

Supplementary information for **Animal daily mobility patterns analysis using resting event networks**

The OSLOM algorithm

In this study we used the Order Statistics Local Optimization Method (OSLOM) [1] to identify the communities in the resting events networks . OSLOM uses an iterative process to detect statistically significant communities with respect to a global null model (i.e. random graph without community structure). The main characteristic of OSLOM is that it is based on a score used to quantify the statistical significance of a cluster in the network [2]. The score is defined as the probability of finding the cluster in a random null model. The random null model used in OSLOM is the configuration model [3] that generates random graphs while preserving an essential property of the network: the distribution of the number of neighbors of a node (i.e. the degree distribution). Therefore, the output of OSLOM consists in a collection of clusters that are unlikely to be found in an equivalent random network with the same degree sequence. This algorithm is nonparametric in the sense that it identifies the statistically significant partition, without defining the number of communities *a priori*. However, the *tolerance* value that determines whether a cluster is significant or not might play an important role for the determination of the clusters found by OSLOM. The influence of this value, fixed initially, is however relevant only when the community structure of the network is not pronounced. When communities are well defined the results of OSLOM do not depend on the particular choice of *tolerance* value [1]. See [1] for a comparison between OSLOM and other community detection algorithms.

Similarity between daily motifs

Let us consider two lists of daily motifs $m_1 = [15 \rightarrow 15, 15 \rightarrow 15, 15 \rightarrow 6, 6 \rightarrow 5]$ and $m_2 = [15 \rightarrow 15, 15 \rightarrow 6, 6 \rightarrow 7, 7 \rightarrow 6, 6 \rightarrow 5]$. Each motif represents a displacement between communities. Displacements inside the same community are considered as valid motifs. It is also important that the same motif may appear several times in the list of daily motif. The similarity between m_1 and m_2 is defined as follows using the Sørensen index,

$$S = \frac{2|m_1 \cap m_2|}{|m_1| + |m_2|} \quad (1)$$

In our example the similarity between m_1 and m_2 is equal to $S = 2 * 3/9 = 2/3$.

