



# Network Neuroscience

Tuesday 20<sup>th</sup> June  
NetSci 2017, Indianapolis

Program, Abstracts, and Guide

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You can find an online version of this program on our website and Facebook page:

Website: <http://www.complexity.es/netsci2017brain>

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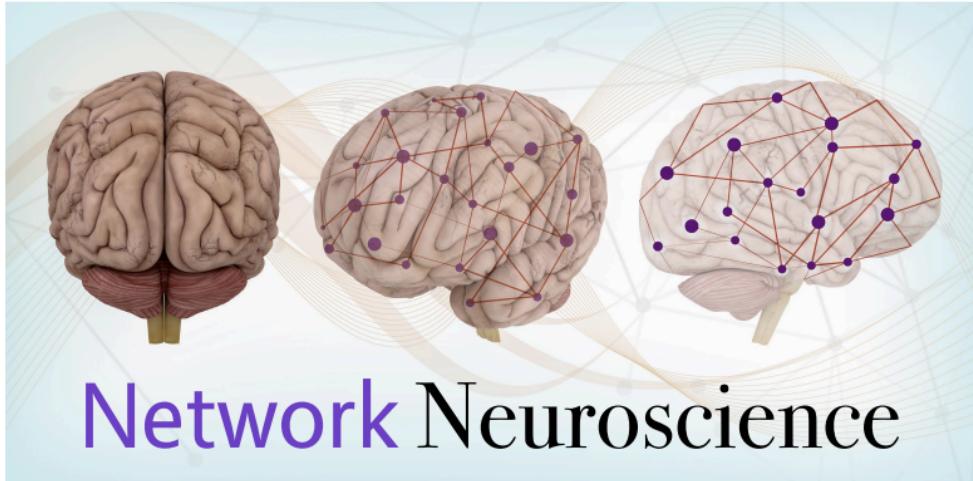


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## Sponsors

We wish to acknowledge the generous support of the **James S. McDonnell Foundation** and the **John Templeton Foundation**. We are extremely grateful for their contributions, which have helped make this Satellite possible, and are proud to be associated with them and their missions.





# Network Neuroscience

Uncovering and understanding the relationship between elements in complex networks has helped propel Network Science in various fields, including neuroscience. The brain is inherently multiscale and multivariate in nature, and understanding each part of the hierarchy and their interconnectedness is vital to understanding brain structure, function and cognition. Genes and proteins interact on the subcellular level. Subsequent populations of cells connect - and integrate within different brain regions - to support and propagate coordinated excitations of neural signals. As dynamic patterns emerge within network circuitry, these signaling patterns integrate to ultimately self-organise the whole organ - itself a cohabitant within the body - which seeks to interact with its external environment and social systems. Studying the brain at these various levels has led to the emergence of Network Neuroscience: a Network Science affiliated field within the brain-based scientific frontier.

Network Science provides a new and natural mathematical framework for investigating functional and anatomical neuroimaging data, and represents a conceptual revolution that goes beyond standard approaches. Network based methods not only refine the outcomes of existing techniques, but also typify a paradigm shift for representing brain structure and dynamics. Equally importantly, the questions posed by neuroscience have the potential to inspire the development of new tools and areas within the broader field of Network Science itself.

As many of you will know, a popular and successful Brain Networks satellite ran in 2015 and 2016 at NetSci. This years' satellite is a natural evolution, promising to expand to envelope the full scope of the emerging field of Network Neuroscience. The themes of this Satellite include, but are not limited to: (i) Interactome networks; (ii) Transcriptional and gene regulation networks; (iii) Structural brain networks (imaging); (iv) Functional brain networks (imaging); (v) Brain networks - theory, modeling and analysis; (vi) Signal processing and information flow; (vii) Circuit dynamics; (viii) Brain-behaviour interactions; (ix) Systems neuroscience. All themes apply to any species.



