

Determining rank of the dynamic fMRI Networks

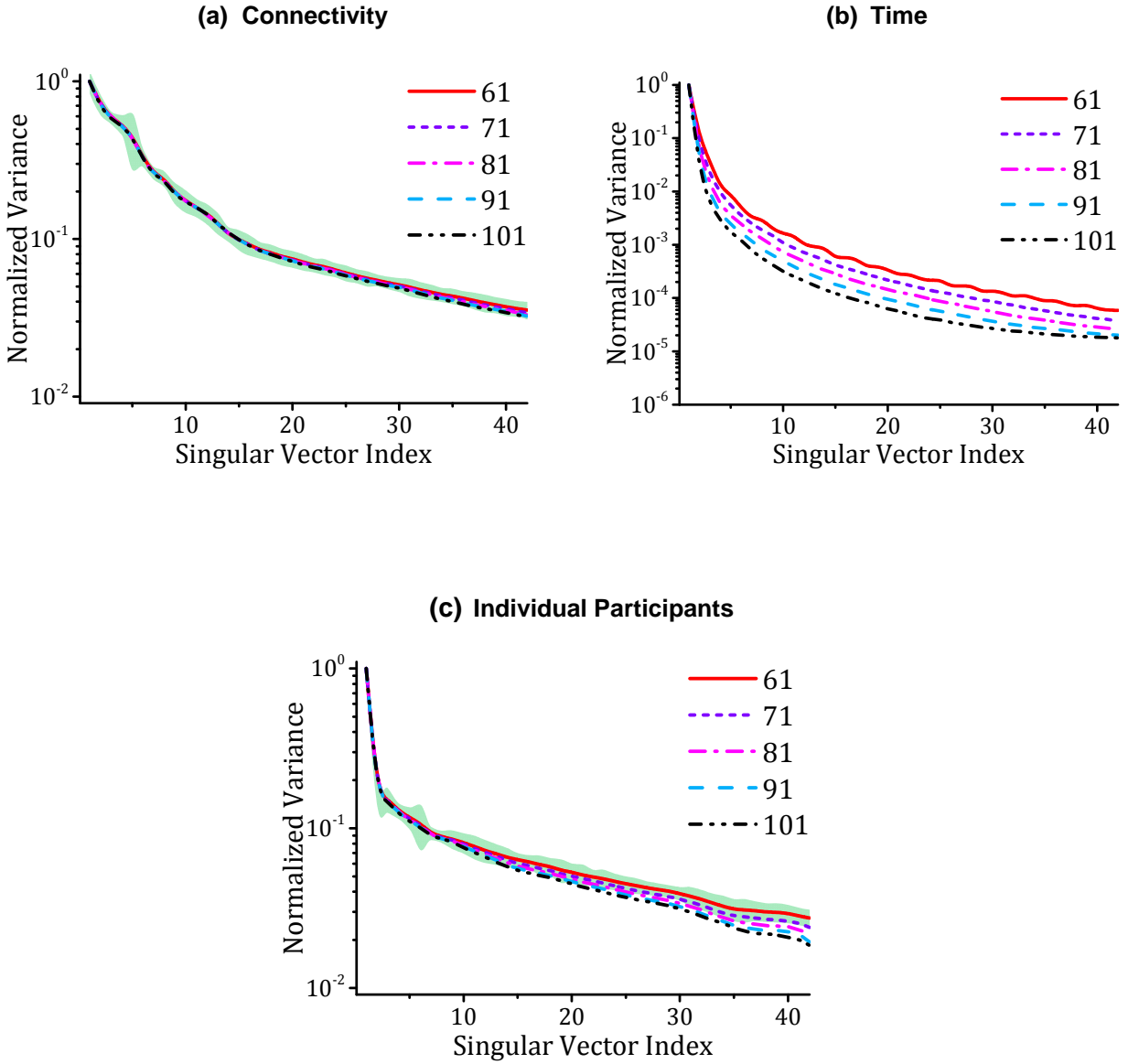


Fig. B.1. The normalized variance represented by the singular vectors of the connectivity tensors thresholded at 10% density in different modes, i.e. connectivity, time and participants. Here, variance of the data along each singular vector, was computed as the square of the corresponding singular value. The resulting measures were normalized to the first singular vector variance and averaged over the 100 validation folds. These figures show that at $R = 21$, the normalized variance decreased to 5%, in all 3 modes. Furthermore, over 85% of the total

variance was captured by the first 21 singular vectors. Hence, $R = 21$ was chosen to reduce the dimensionality of the connectivity tensors. Each curve indicates a specific window size data as depicted by the legend. The shaded area denotes $\pm 3 \times$ standard deviation of the normalized variance for window size 61 time points. For the remaining window sizes the standard deviation was in the same range. The range of standard deviation of time singular vectors was much smaller than the scale of the figures, thus, the shaded area is not observable in (b).