Supplementary Figures

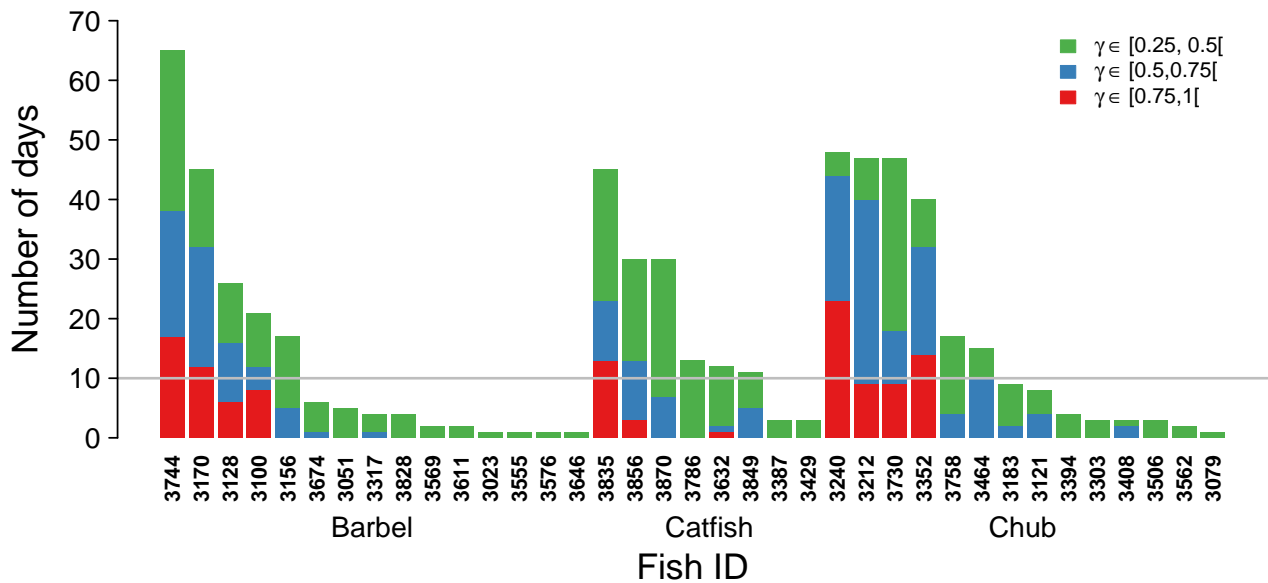


Figure S1: Number of days of presence in the study site. γ represents the fraction of 5-minute periods during which the position of the fish was recorded. Three groups of values have been considered ($\gamma \in [0, 0.5[$, $[0.5, 0.75[$ and $[0.75, 1]$). Four barbels (3744, 3170, 3128 and 3100), two catfishes (3835 and 3856) and four chubs (3240, 3212, 3730 and 3352) have been selected. All selected fish are present in the study area at least half of the day ($\gamma > 0.5$) for at least 10 days (grey line).

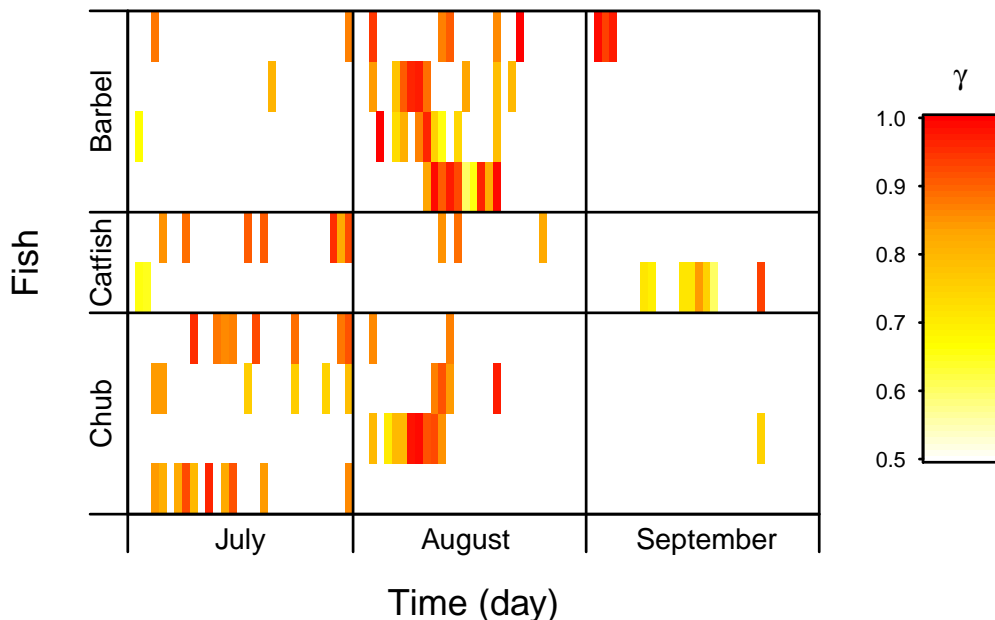


Figure S2: The ten days with highest γ values for each selected fish.

