Activity Report 2016

Team BIOVISION

Biologically plausible Integrative mOdels of the Visual system : towards synergIstic Solutions for visually-Impaired people and artificial visiON

Inria teams are typically groups of researchers working on the definition of a common project, and objectives, with the goal to arrive at the creation of a project-team. Such project-teams may include other partners (universities or research institutions).

RESEARCH CENTER
Sophia Antipolis - Méditerranée

THEME
Computational Neuroscience and Medecine

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Team BIOVISION

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Keywords:

Computer Science and Digital Science:

5.3. - Image processing and analysis
5.4. - Computer vision
5.6. - Virtual reality, augmented reality
6.1.1. - Continuous Modeling (PDE, ODE)
6.1.4. - Multiscale modeling
6.1.5. - Multiphysics modeling
6.2.4. - Statistical methods

Other Research Topics and Application Domains:

1.1.10. - Mathematical biology
1.3.1. - Understanding and simulation of the brain and the nervous system
1.4. - Pathologies
2.1. - Well being
2.5.1. - Sensorimotor disabilities
9.4.2. - Mathematics
9.4.3. - Physics

1. Members

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2. Overall Objectives

2.1. Overall Objectives

Vision is a key function to sense the world and perform complex tasks, with a high sensitivity and a strong reliability, given the fact that most of its input is noisy, changing and ambiguous. Better understanding biological vision will have a strong scientific, medical, societal and technological impact in the near future. In this context, Biovision aims at developing fundamental research as well as technological transfer along two axes:

1. Axis 1 focuses on the development of high tech vision aid systems for low vision patients.
2. Axis 2 focuses on the precise modeling of the visual system for normal and distrophic conditions, targeting applications for low vision and blind patients.

These axes are developed in strong synergy, involving a large network of national and international collaborators with neuroscientists, physicians, and modellers.

3. Research Program

3.1. Introduction

The Biovision team has started on January 1st, 2016. It aims at developing fundamental research as well as technological developments along two axes.

3.1.1. Axis 1: High tech vision aid systems for low vision patients

The most popular class of vision aid systems for low vision patients is based on the idea of magnification. These aids are helpful for tasks such as reading but of course are not useful in other common daily tasks such as navigation.

Video goggles [1] are another kind of device where visual information is captured by a head-mounted camera, processed and then displayed on a near-the-eye display screen. So far, this technology did not encountered a big success essentially due to their narrow field of view. This situation could evolve with the fast progression of technology around virtual reality and augmented reality.

In BIOVISION we mainly focus on this technology to develop new vision aid systems that could take into account the pathologies of low vision patients but also on the tasks performed by the patients. We have three main goals:

1. We plan to focus on three tasks: reading, watching movies and navigating (indoor or outdoor), which are all important daily life activities for patients.
2. We aim at proposing new **scene enhancements** depending on **pathologies**.
3. We want to test them in **immersive** environments with low vision patients, taking into consideration **ergonomics**.

3.1.2. Axis 2: Human vision understanding through joint experimental and modeling studies, for normal and distrophic retinas

A holistic point of view is emerging in neuroscience where one can observe simultaneously how vision works at different levels of the hierarchy in the visual system. Multiple scales functional analysis and connectomics are also exploding in brain science, and studies of visual systems are upfront on this fast move. These integrated studies call for new classes of theoretical and integrated models where the goal is the modeling of visual functions such as motion integration.

[1] Video goggles are marketed by several companies such as, e.g., `eSight`, `Enhanced Vision` and `Lumus`

In BIOVISION we contribute to a better understanding of the visual system with three main goals:

1. We aim at proposing simplified mathematical models characterizing how the **retina** converts a visual scene into spike **population coding**, in **normal and under specific pathological conditions**.
2. We want to design an integrated numerical model of the visual stream, with a focus on motion integration, from retina to **visual cortex** area (e.g., the motion stream **V1-MT-MST**).
3. We plan to develop a simulation platform emulating the retinal spike-response to visual and prosthetic simulations, in normal and pathological conditions.