Descriptive data

Table B.1. Descriptive data, mean (SD) [range] on entire sample, and mean (SD) of weight loss groups. The data indicates that there is not a significant association between sex and weight loss groups, as examined by a chi-squared test (p-value > 0.05). Additionally, the same statistical test showed that interventions and weight loss groups were not significantly associated. Two sample t-test did not reveal a significance difference for Age, BMI, and baseline weight between the two weight loss groups (p-value > 0.05). As expected based on the group assignments using a median split, both weight loss (Kg) and weight loss percent were statistically different between the low and high weight loss groups.

Variable	Entire Sample (N = 52)	Low Weight Loss Group (N = 26)	High Weight Loss Group (N = 26)	P-Value
Sex				
Women	39	19	20	0.75
Men	13	7	6	
Intervention				
WL	14	10	4	0.09
WL + AT	15	8	7	
WL + RT	23	8	15	
Age	67.62 (0.73) [60.70, 79.80]	66.73 (3.88)	68.43 (6.08)	0.23
BMI (Kg/m ²)	34.11 (0.52) [28.14, 41.98]	34.48 (3.63)	33.88 (3.72)	0.56
Baseline Weight (Kg)	93.28 (12.80) [71.76, 129.09]	95.56 (14.58)	91.00 (10.53)	0.20
Weight Loss (Kg)	7.69 (6.66) [-2.81, 23.41]	2.64 (3.42)	12.74 (5.07)	<0.001
Weight Loss (%)	8.41 (7.14) [-2.84, 26.44]	2.87 (3.62)	13.96 (5.18)	<0.001

