

## Introduction

In 1991 Felleman and Van Essen [1] proposed their well-known model of the functional organization of the visual system. Over the last decade, at least two main limitations of the model have been identified. First, Hilgetag and colleagues [2] have shown that the model of Felleman and Van Essen is underconstrained in the sense that their data is consistent with many different cortical-connectivity networks. Second, several authors, most notably Schmolesky [3], have gathered spike timing data that seems to be inconsistent with the hierarchical functional organization as proposed by Felleman and Van Essen [1]. Most notable, the first spikes of areas V4 and FEF are too late and too early respectively.

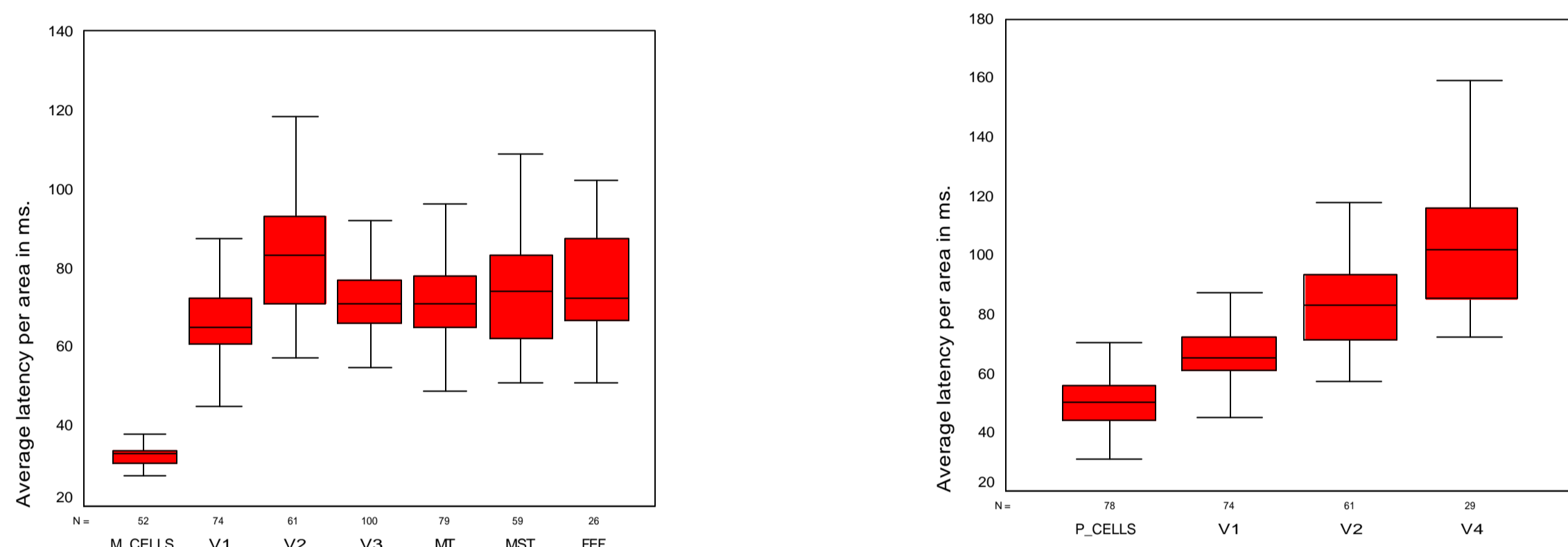


Figure 1: Mean onset latencies in the dorsal and ventral pathways, showing a sequence in the ventral pathway and simultaneous onset in the dorsal pathway. Data used from [3].

In an attempt to address these two limitations, we present a method that combines the data of a large range of studies on structural connectivity with spike timing to generate cortical-connectivity networks in a data-driven manner. We hope to show that 1) this method yields valid models that characterize the visual system and 2) these models fit the available anatomical and latency data better than previous models.

## Methods

### Data collection

The structural connectivity data was gathered from the CoCoMac database (<http://cocomac.org/>) [4]. This database contains tracer data from a large amount of studies conducted on adult macaque monkeys. We applied the Objective Relational Transformation [5] to generalize over the various parcellation schemes used in these studies. The spike-timing data were collected from a number of papers and reviews (e.g., [3], [6]) and combined using the approach of Lamme and Roelfsema [6].

