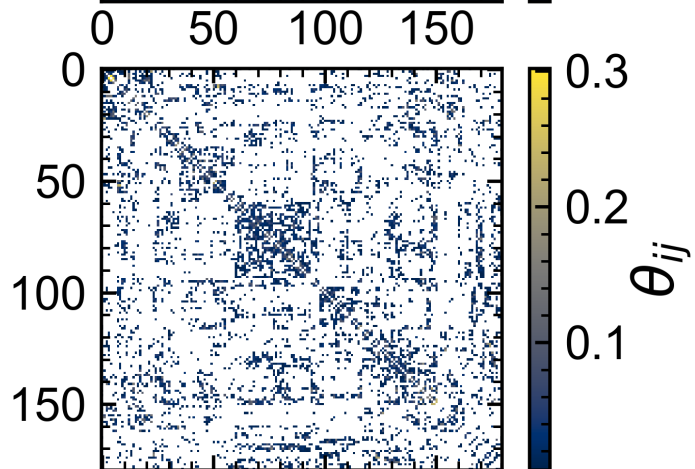
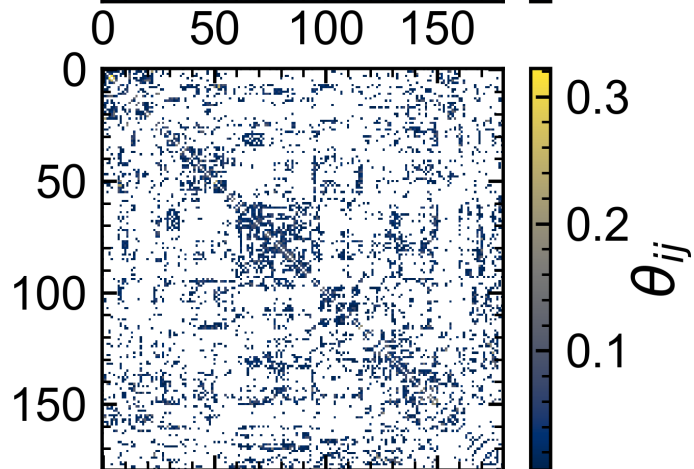
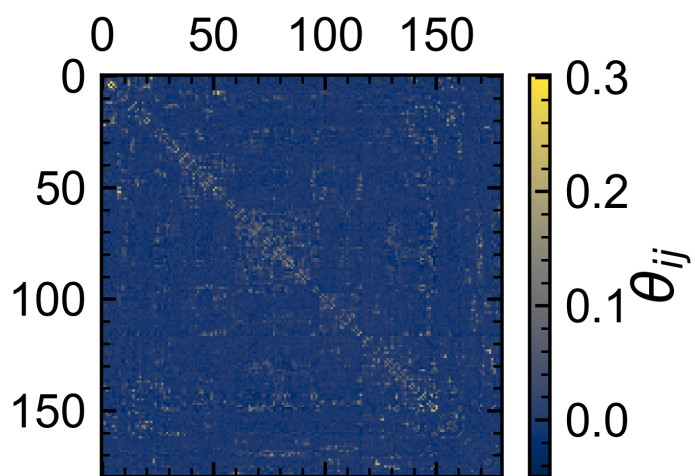
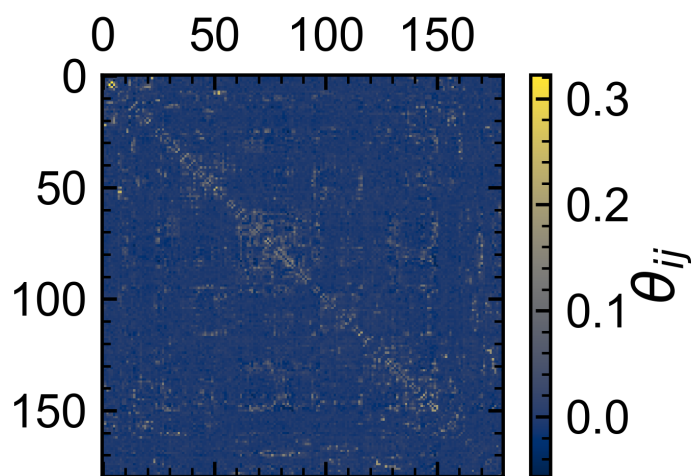
Off-Diagonal:  $\mu_{i \neq j} = 0.00 \pm 0.01$