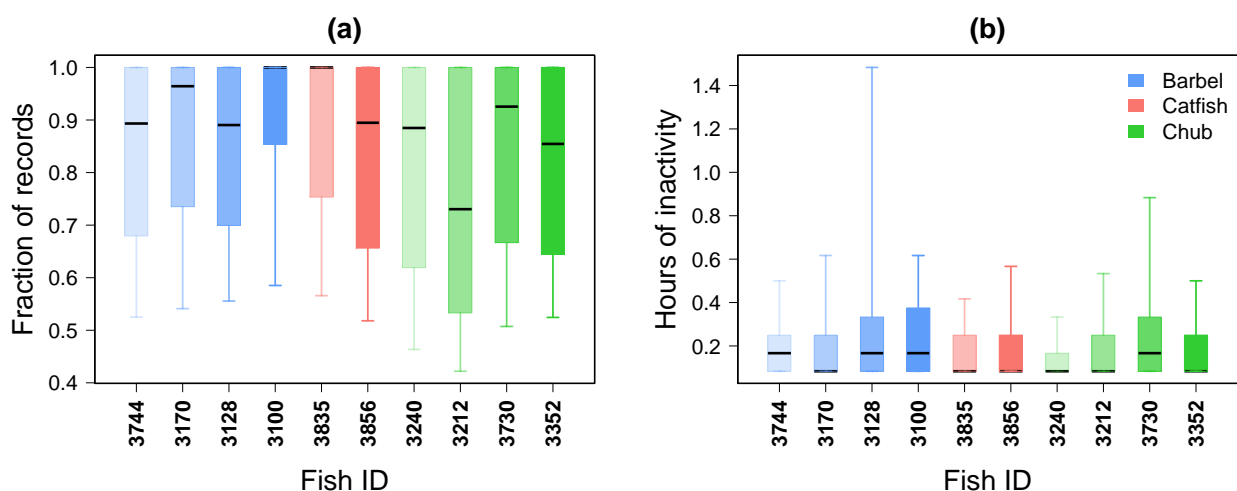


Figure S3: Daily fish trajectory reconstruction accuracy. (a) Boxplots of the fraction of records observed in the location with the highest number of records during a 5-minute period. (b) Boxplots of the duration (in hour) of the sequence during which the presence of a fish is not recorded. The results have been aggregated over the ten selected days for each fish individual. Each boxplot is composed of the first decile, the lower hinge, the median, the upper hinge and the last decile.

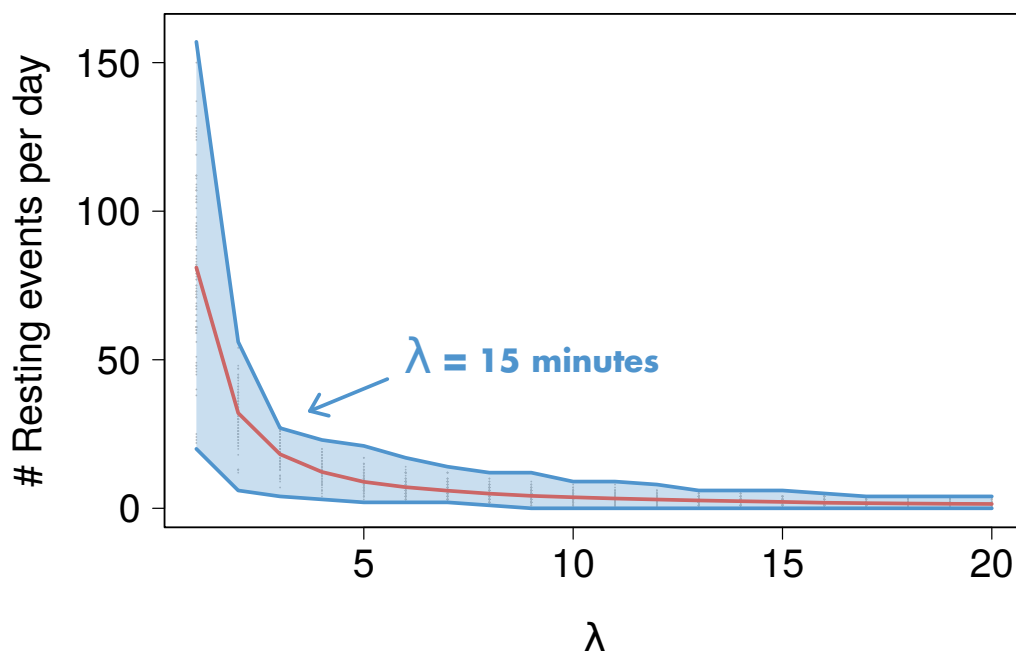


Figure S4: Number of resting events per day as a function of λ . The grey points represent the number resting events for the 100 daily spatio-temporal trajectories. The red line represents the average. The blue lines represent the minimum and maximum values.