Prediction performance of networks created using food cue fMRI

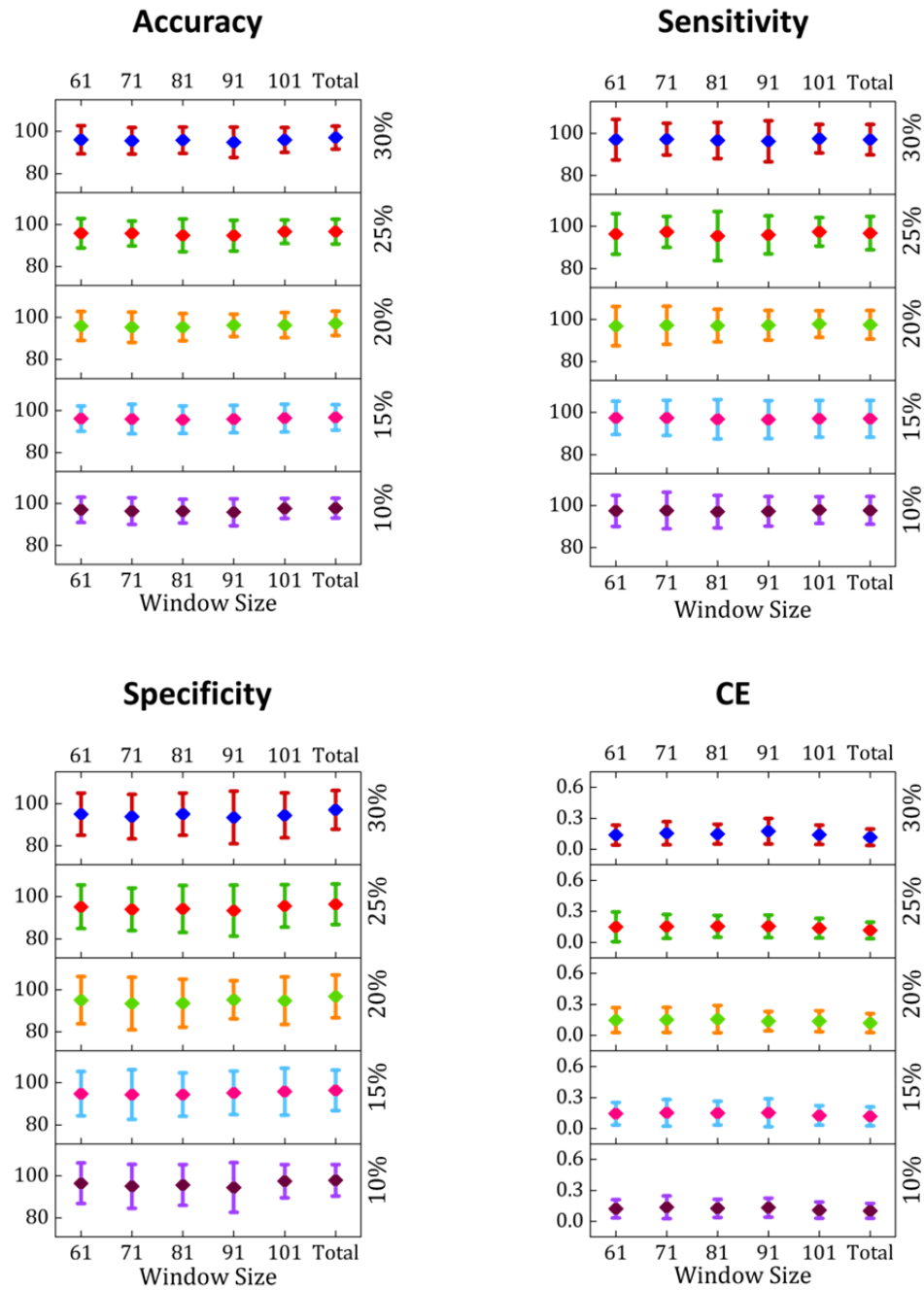


Fig. B.2. The prediction performance measures obtained using the dynamic networks generated by food cue fMRI time series, with different window sizes and different connectivity density thresholds. A paired sample t-test failed to show that classification performance based

on these networks was any different from the prediction performance using the resting state data, $p > 0.05$. This comparison was performed on the networks integrating different window sizes data, namely "Total", and density thresholds of 10%, as these networks showed outperformance for the resting state analysis (see Fig. B.3).

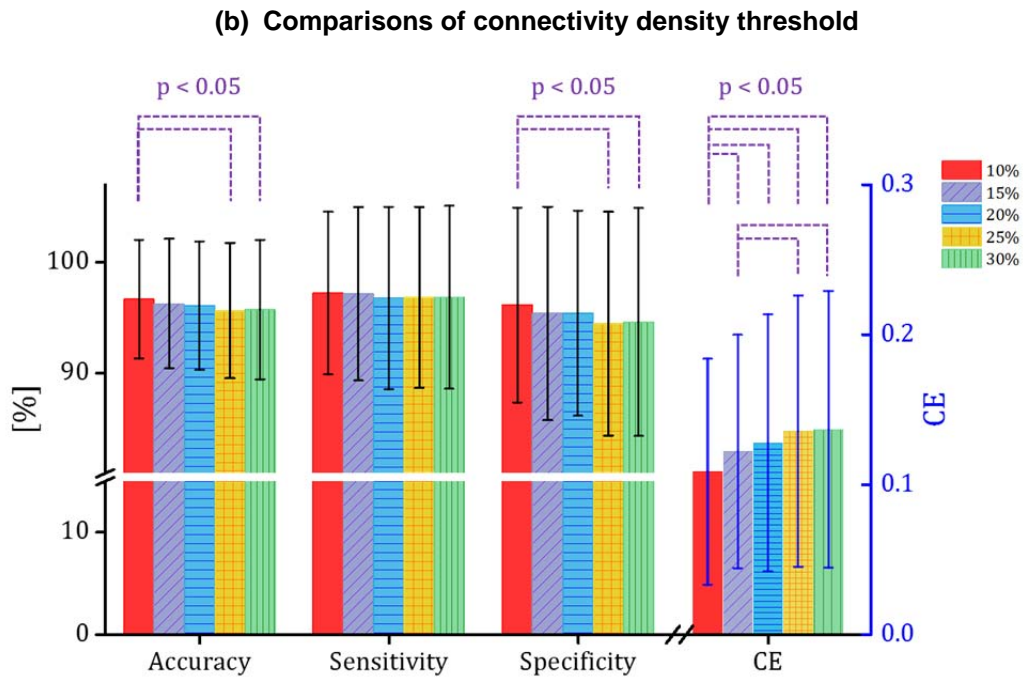
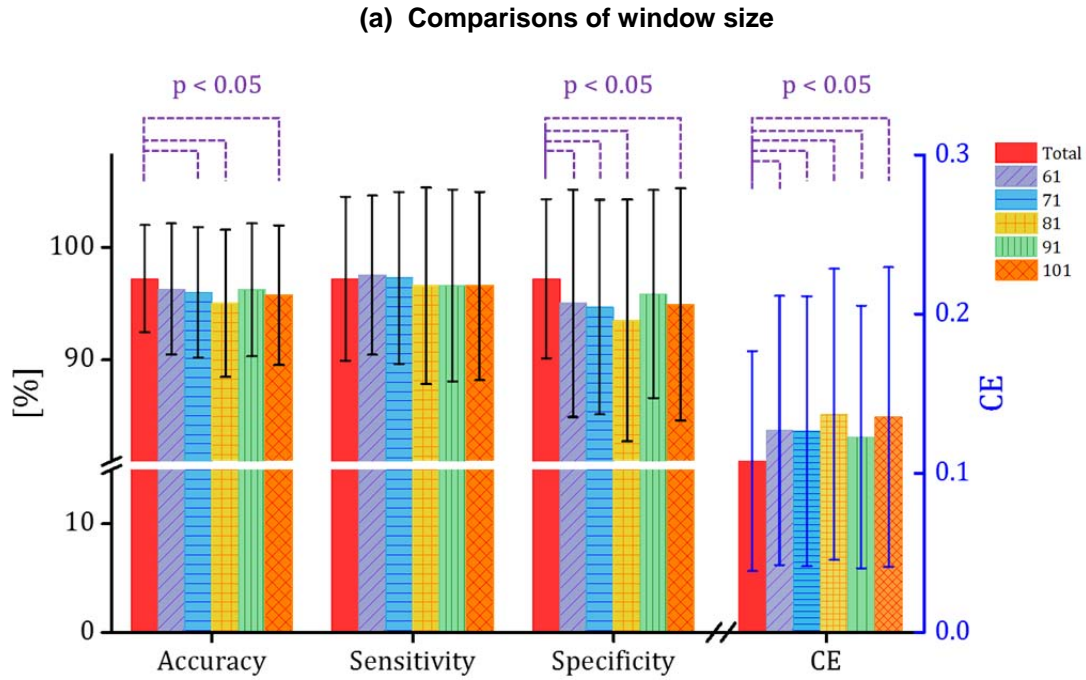