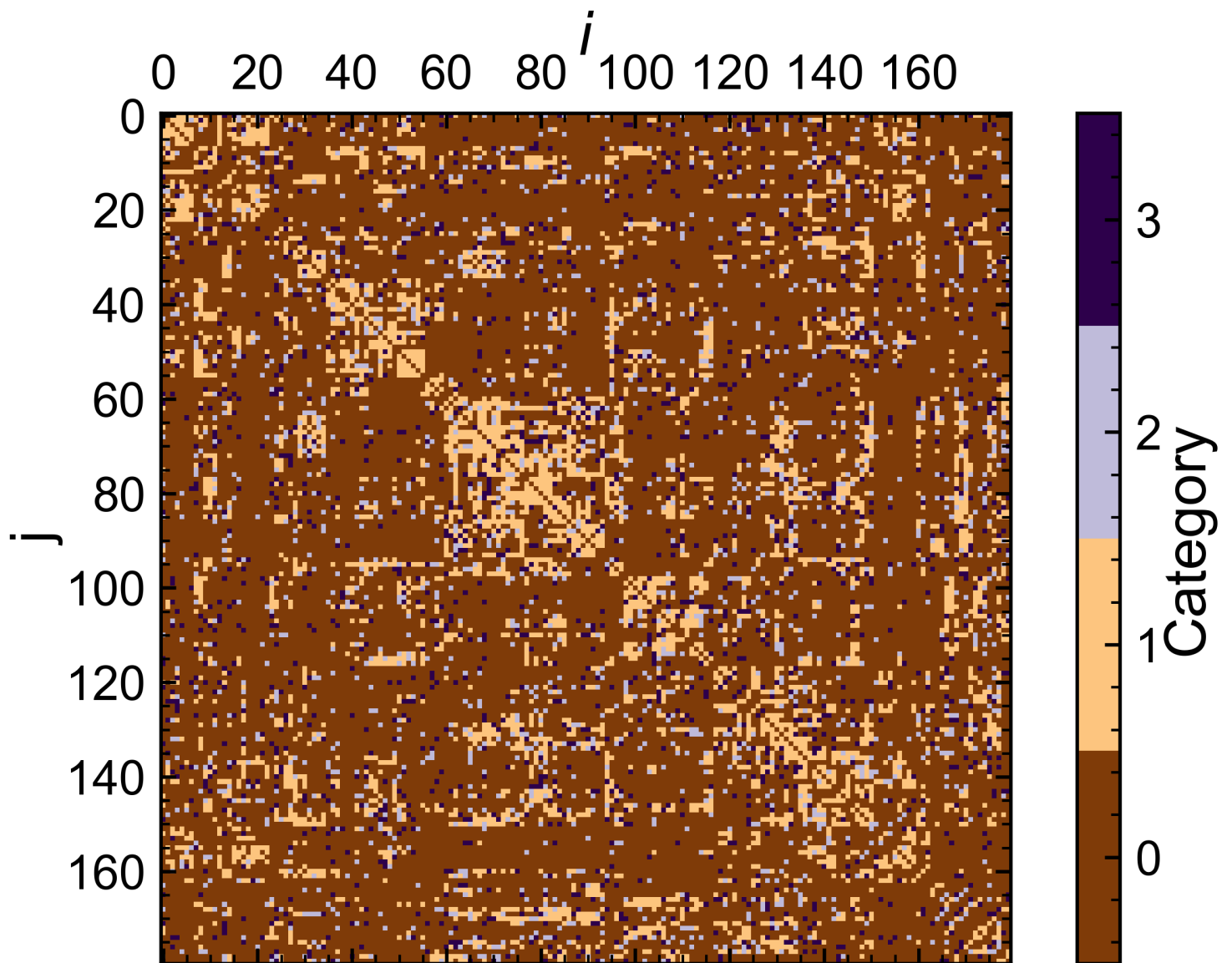


overall positive correlations

## Intra-hemisphere networks (L-L and R-R networks)

include this stuff here and just talk about thresholding afterward makes more sense as a story for your head for now.





theres a strong similarity but how to identify some differnecescomplicated because power law

## Summary

We identify 2 distinct (and similar) networks with do not couple very much with each other except for if  $i=j$ , in the left and right hemispheres

I need to do some summary plots of this!

the strenght of the off L-R couplings can only be interepreted in relation to the L-L and R-R couplings!