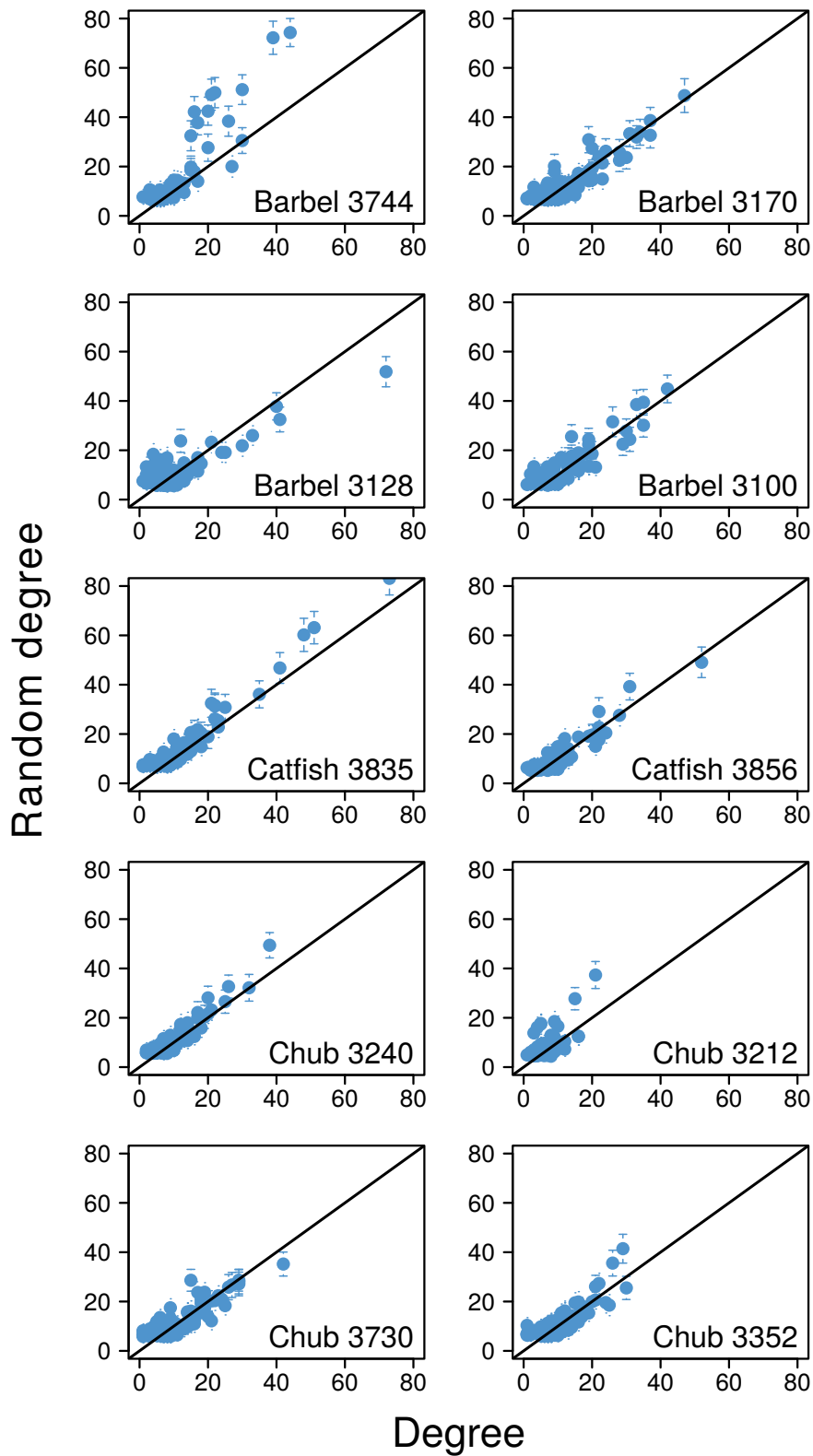


Figure S5: Comparison between observed and average random degree distribution. Each point represents an event with the observed average degree on the x-axis and the average degree obtained with the null model on the y-axis averaged over 100 replications (the error bars represent one standard deviation).