Finally, although this is not the main goal of our team, another natural avenue of our research will be to develop novel synergistic solutions to solve computer vision tasks based on bio-inspired mechanisms.

3.2. Scientific methodology

In this section we briefly describe the scientific methods we use to achieve our research goals.

3.2.1. Adaptive image processing

An impressive range of techniques have been developed in the fields of image processing, computer vision and computer graphics to manipulate and interpret image content for a variety of applications. So far only a few of these techniques have been applied in the context of vision aid systems and even less have been carefully evaluated with patients. However it is worth noticing a recent gain of interest from the artificial vision side to low vision applications [2]. We investigate which techniques could bring a real interest for vision aid systems, how to combine them and how to make them adapted to patient needs, so that they can not only "see" an image but understand it more efficiently.

Some techniques have already been explored. Among the first, enhancing image content (equalization, gamma correction, tone mapping, edge enhancement, image decomposition, cartoonization) seems a natural type of processing to make. Some methods have already been tested with low vision patients [38], [54], [55] or even in retina prosthesis systems as a pre-processing [37]. For some visual impairement it can be useful to consider methods that help patients to focus on the most relevant information, using techniques such as scene retargeting [59], seam carving [40], [39], saliency-based enhancements [71], [82] or 3D-based enhancements when available [64]. All the work done on image understanding could also be extremely useful to help patients navigate in natural cluttered environments both in low vision condition or for prosthetics vision [58]. 3D information, obtained from stereo head systems or RGB-D cameras also bring useful information about the environment [62] and integrated systems combining different expertise are appearing [46].

Our goal will be to take the most of state-of-the-art computer vision methods, in combination with virtual and augmented reality devices (Sec. 3.2.2) to provide patients vision aid system that can adapt to their impairment and so that they can easily change the parameters of the processing in an intuitive way.

3.2.2. Virtual and augmented reality

Our goal is to develop vision-aid systems using virtual and augmented reality [87]. There is a rich continuum of devices between virtual reality (which is *a priori* simpler to use since there is no problem of mobility and environment is well defined), and augmented reality (where information has to be superimposed in real time on top of the real environment to enrich it). Between these two extremes, new hybrid see-through systems are available or under development such as light glasses where additional information can be locally displayed at the center or on the corner (e.g., Google glass improving it). We invest on these technologies which enable new kinds of interaction with visual content which could be very powerful when adapted to low vision patients who want to use their remaining sight. We investigate how low vision patients could take benefits from this technology in their daily life activities [47] [3].

[2] See, e.g., the Special issue on Assistive Computer Vision and Robotics - "Assistive Solutions for Mobility, Communication and HMI" from Computer Vision and Image Understanding (August 2016) or the International Workshop on Assistive Computer Vision and Robotics (ECCV 2016 Sattelite workshop)

We focus on three activities: reading, watching movies and navigating in real world (indoor and outdoor). In these three scenario, this technology should offer crucial advantages for people in low vision. For reading, this could help them solving the page navigation problem or the limitations of magnification encountered when standard CCTVs are used. When watching a movie, the possibility to explore a pre-processed visual scene presented with very high visual angle can help patients to follow the storyline more easily and this poses some interesting questions on the creation of content specifically for virtual reality headsets. Finally, in real scenarios, augmented reality offers promising perspectives to enrich the scene by highly visible visual cues to facilitate low vision patients navigation. Of course the choices of adaptive image processing techniques (see Sec. 3.2.1) will be crucial and this will be the add-on value of our work.

Another important aspect of this work that will progressively need attention is ergonomic which will have to take into account the other potential functional limitations of these patients in addition to low vision (e.g., limitations in mobility, hearing, or agility).