In fact they are some of my strongest couplings overall the (0.5 & 0.4 ones)

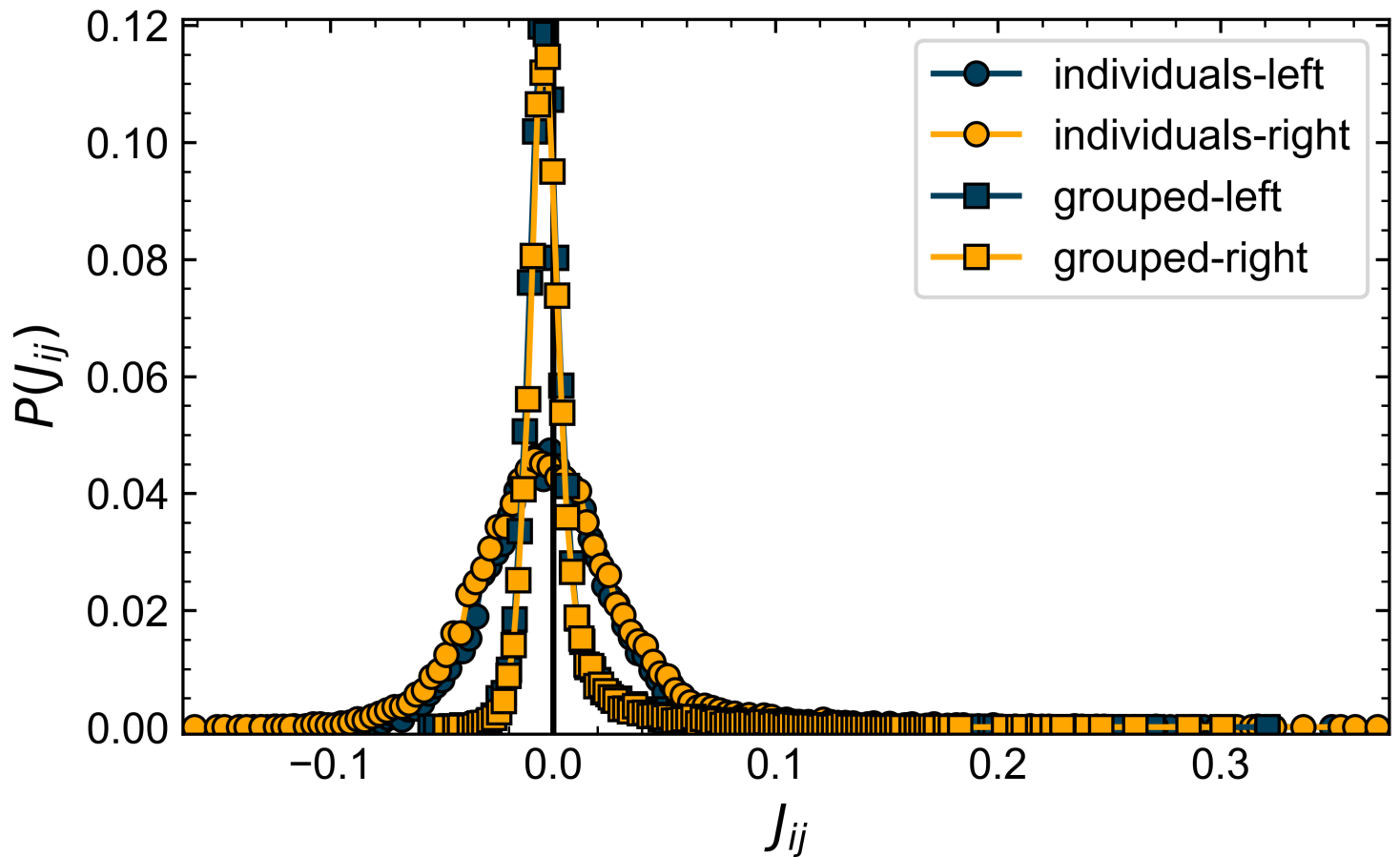
None are significantly anticorrelated

## Distribution Features

# Comparing $J_{ij}$ distributions GRP vs IND(subject=0)

- I work with each hemisphere separately, number of ROIs is  $N = 180$
- GRP -> large B ( $\sim 1e5$ - $1e6$ )
- IND -> small B ( $\sim 1e3$ - $1e4$ )