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# Program: Morning

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Registration: 08:00 - 08:30

## Session I: From Neurons to Anatomy

Chair: Emma Towlson

**08:30** Introduction and Opening Remarks

**08:35** Functional connectivity among hundreds of neurons in cortex (John Beggs)

**08:55** Emergence of slow-switching assemblies in structured neuronal networks (Michael Schaub)

**09:10** From Connectome to Behavior: An Integrated Neuromechanical Model of Forward Locomotion in *C. elegans* (Eduardo Izquierdo)

**09:25** Model of brain activation predicts the neural collective influence map of the brain (Flaviano Morone)

**09:40** Relating topology and dynamics of excitable neural networks (Claus Hilgetag)

Coffee 10:00 - 10:30

## Session II: Computational Approaches

Chair: Fabrizio De Vico Fallani

**10:30** Opening Remarks

**10:35** Data/Tool showcase: The Allen Mouse Brain Connectivity Atlas and the AllenSDK (Nicholas Cain)

**11:35** Visibility graphs for fMRI data: multiplex temporal graphs and their modulations across resting state networks (Daniele Marinazzo)

**11:55** OpenWorm: The network neuroscience of the only complete connectome (Stephen Larson)

**12:15** NeuroCave: A Web-based Immersive Analytics Platform for Visualizing the Connectome (Alex Leow)

Lunch 12:30 - 14:00



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# Program: Afternoon

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## Session III: Function and Dysfunction in the Human Brain

Chair: Robin Wilkins

**14:00** Opening Remarks

**14:05** The Virtual Trial: network intervention modeling in Alzheimer's disease (Willem de Haan)

**14:25** Electrical propagation on Cortical Connectome and Communicability (Masanori Shimono)

**14:40** Global homological conservation versus local reorganization of the psychedelic brain (Esther Ibáñez)

**14:55** Joint exploration and mining of memory-relevant brain anatomic and connectomic patterns via a three-way association model (Jingwen Yan)

**15:10** A Network Neuroscience of Human Learning (Danielle Bassett)

**Coffee 15:30 - 16:00**

## Session IV: Genetics

Chair: Tommaso Gili

**16:00** Opening Remarks

**16:05** Potential to Inform Quantitative Theories of Brain and Behavior (Neda Jahanshad)

**16:25** Imaging genomics of functional brain networks: bridging biological scales with graphs (Jonas Richiardi)

**16:45** Topological co-expression networks capture spatial and gene-gene interactions (Alice Patania)

## Session V: The Future of Network Neuroscience

**17:00** Network Neuroscience Journal (Olaf Sporns)

**17:05** Panel Discussion

## Session VI: Posters

**18:00** Contributed Posters

**19:30** End



## Invited Speakers

### Functional connectivity among hundreds of neurons in cortex - John M.

Beggs

Indiana University, USA

08:35 - 08:55



The fantastic progress of functional connectomics has occurred mainly at the scale of the human brain and has been fueled by fMRI technology. Within each fMRI voxel, though, there are several hundred thousand cortical neurons, forming functional networks at a vastly smaller scale. Here, collective computations like associative memory and pattern recognition are first expected to emerge. By using high-density microelectrode arrays, we have probed functional connectivity among ~300 closely-spaced neurons in cortex. Sub-millisecond temporal resolution allows us, for the first time, to construct directed networks and identify neurons where information converges synergistically to support computations. Our results show that information flow in these networks does not involve all neurons equally. Rather, a small percentage of hub neurons dominates information traffic. Interestingly, synergistic computations do not occur primarily at these hub neurons, but rather in neurons that receive hub neuron connections. This emerging picture is expected to offer clues to how the cortex achieves its remarkable computational power.



### Relating topology and dynamics of excitable neural networks - Claus

Hilgetag

Boston University & Hamburg University, USA/Germany

09:40 - 10:00

Brain networks are characterised by a number of distinctive topological features, such as a heterogeneous degree distribution with hubs, hierarchically organised modules, as well as a characteristic spectrum of motifs and cycles. These features have consequences for different aspects of brain dynamics, such as self-sustained network activity, the wave-like propagation of activity as well as correlations and anti-correlations of activity patterns. We have systematically investigated the relation between neural network topology and dynamics with the help of a general excitable (cellular automaton) model which allows a mechanistic understanding of the contribution of different topological features of brain networks to brain dynamics.



# Invited Speakers



## Data/Tool showcase: The Allen Mouse Brain Connectivity Atlas and the

**AllenSDK** - Nicholas Cain

Allen Institute for Brain Science, USA

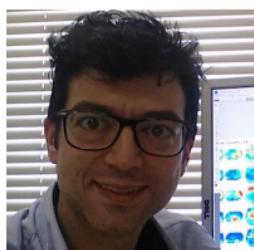
10:35 - 11:35

The Allen Mouse Brain Connectivity Atlas is a high-resolution map of neural connections in the mouse brain, built on an array of transgenic mice genetically engineered to target specific cell types. This presentation will focus on the several key aspects of the data that comprise the atlas, a tour of the web-based Atlas browser (<http://connectivity.brain-map.org/>) and a tutorial session that demonstrates the use of python API to access and manipulate preprocessed data from the experiments. The tutorial will demonstrate connectivity atlas-specific functionality of the API, as well as some of the generally relevant informatics functionality used across projects at the Allen Institute. If you would like to participate in the tutorial, please bring your (python) jupyter notebook-equipped laptop with the AllenSDK (<http://alleninstitute.github.io/AllenSDK/install.html>) installed.