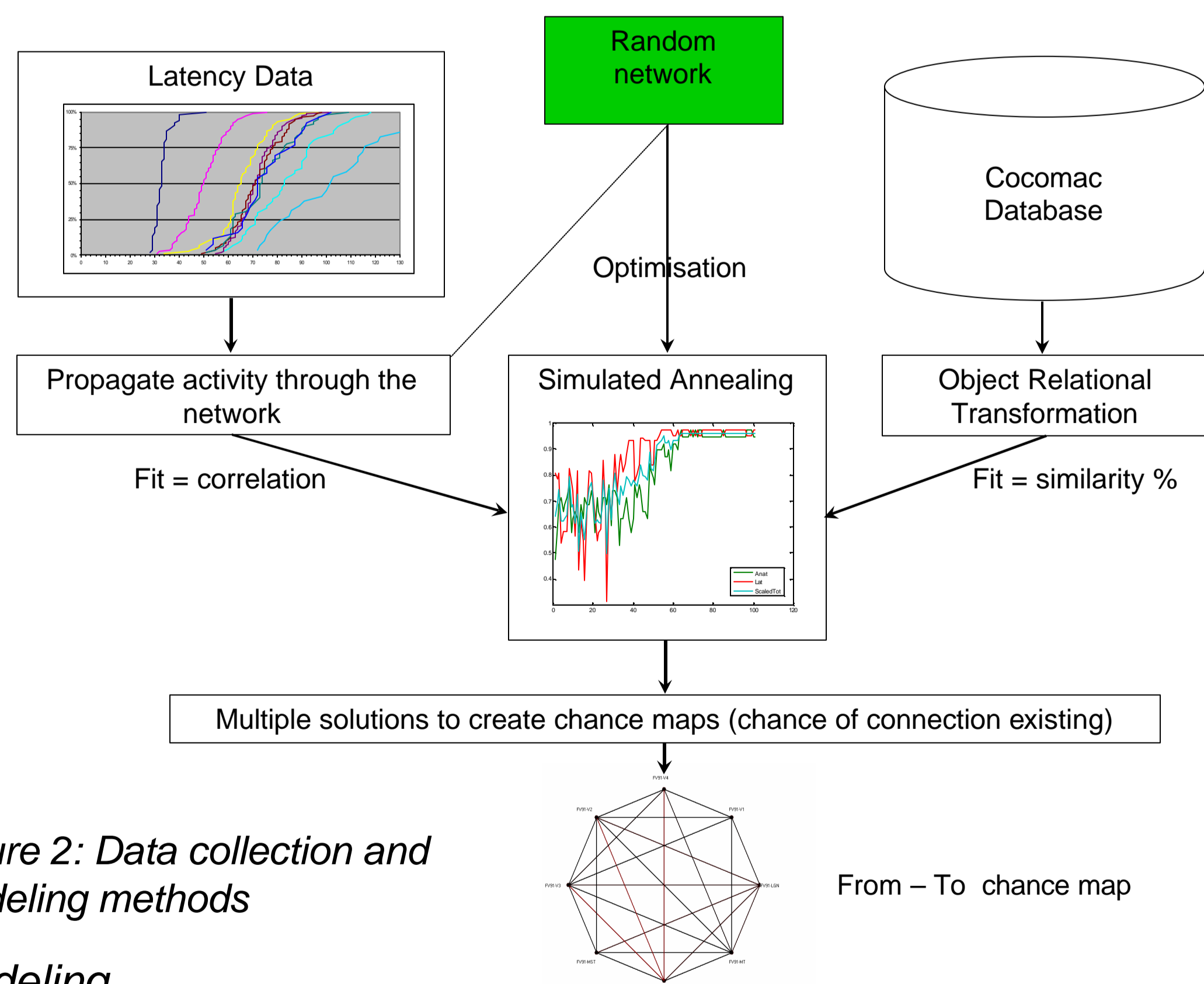


Figure 2: Data collection and modeling methods

### Modeling

To generate cortical-connectivity networks in a data-driven manner we used an optimization method known as simulated annealing. We started with a random connectivity matrix and turned individual connections on or off to optimize the fit with the data in a stochastic way. The amount of fit with the structural-connectivity data was expressed in a percentage of fit with the CoCoMac database [4] records. The spike-time fit was obtained by propagating activity through the generated cortical-connectivity networks and computing a rank-order correlation with the actual spike-time data.