## Distribution of parameter values $P(J_{ij})$ (linear scale)



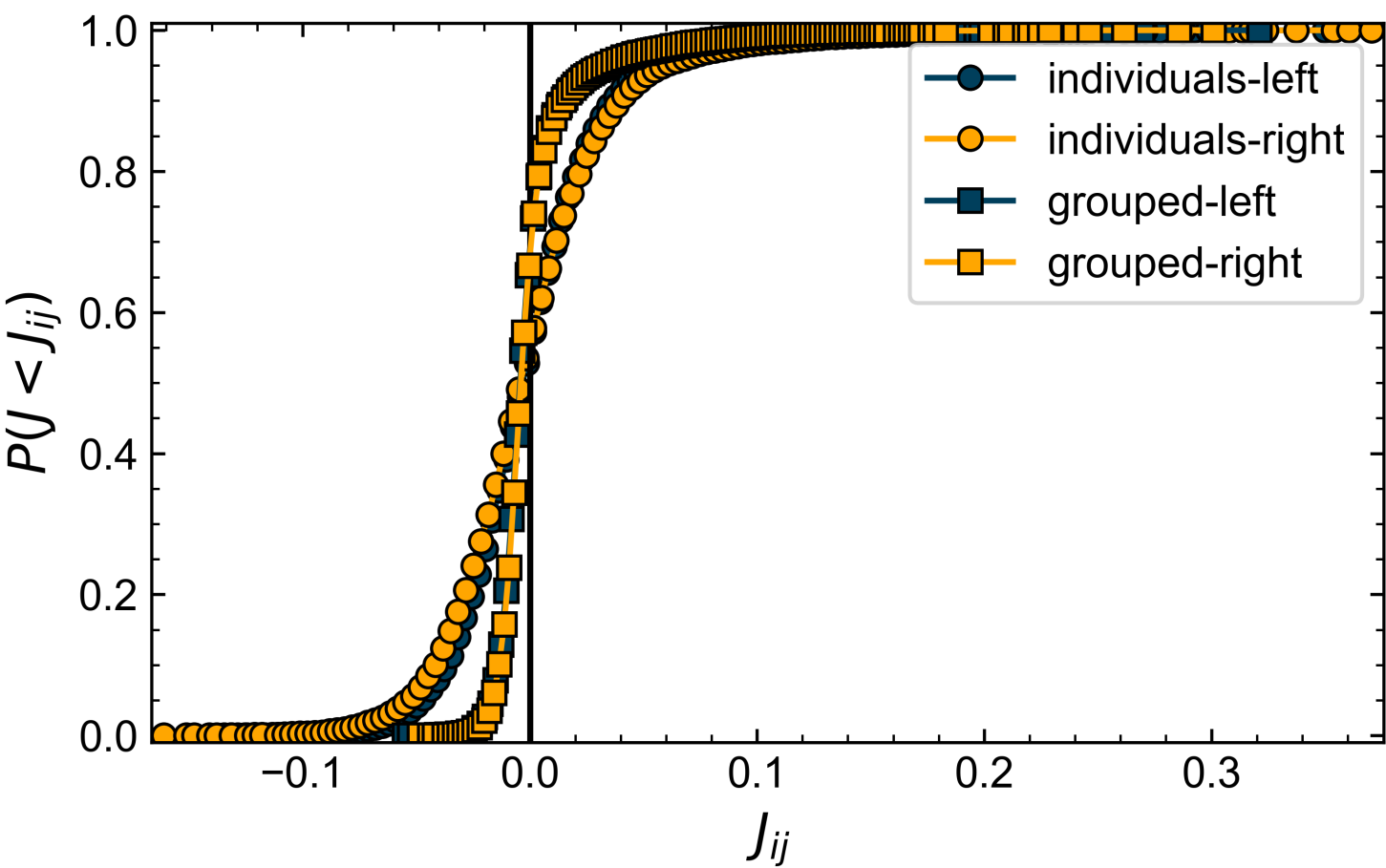
SUMMARY-OBS	IND-L	IND-R	GRP-L	GRP-R
$\mu_J N$	0.17	0.09	0.20	0.25
$\sigma_J N^{1/2}$	0.45	0.52	0.28	0.27
$\mu_J N / \sigma_J N^{1/2}$	0.37	0.17	0.71	0.92
$\text{argmax}(P(J_{ij}))$	-0.0013	-0.0083	-0.0057	-0.0026