## Visibility graphs for fMRI data: multiplex temporal graphs and their modulations across resting state networks - Daniele Marinazzo

Ghent University, Belgium

11:35 - 11:55



Visibility graphs have proved a convenient tool to describe the dynamics of time series, finding applications across several disciplines. Recently an approach has been proposed to extend this framework to multivariate time series, allowing a novel way to describe collective dynamics. I will propose their application to fMRI time series and give some explanation on why we think that it's an interesting thing to do.





### **OpenWorm: The network neuroscience of the only complete connectome**

- Stephen Larson  
OpenWorm, USA  
11:55 - 12:10

Of great interest in modern science are the questions of how the brain produces behavior and experience and how we may be able to build brains within computers. Central to answering both questions is to understand how the cells of the nervous system process information. The deepest understanding would be achieved if it were possible to engineer models of cells to produce arbitrary information processing operations. A good place to reverse-engineer the understanding necessary for this would be with a simple biological organism with relatively few cells and for which a lot of observations and measurements have already been made.

To tackle this challenge, OpenWorm aims to build the first comprehensive computational model of the *Caenorhabditis elegans* (*C. elegans*), a microscopic roundworm. With only a thousand cells-- three hundred of which are brain cells-- it solves non-trivial survival challenges such as feeding, mate-finding and predator avoidance. Despite being the only organism with a complete wiring diagram of its brain cells, discovered thirty years ago, there is still no principled understanding of how even simple crawling or swimming behaviors are produced by its cells.

At OpenWorm, we are using a bottom-up approach, aimed at observing the worm behavior emerge from simulations using cellular data derived from scientific experiments carried out over the past decade. To do so, we are incorporating the data available in the scientific community into computational models. We are engineering Geppetto, c302, and Sibernetic, open-source simulation platforms, to be able to run these different models in concert. We are also forging new collaborations with universities and research institutes to collect new data that fill in gaps.

In this talk, I will discuss recent progress with the project and steps forward to begin deriving deep insight from the modelling and simulation work that has been done.



# Invited Speakers

## The Virtual Trial: network intervention modeling in Alzheimer's disease -

Willem de Haan

VU University Amsterdam, The Netherlands

14:05 - 14:25



Although brain network knowledge has been expanding rapidly over the past years, it has not yet translated into 'killer feature' clinical applications in the medical field, and many doctors regard brain connectivity research as a wonderful but exotic research niche that is too technical and abstract to benefit patients directly. One way brain network research may get closer to obtaining a clinical role may be by focusing on treatment strategies. More specifically, in my presentation I will argue that a computational approach which unites the strengths of graph theoretical analysis and neural mass modeling, is a great candidate for this purpose, as it can offer an attractive test environment in which positive and negative influences on network integrity can be explored, with the ultimate aim to find effective countermeasures against neurodegenerative network damage. As an example, I will present a modeling study that focuses on countering neuronal hyperactivity in early stage Alzheimer's disease. The effect of altering neuronal excitability on preserving large-scale network integrity is examined, and the most successful strategy turns out to be quite contrary to our initial hypothesis. The virtual trial approach might become a versatile tool that turns our growing connectome knowledge into clinical predictions, providing a more solid theoretical basis for clinical trial design.



## A Network Neuroscience of Human Learning - Danielle Bassett

University of Pennsylvania, USA

15:10 - 15:30

Humans adapt their behavior to their external environment in a process often facilitated by learning. Efforts to describe learning empirically can be complemented by quantitative theories that map changes in neurophysiology to changes in behavior. In this talk, I will highlight recent advances in network science that offer a set of tools and a general perspective that may be particularly useful in understanding types of learning that are supported by distributed neural circuits. I will describe recent applications of these tools to neuroimaging data that provide unique insights into adaptive neural processes, their dynamics during normative neurodevelopment, their alteration in psychiatric disease, and their susceptibility to external modulation. While promising, the tools have yet to be linked to well-formulated models of behavior commonly utilized in cognitive psychology. I will conclude by suggesting that continued progress will require the explicit marriage of network approaches to neuroimaging data and quantitative models of behavior.