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## Results

The results show that the hierarchical organization of the visual system as proposed by Felleman and Van Essen does not yield the best fit with the structural-connectivity and spike-timing data. Our networks have a higher fit and contain several remarkable features. First, the best-fitting network contains direct, subcortical pathways to FEF, which are absent in the Felleman and Van Essen hierarchy. This result is supported by biological data. Both Beaulieu [7] and Romansky [8] found a subcortical pathway between LGN and FEF. Second, the pathway to V4 in our networks is less direct than in the Felleman and Van Essen network.

From:	To:	LGN	MT	FEF	MST	V3	V2	V4	V1
LGN									
MT				1	1	1	1	1	1
FEF		1			1	1	1	1	0
MST		1	1						1
V3		1		1			1	1	1
V2		1		1	1			1	1
V4		1		0	1	1			1
V1	1	1	0	0	1	1	1		

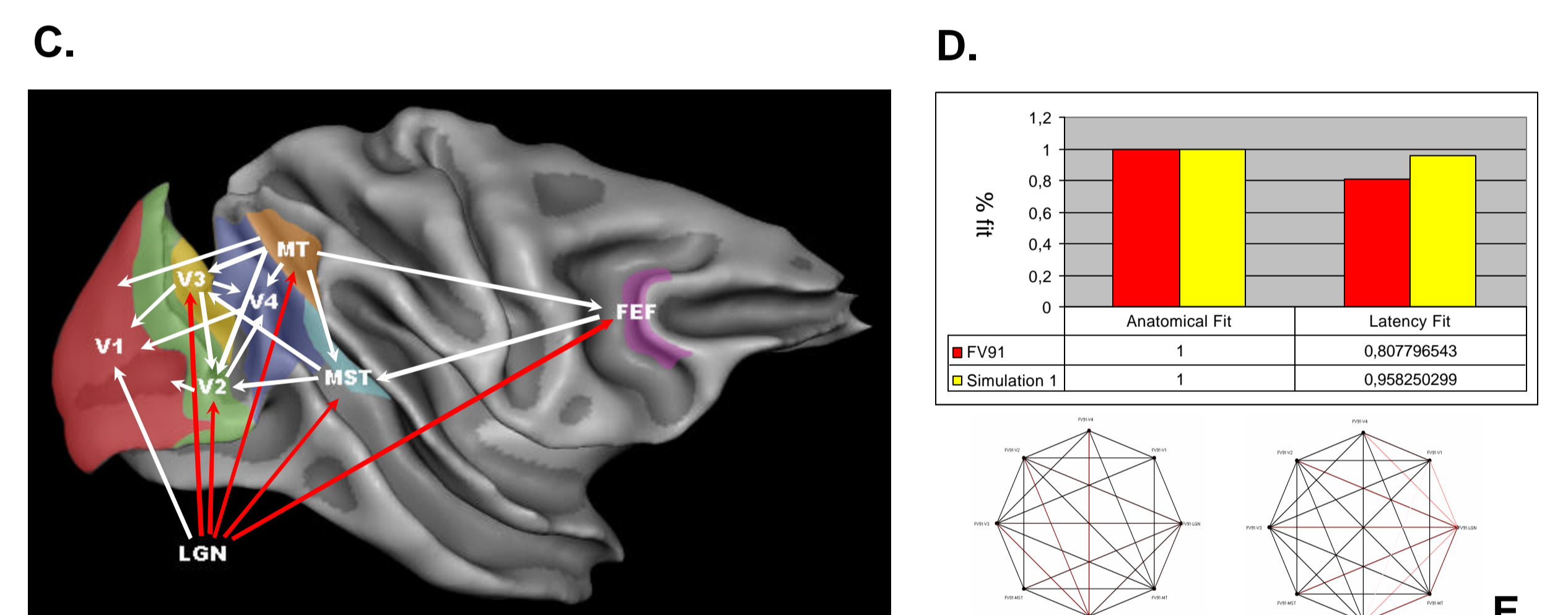


Figure 3: Results of simulation with 8 areas. A) Connection matrix of the areas in which Schmolesky et al. [3] measured. The 'parcellation-scheme' is that used by Felleman & Van Essen [1] and was extracted from the CoCoMac database [4] B) Connection matrix optimized for both anatomic and timing fit. Changes from 'original' (A) are marked in green and red. D) This network has the same anatomic fit but improved fit to the timing data. C) Connections in our solution shown on anatomical image of the macaque brain (only lower triangle of the connection matrix is shown) E) Whole connection matrix shown in graph theoretical maps (lower and upper triangle respectively)