- IND (small B condition) is more spread, **almost twice as spread!**
- Corresponds to lower temperature state-point in SK formalism.
- Mean also shifts further positive



- Relevant variable in SK-PD is the ratio  $\mu_J N / \sigma_J N^{1/2} \rightarrow \sim 1$  in GRP
- Peaks of gaussian are negative, i.e. a large proportion of population is slightly inhibitory.
- Long positive tail is responsible for positive mean

## Cumulative distribution of parameter values $P(J < J_{ij})$ (linear scale)

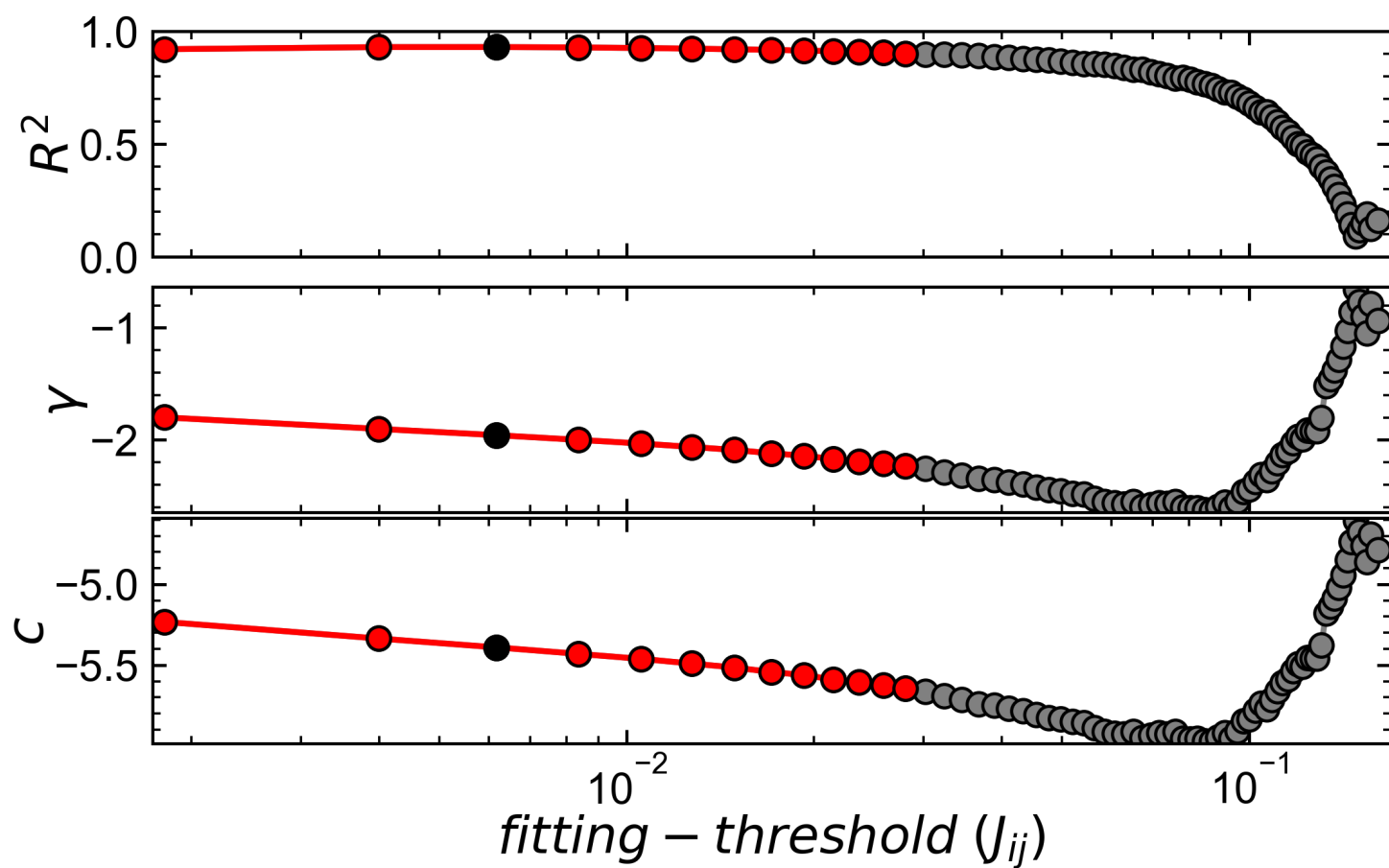
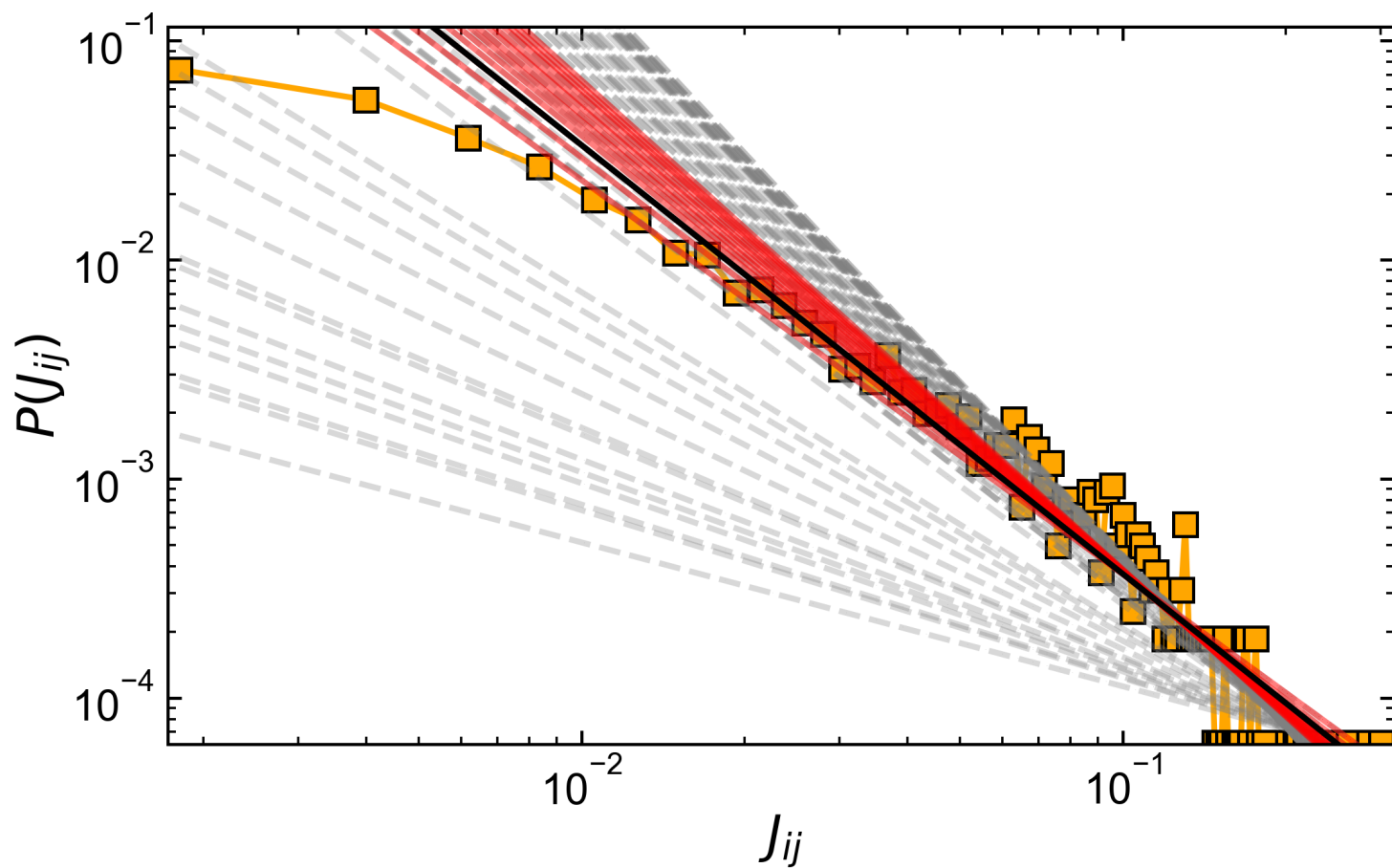