## Invited Speakers



**Potential to Inform Quantitative Theories of Brain and Behavior - Neda Jahanshad**  
Keck School of Medicine USC, USA  
16:05 - 16:25

In collaborative efforts involving over 300 scientists from around the world, the Enhancing Neuro Imaging and Genetics through Meta-Analysis Consortium, ENIGMA, has led the discovery of common genetic variants that shape the structure of the living brain as seen through MRI. Genome-wide association studies of regional brain volumes in over 30,000 individuals have identified genetic loci that significantly impact brain structural variations. ENIGMA has extended its efforts to discover the genetic influence over variability in cortical structure and its white matter connections, identifying many more genetic loci that influence brain structure. However, genetic contributions are not unique to single brain regions and we are discovering interconnected networks of genetic influences that shape the human brain. These networks not only influence brain structure, but also, cognitive function and risk for neuropsychiatric disease. Here, we will highlight common practices in identifying genetic correlations in the human brain and feature preliminary results from the largest and most powerful study of the genetic influences over the human cortex.

**Imaging genomics of functional brain networks: bridging biological scales with graphs - Jonas Richiardi**

University of Geneva, Switzerland

16:25 - 16:45



During rest, brain activity is intrinsically synchronized between different brain regions, forming networks of coherent activity. These functional networks, consisting of multiple regions widely distributed across lobes and hemispheres, appear to be a fundamental theme of neural organization in mammalian brains. The recent availability of high spatial resolution post-mortem brain gene expression datasets, together with several large-scale imaging genetics datasets, opens intriguing data analysis avenues to go beyond conventional twin studies for heritability or candidate gene approaches in studying the relationship between genomics and functional networks. Using a graph-based statistical testing approach inspired by community detection, we show that functional brain networks defined with resting-state fMRI can be recapitulated using measures of correlated gene expression, and that the relationship is not driven by gross tissue types or spatial distance. The set of genes we identify is significantly enriched for certain types of ion channels and synapse-related genes. We validate results by showing that polymorphisms in this set significantly correlate with alterations of in-vivo resting-state functional connectivity in a group of 259 adolescents. We further validate results on another species by showing that orthologs of our list of genes are significantly associated with neuronal connectivity in the mouse brain, again independently of distance. These results provide convergent, multimodal evidence that resting-state functional networks emerge from the orchestrated activity of dozens of genes, in particular linked to ion channel activity and synaptic function.



**Emergence of slow-switching assemblies in structured neuronal networks** - Michael Schaub, Yazan N. Billeh, Costas A. Anastassiou, Christof Koch and Mauricio Barahona

**08:55 - 09:10**

Unraveling the interplay between structure and spatio-temporal dynamics in neuronal networks is paramount to advance our understanding of neuronal processing. Here we investigate how particular features of network connectivity underpin the propensity of neuronal networks to generate slow-switching assembly dynamics -- sustained epochs of increased firing within neural-assemblies which transition slowly between different groups.

**From Connectome to Behavior: An Integrated Neuromechanical Model of Forward Locomotion in *C. elegans*** - Eduardo J. Izquierdo and Randall D. Beer

**09:10 - 09:25**

With 302 neurons, a near-complete connectome, and a rich behavioral repertoire, *C. elegans* is an ideal organism to understand how behavior is grounded in the interaction between brain, body, and environment. We evolve neuromechanical models of the worm to match behavior and we analyze the resulting ensemble of solutions to generate hypotheses about how they operate.

**Model of brain activation predicts the neural collective influence map of the brain** - Flaviano Morone

**09:25 - 09:40**

The brain is arranged in functionally specialized modules to form a network of networks (NoN). We introduce a model of brain NoN, which is robust against random node failures, and describes the binding of segregated modules through the optimization of the influence of the minimal set of essential nodes responsible for broadcasting information to the whole brain NoN.

**NeuroCave: A Web-based Immersive Analytics Platform for Visualizing the Connectome** - Johnson Keiriz, Angus Forbes, Olusola Ajilore and Alex Leow

**12:15 - 12:30**

NeuroCave is a novel immersive visual analytics system that facilitates the visual inspection of structural and functional connectome datasets. With NeuroCave, neuroscientists can interact with the connectome while wearing portable VR headsets, in any coordinate system or topological space, as well as cluster brain regions into different modules on demand.