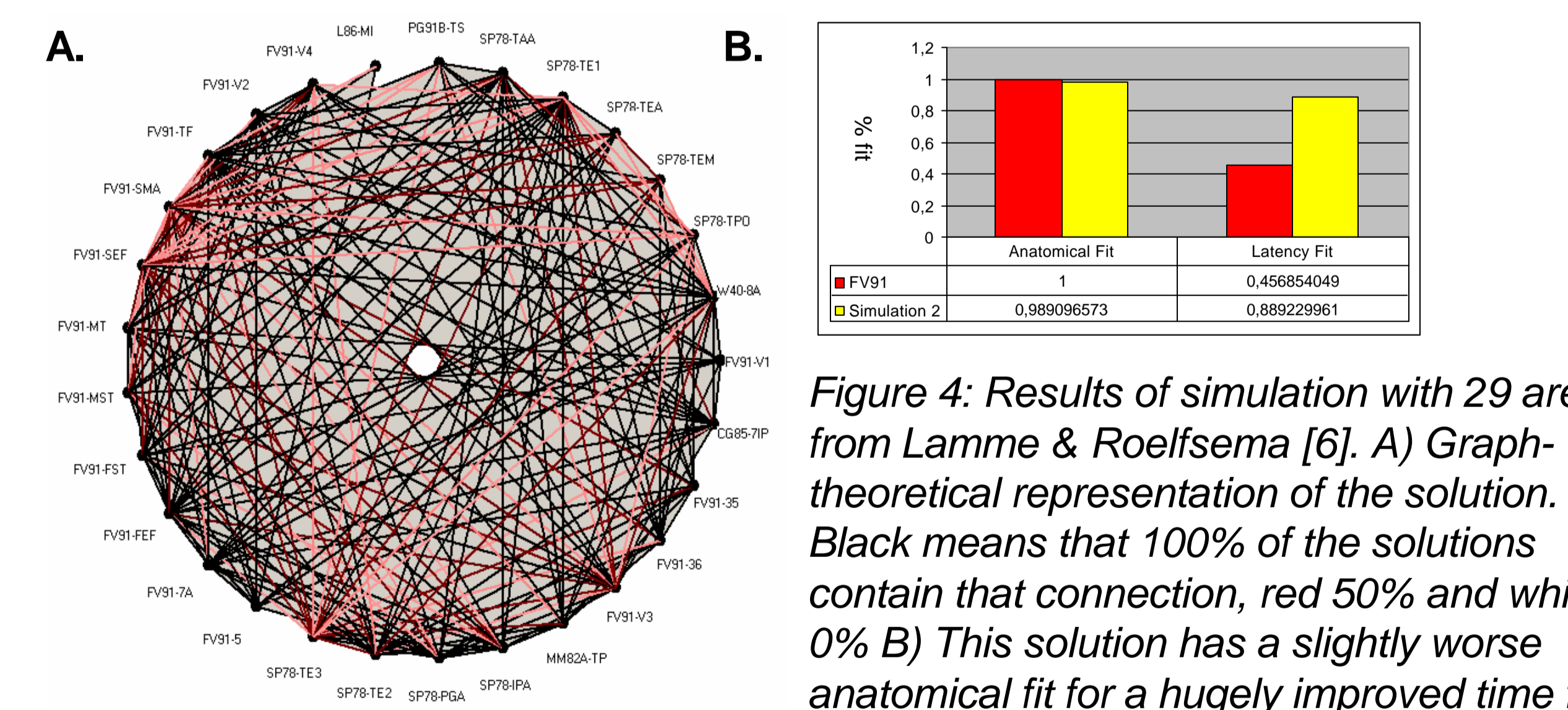


Figure 4: Results of simulation with 29 areas from Lamme & Roelfsema [6]. A) Graph-theoretical representation of the solution. Black means that 100% of the solutions contain that connection, red 50% and white 0% B) This solution has a slightly worse anatomical fit for a hugely improved time fit.

## Discussion and Conclusion

Our results depend critically on two assumptions. 1) The difference in myelination between magno- and parvo-cellular pathways does not sufficiently explain the (absence of) latency differences. 2) It takes time for a neural signal to pass a module in the visual system.

Under these assumptions we conclude that our method provides an effective means of generating models of cortical connectivity that are consistent with the available data on structural connectivity and spike-timing data. The generated models show an improved fit with these data.

### References:

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2. Hilgetag, O'Neill & Young, 1996, *Science*
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7. Beaulieu & Colonnier, 1983, *The Journal of Comparative Neurology*
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