SUMMARY-OBS	IND-L	IND-R	GRP-L	GRP-R
$P(J_{ij} < 0)$	0.53	0.54	0.65	0.66

split this once I know what's in the tail!

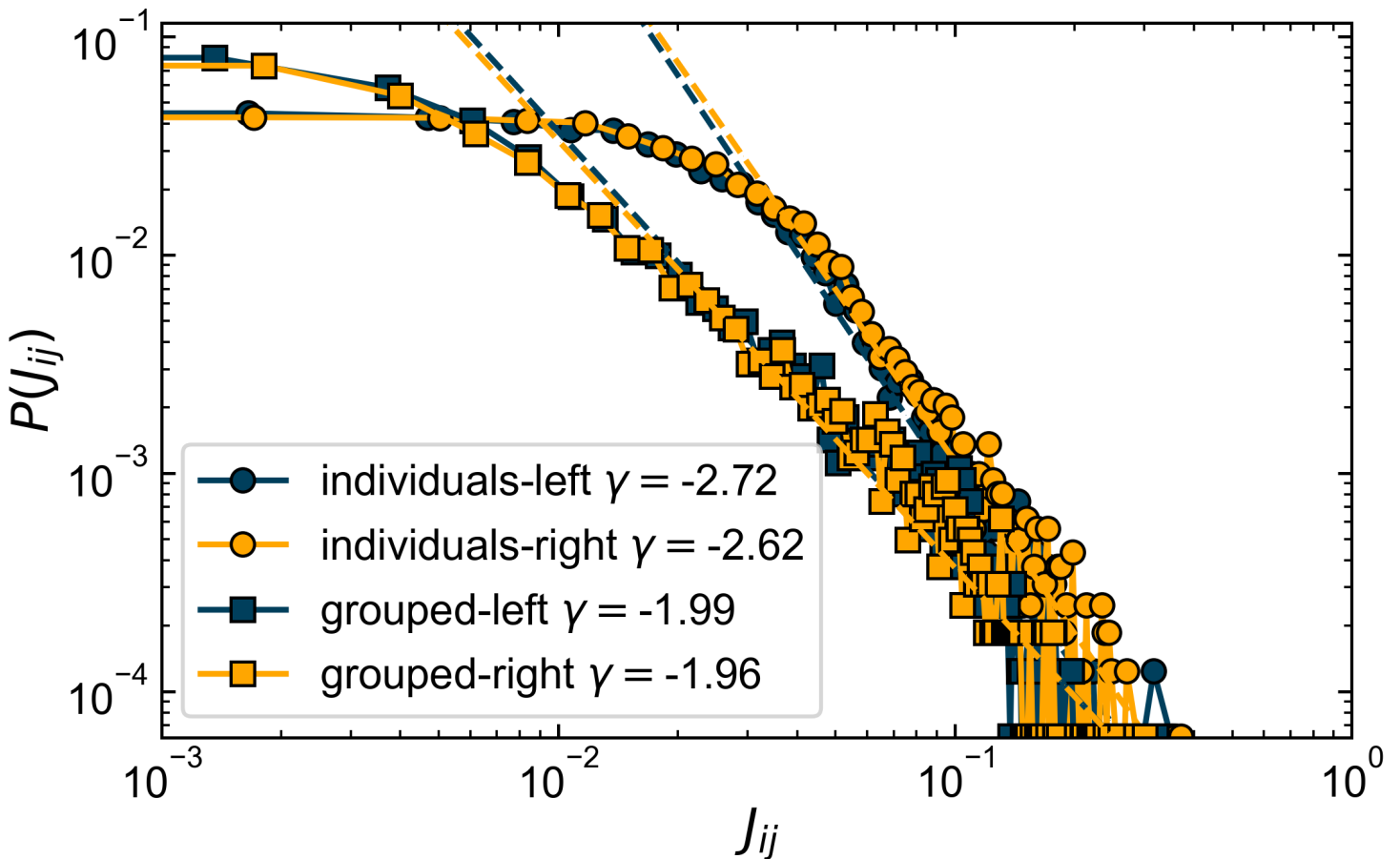
- So what does this reveal? The bias causes  $J_{ij}$  population to look more symmetric about 0
- This makes sense if we think it "stretches" the tail
- In "reality" i.e. the large B setting (GRP),  $\sim 2/3$  of the population of neurons is inhibitory. The other third is positive and sits in the tail
- Visual inspection of PDF shows that positive tail of coupling distribution follows a power-law like tail

## Fitting the Power Law tail:



- I vary the value  $J_{\text{tail}}$  and fit a straight line to  $y = \log_{10}(P(J_{ij}))$ ,  $x = \log_{10}(J_{ij})$  for  $J_{ij} > J_{\text{tail}}$
- I look at the  $R^2$  values obtained for all these fits
- I pick the value of  $J_{\text{tail}}$  which maximizes  $R^2$
- Red lines show all fits, with  $R^2 > 0.9$ , black spot is best fit
- Curvature of  $R^2$  is flat, meaning there is a reasonably large range of suitable fitting exponents, i.e. error, as shown by red points which satisfy the  $R^2 > 0.9$  condition