3.2.3. Biophysical modeling

Modeling in neuroscience has to cope with several competing objective. On one hand describing the biological realm as close as possible, and, on the other hand, providing tractable equations at least at the descriptive level (simulation, qualitative description) and, when possible, at the mathematical level (i.e., affording a rigorous description). These objectives are rarely achieved simultaneously and most of the time one has to make compromises. In Biovision team we adopt the point of view of physicists: try to capture the phenomenological description of a biophysical mechanism, removing irrelevant details in the description, and try to have a qualitative description of equations behaviour at least at the numerical simulation level, and, when possible, get out analytic results. We do not focus on mathematical proofs, instead insisting on the quality of the model in predicting, and, if possible proposing new experiments. This requires a constant interaction with neuroscientists so as to keep the model on the tracks, warning of too crude approximation, still trying to construct equations from canonical principles [4],[33], [22].

3.2.4. Methods from theoretical physics

Biophysical models mainly consist of differential equations (ODEs or PDEs) or integro-differential equations (neural fields). We study them using dynamical systems and bifurcation theory as well as techniques coming from nonlinear physics (amplitude equations, stability analysis, Lyapunov spectrum, correlation analysis, multi-scales methods).

For the study of large scale populations (e.g., when studying population coding) we use methods coming from statistical physics. This branch of physics gave birth to mean-field methods as well statistical methods for large population analysis. We use both of them. Mean-field methods will be applied for large scale activity in the retina and in the cortex [7], [11],[15].

For the study of retina population coding we use the so-called Gibbs distribution, initially introduced by Boltzmann and Gibbs. This concept includes, but *is not limited to*, maximum entropy models [60] used by numerous authors in the context of the retina (see, e.g., [73], [75], [57], [56], [78]). These papers were restricted to a statistical description without memory neither causality: the time correlations between successive times is not considered. A paradigmatic example of this is the Ising model, used to describe the retinal activity in, e.g., [73], [75]. However, maximum entropy extends to spatio-temporal correlations as we have shown in, e.g., [13], [5].

More generally, while maximum entropy models rely heavily on the questionable assumption of stationariy, the concept of Gibbs distribution does not need this hypothesis. Beside, it allows to handle models with large memory; it also provides a framework to model anticipation [16]. It includes as well existing models to explain retina statistics such as the Generalized Linear Model (GLM) [44].

[3] Note that wearing such headsets may not be easily accepted by patients who do not want to advertise their disability. More generally, this poses the general question of how users come to accept and use a technology. This question is debated in the Technology Acceptance Model (TAM) which postulates that two specific perceptions about technology determine one behavioral intention to use a technology: perceived ease of use and perceived usefulness (see, e.g., [50]).

4. Application Domains

4.1. High tech vision aid systems for low vision patients

Vision aid systems for low vision patients is an application domain with commercial products already existing. A variety of solutions are on the market and can be distinguished by their functioning (in virtual or augmented reality), the tasks targeted by the systems (e.g., face and object recognition, reading), the platform they use (dedicated platform or general existing one). Our goal is to propose competing solutions based on wide-spread and cheap platforms (e.g., mobile phone and cheap headset) to facilitate transfer to consumer market.

4.2. Human vision understanding through joint experimental and modeling studies, for normal and distrophic retinas

4.2.1. Cells characterization from their spike response

A prior step toward understanding how the retina extracts the information from a visual scene is the characterization of retinal ganglion cells receptive fields. The receptive field allows to classify retinal ganglion cells in sub-types such as direction sensitive cells. Each of these type extracts a local and definite piece of information from the visual scene, transmitted to the visual cortex. Hence receptive fields are somewhat the fundamental bricks of vision.

Current techniques of receptive fields estimation are based on Spike-Triggered Average [70]. However, this method heavily relies on the assumption that the static non linearity is convex (typically this is an exponential). Unfortunately, this violates a fundamental biophysical property of neurons: firing rate is bounded due to the refractory period. Additionally, this method is slow and of low precision.