Fig. B.3. Comparisons of the average prediction performance measures obtained using (a) different window sizes, for each window size the average of prediction performance was calculated over 5×100 (number of density thresholds × number of permutations in each run of

analysis) prediction measures obtained using the same window size; and (b) connectivity density thresholds, for each density threshold the average of prediction performance was calculated over 6×100 (number of window sizes \times number of permutations in each run of analysis) prediction measures obtained using the same density threshold. The significantly different pairs are marked with the corresponding p-value.

HOSVD coefficient time series of the 9 highest-ranked principal components

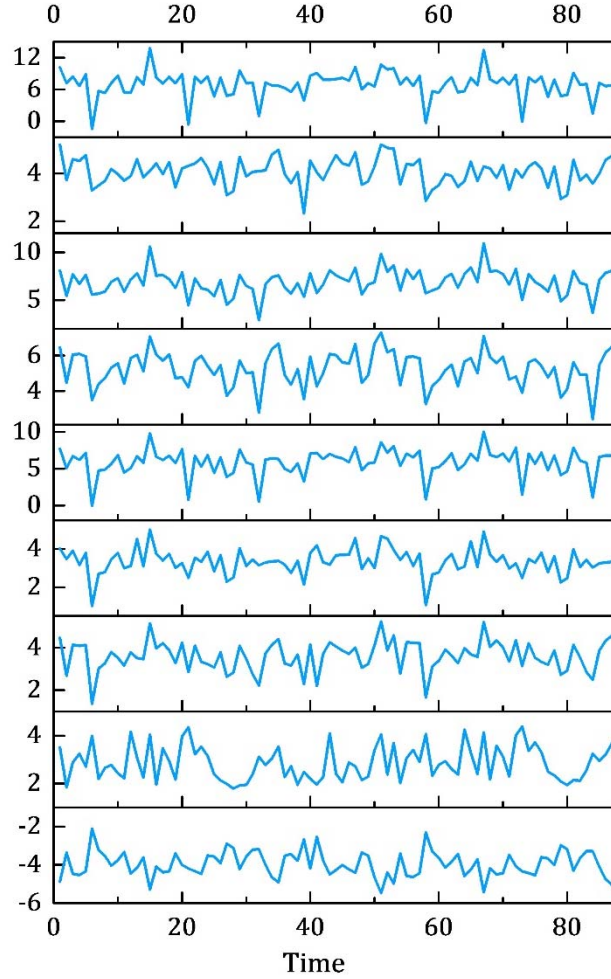


Fig. B.4. Coefficient time series of the 9 highest-ranked principal components, sorted from highest-ranked (top) to lowest-ranked (bottom), for a randomly-chosen individual participant. Using the core idea of SVD, each participant's connectivity tensor can be written as a linear composition of the principal components, for which the coefficient of each principal component is in the form of a time series. As described in the main document (subsection 2.6), the time series are computed as $\mathbf{C} = \mathbf{G}_r \left(\mathbf{U}_r^{(3)} \otimes \mathbf{U}_r^{(4)} \right)^T \in \mathbb{R}^{R^2 \times TM}$ which was then reshaped to reconstruct the reduced-rank connectivity tensor $\mathcal{C} \in \mathbb{R}^{R \times R \times T \times M}$. Time series of the first 9 diagonal entries (corresponding with the 9 highest-ranked principal components) of the tensor \mathcal{C} are shown in

the figure. It was previously explained in the main document (see Figure 5) that diagonal entries over-contributed to the group discrimination, as compared with off-diagonal entries.