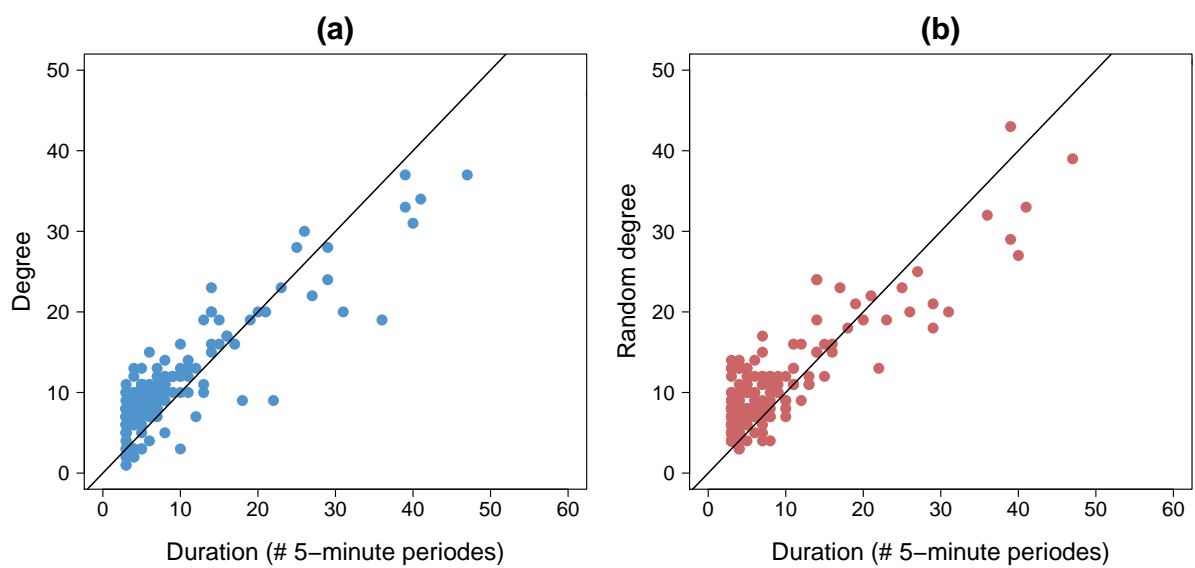


Figure S6: Relationship between event degree and event duration. Each point represents an event with its duration (in number of 5-minute periods) on the x-axis and the observed degree (a) and the one obtained with one realization of the nul model (b) on the y-axis averaged.