## $P(J_{ij})$ distribution tail features



- Plotting  $P(J_{ij})$  on a log-log axis shows that tail of coupling distribution looks like a straight line, i.e. a power law. Connects to criticality (sometimes)
- Can fit this power law and get exponents. Smaller (magnitude) exponents for GRP, i.e. as the parameters in IND are stretched the power law looks like it decays more slowly.
- Using the tail cut-off value  $J_{\text{tail}}$  and the CDF above, I can see what the probability is that a coupling value lies in the tail

SUMMARY-OBS	IND-L	IND-R	GRP-L	GRP-R
$J_{\text{tail}}$	0.0198	0.0216	0.00606	0.00617

SUMMARY-OBS	IND-L	IND-R	GRP-L	GRP-R
$P(J_{ij} < J_{\text{tail}})$	0.792	0.796	0.833	0.830

So for remaining analysis I want to return this cutoff value (use it to calculate  $N(J > J_{\text{tail}})$ ), and  $r_{2mc}$  to analyze the individual variation and compare it to the GRP values. so return  $J_{\text{tail}}$  and  $r_{2mc}$  from my tail functions

- so distro of L/R seem very similar especially for GRP. Comment on this!

So for analysis i want tail to return J cutoff + best fit params. I

For now I will define the tail as beginning where  $R^2$  is best for linear fit, i can clearly see that this is not super true though!

I won't analyse every distribution in detail for every individual..

I should have a look at the average vs the grped distros!

analysing the matricies of the tails  
start by introducing matrix and that we can threshold it above  
then talk about the power law tails  
then talk about the tresholded stuff and the assymetries we find  
I can only do this in broad strokes at the moment

Thoughts for next week:

- When I'm compairng my tresholded models, a lot of the similariteis comes from LR both containing couplings that are not in the tail. So my ~10% measure reflects similarity of the whole network (including the couplings I've thresholded out)
- I should try to also see similarity only in tail, i.e. by masking and doing simlarity analysis on a flattend version of the array (i.e. excluding all the zeros / nans)
- look through comments in notes
- Final numbers will be a % whole network similarity and a % tail similarity
- tail issue is that couplings don't overlap i.e.  $iL$  might not be in tail in right. Rethink this, because what I've just written above now doesn't really make sense anymore...
- I will have to threshold in some what no matter what... I could do the analysis for  $J_{\text{th}} = 0$  and  $J_{\text{th}} = J_{\text{tail}}$  and see how it changes?
- this is all very subjective at the end of the day. Maybe best I just stick with the simplest thing, which is similarity after threshold and only keeping the tail
- I.e. I regard couplings in the tail to be "real" and connected for this similarity analysis; although the strength of them may vary somewhat

- Put in the intro plots of the whole matrix where I identify that Mat(L) and Mat(R) look similar, **this is the basis of why I analyze the two hemispheres separately**

## Remaining Questions:

What if I infer each hemisphere separately?

**Q: what Number of neurons is in the tail? i.e.  $P(J > \text{cutoff})$ ?**

**Q: what is the exponent of the tail? + how many decades**

**Q: how do I determine if the couplings near zero are real/significant**

**Q: what happens to all these results when I do the correction -> not done for full case at the moment, too many samples!**

```
# I'll want one more thing that looks at the different r2mcs for each individual
# that will be another section: Individuals comparison
# Need to fill in the ratio B/N thing to get an idea of how good my inference is?
# this will be quite insightful in the end I think!
```

```
# I think I want to set them to the TH, 0 or NaN?
# measure how different the two networks are?
# just in terms of connectivity i.e. not strength of connectivity?
# analyse this subnetwork?
```

```
# I won't be able to recycle for multiple analysis
# yes I can if I have option to stop plotting, and return NP and other measures!
# I'm doing a lot here, maybe too much for one function / set of plots...
# but it's ok, makes sense for now
# next I want to compare "similarity" of networks
```

I STILL WANT A PLOT WHERE I COMPARE THE NETWORK TO WHAT THE CORRELATIONS WOULD IMPLY i.e. why is this better than simple functional connectivity networks

I can also still talk about the hs somewhere... which I currently ignore to be honest