We are working on more efficient techniques based on non-convex analysis, faster, more precise, and working for a non-convex (typically sigmoidal) non linearity. Additionnally we are also working on designing better stimuli for receptive fields estimations.

4.2.2. Understanding the role of spatio-temporal correlations in visual scene encoding

Retinal response to stimuli is related, on one hand, to spatio-temporal correlations of the stimulus [76], and, on the other hand to the intrinsic spatio-temporal correlations of the retinal activity induced by its vertical and lateral connectivity [81]. However, the role of spatio-temporal correlations in retinal coding is still controversial. With the current evolution of multi-electrode arrays recordings, it is possible to record from tens to thousands of neurons [42], [51], [63], [86], studying not only the correlations between few neurons, but also the correlations present in a whole population of retinal ganglion cells [73], [75], [77], [80]. The BIOVISION team has proposed a framework to study this correlation structure using Gibbs distributions (Sec. 3.2.4). Based upon the mathematical results presented in the papers [5] [45], we have developed algorithms to analyse and reproduce spatio-temporal correlations in neural assemblies containing up to a few hundreds of neurons [13], [69], [68].

We are now applying these methods for the analysis of retina data so as to better understand the role of spatio-temporal spike correlations in vision encoding.

4.2.3. Retinal waves

Retinal waves are bursts of activity occurring spontaneously in the developing retina of vertebrate species, contributing to the shaping of the visual system organization: retina circuitry shaping, retinotopy, eye segregation [83], [52], [74], [53]. They stop a few weeks after birth. Wave activity begins in the early development, long before the retina is responsive to light. It was recently found that they can be reinitiated pharmacologically in the adult mammalian retina [48]. This could have deep consequences on therapy for several degenerative retinal diseases. The mechanism of their generation, in imature, or adult retinas, remains however incompletely understood [84].

We aim at proposing a dynamical model of retinal waves depending on a few canonical parameters (e.g. concentration of a pharmacological agent) controlling the arousal of retinal waves as well as their shape/intensity. We want, on one hand, to design a model sufficiently close to biophysics so that it can reproduce and predict experimental results, and, on the other hand, sufficiently general to provide a generic mechanisms of retinal waves arousal also describing their different types.

4.2.4. Trajectory anticipation, from retina to V1

Global motion processing is a major computational task of biological visual systems. When an object moves across the visual field, the sequence of visited positions is strongly correlated in space and time, forming a trajectory. These correlated images generate a sequence of local activation of the feedforward stream. At the present stage of knowledge, it is still unclear how the early visual system processes motion trajectories. Motion integration, anticipation and prediction would be jointly achieved through the interactions between feed-forward, lateral and feedback propagations within a common spatial reference frame, the retinotopic maps. Addressing this problem is particularly challenging, as it requires to probe these sequences of events at multiple scales (from individual cells to large networks) and multiple stages (retina, primary visual cortex (V1)).

In the context of the ANR Trajectory we are working on such an integrated approach. We aim at modelling the population responses at two key stages of visual motion encoding: the retina and V1 based on simultaneous micro- and mesoscopic recordings made by our partners Institut des Neurosciences de la Timone and Institut de la Vision, and design a simulator of retinal output feeding V1. This study is a step toward understanding mechanisms of motion coding and anticipation with strong impact on our understanding of the visual system.

4.2.5. Simulating and analysing retina's response to visual stimuli

We want to design a retina simulator integrating the most recent advances on retina modeling. We will propose a user-friendly simulator, using parallel (multi-threads) programming, in order to simulate rapidly a large piece of the retina. This platform is further described in the section Software.