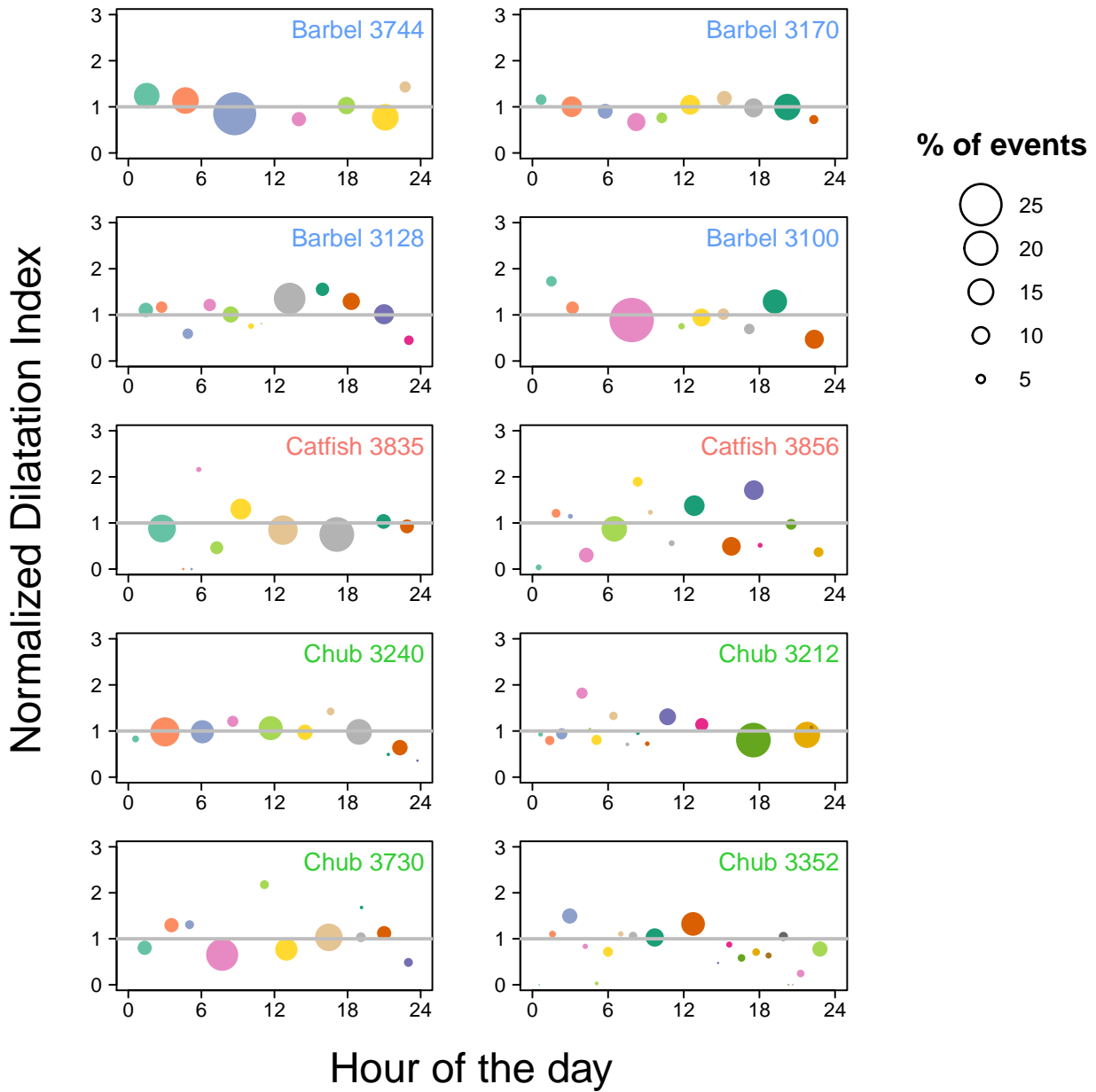


Figure S7: Analysis of the event networks' community structure obtained with the null model. The plots display the communities characteristics for every fish. Each point represents a community with the average resting time on the x-axis and the community dilatation index on the y-axis. The community dilatation index is normalized by the dilatation index DI_{NM} . The size of the dots is proportional to the fraction of events. Only results with one random network are shown.

Supplementary Tables

Table S1: Statistical properties of the resting event networks (standard deviations). Number of events (#Nodes), number of links (#Links), average degree (Degree) and dilatation indices (express in meters). Standard deviations associated with the average values displayed in Table 1.

Fish ID	Species	#Nodes	#Links	#Links (NM)	Degree	Degree (NM)	DI	DI _{tot}	DI _{NM}
3744	Barbel	NA	NA	33.64	NA	0.42	NA	NA	20.14
3170	Barbel	NA	NA	33.25	NA	0.34	NA	NA	15.89
3128	Barbel	NA	NA	26.95	NA	0.31	NA	NA	18.67
3100	Barbel	NA	NA	31.39	NA	0.40	NA	NA	25.99
3835	Catfish	NA	NA	34.04	NA	0.36	NA	NA	11.97
3856	Catfish	NA	NA	23.64	NA	0.29	NA	NA	12.49
3240	Chub	NA	NA	26.56	NA	0.27	NA	NA	17.63
3212	Chub	NA	NA	21.39	NA	0.25	NA	NA	15.41
3730	Chub	NA	NA	31.86	NA	0.35	NA	NA	20.97
3352	Chub	NA	NA	32.30	NA	0.30	NA	NA	11.33

Table S2: Number of resting event network communities. Standard deviations associated with the average values displayed in Table 2.

Fish ID	Species	#Com	#Com (NM)
3744	Barbel	NA	1.34
3170	Barbel	NA	0.97
3128	Barbel	NA	0.76
3100	Barbel	NA	0.90
3835	Catfish	NA	1.44
3856	Catfish	NA	1.12
3240	Chub	NA	0.85
3212	Chub	NA	0.87
3730	Chub	NA	1.11
3352	Chub	NA	1.81

References

- [1] A. Lancichinetti, F. Radicchi, J. J. Ramasco, and S. Fortunato. Finding Statistically Significant Communities in Networks. *PLOS ONE*, 6(4):e18961, 2011.
- [2] A. Lancichinetti, F. Radicchi, and J. J. Ramasco. Statistical significance of communities in networks. *Physical Review E*, 81(4):046110, 2010.
- [3] M. Molloy and B. Reed. A critical point for random graphs with a given degree sequence. *Random Structures & Algorithms*, 6(2-3):161–180, 1995.