**Electrical propagation on Cortical Connectome and Communicability** - Masanori Shimono and Naomichi Hatano  
14:25 - 14:40

This presentation provides a new connection between Network Science and Neuroscience in terms of dynamical propagation. Propagating neuronal signals run through a vast number of possible Walks to reach a specific target region with decaying the amplitude. We will demonstrate a systematic approach to characterize the complex dynamics using Communicability, and will also discuss the estimated representative propagation speed. See also: <http://nori417.sakura.ne.jp/wp/>

**Global topological conservation versus local reorganization of the psychedelic brain** - Esther Ibáñez, Angkoon Phinyomark, Paul Expert, Robin Carhart-Harris, Francesco Vaccarino and Giovanni Petri

14:40 - 14:55

Using TDA (topological data analysis) we analyse fMRI data of subjects before and after the subministration of LSD. TDA techniques abandon the standard pairwise measures between points and focus on extracting and understanding the shape of data extracting meaningful high-dimensional features. Results show an overall global conservation mediated by local differences in the fMRI homological structure and an adaptative behaviour while the drug is being metabolized.

**Joint exploration and mining of memory-relevant brain anatomic and connectomic patterns via a three-way association model** - Jingwen Yan, Kefei Liu, Huang Li, Enrico Amico, Shannon Risacher, Yu-Chien Wu, Shiaofen Fang, Olaf Sporns, Andrew Saykin, Joaquin Goni and Li Shen

14:55 - 15:10

We propose a new sparse association model (OSCCA) and an efficient algorithm to enable the three-way association among brain connectivity, structure and episodic memory performance. Using the data from the HCP cohort, we identified a small set of associated brain fibers and structures in relation to the episodic memory profiles.

**Topological co-expression networks capture spatial and gene-gene interactions** - Alice Patania, Mattia Veronese, Paul Expert, Pierluigi Selvaggi, Francesco Vaccarino, Federico Turkheimer and Giovanni Petri

16:45 - 17:00

We produce a topological summary network of genes co-expression, akin to a coarse-grained backbone, via an extension of the topological simplification algorithm Mapper. We use this technique to understand the interactions between the genetic pathways of neurotransmitters. The resulting backbone encodes the two components of the ABA dataset -- gene-expression and brain structure --, it preserves the shape of the original dataset while strongly reducing its dimensionality, and yields a notion of network connectivity across the gene expression samples.



- 1. The geometric, genetic, and structural basis of functional connectivity in whole-brain intracranial EEG networks -**  
Richard Betzel and Danielle Bassett
- 2. Out-degree rich clubs in networks of spiking cortical neurons feed neural computations while in-degree rich clubs perform neural computations -** Samantha Faber, Nicholas Timme, John Beggs and Ehren Newman
- 3. Oscillatory network dynamics of non-rapid eye movement sleep -** Roy Cox, Anna Schapiro and Robert Stickgold
- 6. Graph embedded sparse association model for joint identification of discriminative imaging proteomic markers and their associations -** Jingwen Yan, Kefei Liu, Shannon Risacher, Kwangisk Nho, Andrew Saykin and Li Shen
- 10. Distinguishing individuals with schizophrenia from healthy controls using fMRI brain networks -** Sarah Morgan, Jonathan Young, Therese van Amelsvoort, Jim van Os, Machteld Marcelis and Ed Bullmore
- 11. From connectome to behavior: Circuit motifs that generate oscillations to drive forward and backward locomotion in C.elegans -** Erick Olivares, Eduardo Izquierdo and Randall Beer
- 12. Modeling multiple brain networks through linear mixed effects models -** Yura Kim and Elizaveta Levina
- 13. Geometric and Topological Analysis at Different Scales of Organization of the Mouse Brain Connectivity Network -** Jose Brum, Emma Towlson, Soodabeh Milanlouei and Albert-László Barabási
- 14. Structure-function relationships in segregated and integrated states of time-resolved brain networks -** Makoto Fukushima, Richard F. Betzel, Ye He, Marcel A. de Reus, Martijn P. van den Heuvel, Xi-Nian Zuo and Olaf Sporns
- 15. Reconfiguration of Brain Functional Network Community Structure in Major Depressive Disorder -** Ye He, Sol Lim, Santo Fortunato, Lei Zhang, Xi-Nian Zuo, Jiang Qiu and Olaf Sporns
- 16. Altered Dynamic Brain Network Modularity in Adolescent Remitted Depression -** Olu Ajilore, Rachel Jacobs, Katie Bessette, Claudia Feldhaus, Alyssa Barba, Lisanne Jenkins, Alex Leow and Scott Langenecker
- 17. Development of Community Structure in the Human Connectome across the Life Span: An Application of Weighted Stochastic Blockmodels -** Joshua Faskowitz, Xiaoran Yan, Xi-Nian Zuo and Olaf Sporns