5. New Software and Platforms

5.1. Virtual Retina: A biological retina model with contrast gain control for large scale simulations

KEYWORDS: Neurosciences - Simulation - Biology - Health
SCIENTIFIC DESCRIPTION

The Virtual Retina software allows large-scale simulations of biologically-plausible retinas, with customizable parameters. Virtual Retina has been shown to reproduce a wide range of experimental data from salamander, cat and primate retinas [14], and has been used in several theoretical studies [65], [66], [67], [41], [17]. It has recently been shown to predict spikes in a mouse retina more accurately than linear-nonlinear (LN) models [79]. The underlying model includes a non-separable spatio-temporal linear model of filtering in the Outer Plexiform Layer, a shunting feedback at the level of bipolar cells, and a spike generation process using noisy leaky integrate-and-fire neurons to model RGCs. All parameters for the different stages of the model are customizable so that the visual field can be paved with different RGC types.

FUNCTIONAL DESCRIPTION.

Virtual Retina is a simulation software that allows large-scale simulations of biologically-plausible retinas.

- Participants: Bruno Cessac, Maria-Jose Escobar, Pierre Kornprobst, Selim Kraria, Daniela Pamplona, Selma Souihel, Thierry Vieville and Adrien Wohrer.
- Contact: Pierre Kornprobst
- URL: https://enas.inria.fr/virtual-retina.html

5.2. ENAS: Event Neural Assembly Simulation

KEYWORDS: Neurosciences - Health - Physiology
SCIENTIFIC DESCRIPTION

As one gains more intuitions and results on the importance of concerted activity in spike trains, models are developed to extract potential canonical principles underlying spike coding. These methods shed a new light on spike train dynamics. However, they require time and expertise to be implemented efficiently, making them hard to use in a daily basis by neuroscientists or modelers. To bridge this gap, we developed the license free multiplatform software ENAS (https://enas.inria.fr) integrating tools for individual and collective spike analysis and simulation, with some specificities devoted to the retina. The core of ENAS is the statistical analysis of population codes. One of its main strength is to provide statistical analysis of spike trains using Maximum Entropy-Gibbs distributions taking into account both spatial and temporal correlations as constraints, allowing to introduce causality and memory in statistics. It also generates simulated population raster from an user-specified Gibbs distribution.

We hope that ENAS will become a useful tool for neuroscientists to analyse spike trains and we hope to improve it thanks to user feedback. Our goal is to progressively enrich it with the latest research results, in order to facilitate transfer of new methods to the community.

FUNCTIONAL DESCRIPTION. ENAS is developed joinly by the Biovision, CORTEX/Mnemosyne, and DREAM Inria teams, under CeCILL-C licence, APP logiciel ENAS : IDDN.FR.OO1.190004.000.S.P.2014.000.31235. It can be freely loaded. ENAS has a friendly Graphical User Interface that avoids any scripting or writing code from user. Most methods have been implemented to run in parallel to reduce the time and memory consumption.

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- URL: https://enas.inria.fr

5.3. The Enas–Virtual Retina platform

In 2016 we merged Enas and Virtual Retina to produce the Enas platform https://enas.inria.fr. The initial version of Virtual retina has been extended to include lateral connections in the Inner Plexiform Layer. We can then simulate the response of the retina to visual stimuli (movies), including the effect of lateral connectivity, analyse the collective spike response to this stimulus using Gibbs distributions, and reproduce a similar raster using learning methods shaping the connectivity in the Inner Plexiform Layer.

This work has been presented in [27] and submitted to Frontiers in Neuroinformatics [3].

6. New Results

6.1. High tech vision aid systems for low vision patients

This is a new axis in the team that we started this year. We do not have results yet available but one project has started to allow real-time enhancement of environments in Virtual Reality (equipement: Samsung S6 and Samsung VR headset). This is the internship work of Alberto Patino (grant: CONACYT) who is co-supervised by Pierre Kornprobst and Fabio Solari (University of Genoa, Italy). We plan to submit an abstract to Vision 2017 conference, the 12th International Conference by the International Society for Low Vision Research and Rehabilitation.

Another project is in preparation, involving Fabio Solari (University of Genoa, Italy) and other colleagues from Université Cote d'Azur. New results are expected in 2017.

6.2. Human vision understanding through joint experimental and modeling studies, for normal and distrophic retinas

6.2.1. Cells characterization from their spike response

6.2.1.1. A new nonconvex variational approach for sensory neurons receptive field estimation

Participants: Audric Drogoul, Gilles Aubert [UCA, Laboratoire Jean Alexandre Dieudonné, Nice, France], Bruno Cessac, Pierre Kornprobst.

Determining the receptive field of a visual sensory neuron is a first but crucial step to- wards the characterization of neurons response to local spatio-temporal stimuli. Existing methods are based on convex optimization methods neglecting biophysical constraints of neurons (bounded firing rate), and they are relatively poor in terms of accuracy and running time. We propose a new method to estimate receptive fields by a nonconvex variational approach, thus relaxing the simplifying and unrealistic assumption of convexity made by standard approaches. The method consists in studying a relaxed discrete energy minimized by a proximal alternating minimization algorithm. We compare our approach with the classical spike-triggered-average technique on simulated data, considering a typical retinal ganglion cell. Results show a high improvement in terms of accuracy and convergence with respect to the duration of the experiment.

This work was presented in [29], [21] and has been submitted, see [24] .

6.2.1.2. Pan-retinal characterization of Light Responses from Ganglion Cells in the Developing Mouse Retina

Participants: Gerrit Hilgen [Institute of Neuroscience, Medical School, Newcastle University, Newcastle UK], Sarah Pirmoradian [ANC - Institute for Adaptive and Neural Computation, Edimburgh, UK], Daniela Pamplona, Pierre Kornprobst, Bruno Cessac, Matthias Hennig Pirmoradian [ANC - Institute for Adaptive and Neural Computation, Edimburgh, UK], Evelyne Sernagor [Institute of Neuroscience, Medical School, Newcastle University, Newcastle, UK].

We have investigated the ontogeny of light-driven responses in mouse retinal ganglion cells (RGCs). Using a large-scale, high-density multielectrode array, we recorded from hundreds to thousands of RGCs simultaneously at pan-retinal level, including dorsal and ventral locations. Responses to different contrasts not only revealed a complex developmental profile for ON, OFF and ON-OFF RGC types, but also unveiled differences between dorsal and ventral RGCs. At eye-opening, dorsal RGCs of all types were more responsive to light, perhaps indicating an environmental priority to nest viewing for pre-weaning pups. The developmental profile of ON and OFF RGCs exhibited antagonistic behavior, with the strongest ON responses shortly after eye-opening, followed by an increase in the strength of OFF responses later on. Further, we found that with maturation receptive field (RF) center sizes decrease, responses to light get stronger, and centers become more circular while seeing differences in all of them between RGC types. These findings show that retinal functionality is not spatially homogeneous, likely reflecting ecological requirements that favour the early development of dorsal retina, and reflecting different roles in vision in the mature animal.

This work is under revision, submitted to EScience [25]

6.2.2. Understanding the role of spatio-temporal correlations in visual scene encoding

6.2.2.1. Spike train analysis and Gibbs distributions

Participants: Bruno Cessac, Rodrigo Cofré [Département de Physique Théorique, Université de Genève].

Spikes in sensory neurons are conveyed collectively to the cortex using correlated binary patterns (in space and time) which constitute “the neural code”. Since patterns occur irregularly it is appropriate to characterize them using probabilistic descriptions or statistical models. Two major approaches attempt to characterize the spike train statistics: The Maximum Entropy Principle (MaxEnt) and Neuronal Network modeling (N.N). Remarkably, both approaches are related via the concept of Gibbs distributions. MaxEnt models are restricted to time-invariant Gibbs distributions, via the underlying assumption of stationarity, but this concept extends to non-stationary statistics (not defined via entropy), allowing to handle as well statistics of N.N models and GLM with non-stationary dynamics. We show in this poster that, stationary N.N, GLMmodels and MaxEnt models are equivalent via an explicit mapping. This allows us, in particular, to interpret the so-called "effective interactions" of MaxEnt models in terms of “real connections” models.