- 22. Navigational Core vs Link Prevalence Score in Structural Networks of the Human Brain** - Andras Majdan, Andras Gulyas, Zalan Heszberger and Jozsef Biro
- 24. Optimal modularity in rodent cortical slices** - Nathaniel Rodriguez, John Beggs, Yong-Yeol Ahn and Zachary Tosi
- 25. Curvature-based Analysis of Brain Networks** - Melanie Weber, Emil Saucan, Johannes Stelzer, Gabriele Lohmann and Jürgen Jost
- 26. Dynamic Multivariate Kurtosis as a measure of temporal variations in task-rest functional connectivity with applications to family history of alcoholism** - Vibha Viswanathan, Mario Dzemidzic, David Kareken and Joaquín Goñi
- 28. Detecting optimal subgraphs in connectomes across individuals and species** - Filip Miscevic and Olaf Sporns
- 30. Loss of brain inter-frequency hubs in Alzheimer's disease** - Jeremy Guillou, Yohan Attal, Oliver Colliot, Valentina La Corte, Bruno Dubois, Denis Schwartz, Mario Chavez and Fabrizio De Vico Fallani
- 31. A statistical model for brain networks inferred from large-scale electrophysiological signals** - Catalina Obando Forero and Fabrizio De Vico Fallani
- 32. Functional resilience in dynamical complex networks with adaptive connectivity** - Edward Laurence, Patrick Desrosiers, Nicolas Doyon and Louis J Dubé
- 34. Organization and hierarchy of the human functional brain network lead to a chain-like core** - Rossana Mastrandrea, Andrea Gabrielli, Fabrizio Piras, Gianfranco Spalletta, Guido Caldarelli and Tommaso Gili
- 35. Inhibitory synapses are central to structural balance in *C. elegans* neuronal network** - Rahul Badhwar and Ganesh Bagler
- 37. Music and Emotion in Context: A Constructionist Approach to a Network Neuroscience Investigation into Changes in Functional Brain Network Connectivity Based on Emotional Responses to Music Stimuli** - Robin.W. Wilkins, Sahana Giridharan, Kristen A. Lindquist, Jeffrey A. Brooks, Megan Johnston and Robert A. Kraft.
- 38. Chaos and Correlated Avalanches in Excitatory Neural Networks with Synaptic Plasticity** - Fabrizio Pittorino, Miguel Ibanez Berganza, Matteo Di Volo, Alessandro Vezzani and Raffaella Burioni
- 39. Experimental Test of Network Control: Functional predictions in the *C. elegans* nervous system** - E.K. Towlson, G. Yan, P.E. Vértes, Y.L. Chew, D.S. Walker, W.R. Schafer, and A-L Barabási



# Network Neuroscience: Focus Feature 2018

We are delighted to announce that the new journal dedicated to this emergent field, Network Neuroscience (MIT Press), is inviting submissions from all presenters at the Network Neuroscience satellite for a Focus Feature: **Bridging Scales and Levels**. We anticipate online publication in Spring 2018.

**Editor:** Olaf Sporns

**Guest Editors:** Emma Towlson, Robin Wilkins, Tommaso Gili, & Fabrizio De Vico Fallani

**Journal Website:** <http://www.mitpressjournals.org/netn>



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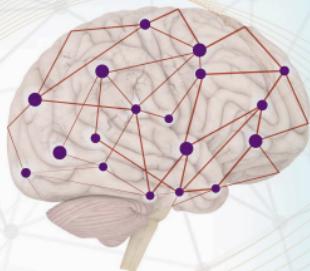
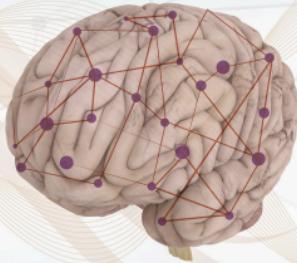
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## Questionnaire

We want to hear your thoughts on Network Neuroscience! Please, provide us with your feedback and dreams for the future at: <https://goo.gl/forms/M15EvW4EN93tVKzf1>





# Network Neuroscience

Thank you for joining us,  
we hope to see you in 2018!

Have your say on what you would like to see:  
<https://goo.gl/forms/MI5EvW4EN93tVKzf1>