This work was presented in the Bernstein Conference 2016 [28] and will be soon submitted to Journal of Statistical Physics.

6.2.2.2. Dimensionality Reduction in spatio-temporal MaxEnt models and analysis of Retinal Ganglion Cell Spiking Activity in experiments

Participants: Rubén Herzog [CINV - Centro Interdisciplinario de Neurociencia de Valparaíso], Maria-Jose Escobar [Univ Tecnico Federico Santa María], Adrian Palacios [CINV - Centro Interdisciplinario de Neurociencia de Valparaíso], Bruno Cessac.

Retinal spike response to stimuli is constrained, on one hand by short range correlations (receptive field overlap) and on the other hand by lateral connectivity (cells connectivity). This last effect is difficult to handle from statistics because it requires to consider spatio-temporal correlations with a time delay long enough to take into account the time of propagation along synapses. Although MaxEnt model are useful to fit optimal model (maximizing entropy) under the constraints of reproducing observed correlations, they do address spatio-temporal correlations in their classical form (Ising or higher order interactions but without time delay). Binning in such models somewhat integrates propagation effects, but in an implicit form, and increasing binning severely bias data [1]. To resolve this issue we have considered spatio-temporal MaxEnt model formerly developed e.g. by Vasquez et al. [2]. The price to pay, however is a huge set of parameters that must be fitted to experimental data to explain the observed spiking patterns statistics. There is no a priori knowledge of which parameters are relevant and which ones are contributing to overfitting. We propose here a method of dimension reduction, i.e. a projection on a relevant subset of parameters, relying on the so-called Susceptibility matrix closely related to the Fisher information. In contrast to standard methods in information geometry though, this matrix handle space and time correlations. We have applied this method for retina data obtained in a diurnal rodent (Octodon degus, having 30% of cones photoreceptors) and a 252-MEA system. Three types of stimuli were used: spatio-temporal uniform light, white noise and a natural movie. We show the role played by time-delayed pairwise interactions in the neural response to stimuli both for close and distant cells. Our conclusion is that, to explain the population spiking statistics we need both short-distance interactions as well as long-distance interactions, meaning that the relevant functional correlations are mediated not only by common input (i.e. receptive field overlap, electrical coupling; spillover) but also by long range connections.

This work has been presented in the Bernstein 2016 conference [31] and has been submitted to Plos Comp Bio.

6.2.2.3. On the mathematical consequences of binning spike trains

Participants: Bruno Cessac, Arnaud Le Ny [LAMA - Laboratoire d'Analyse et de Mathématiques Appliquées], Eva Loecherbach [AGM - Laboratoire d'Analyse, Géométrie et Modélisation and Département de Mathématiques, [Cergy-Pontoise].

We initiate a mathematical analysis of hidden effects induced by binning spike trains of neurons. Assuming that the original spike train has been generated by a discrete Markov process, we show that binning generates a stochastic process which is not Markovian any more, but is instead a Variable Length Markov Chain (VLMC) with unbounded memory. We also show that the law of the binned raster is a Gibbs measure in the DLR (Dobrushin-Lanford-Ruelle) sense coined in mathematical statistical mechanics. This allows the derivation of several important consequences on statistical properties of binned spike trains. In particular, we introduce the DLR framework as a natural setting to mathematically formalize anticipation, i.e. to tell "how good" our nervous system is at making predictions. In a probabilistic sense, this corresponds to condition a process by its future and we discuss how binning may affect our conclusions on this ability. We finally comment what could be the consequences of binning in the detection of spurious phase transitions or in the detection of wrong evidences of criticality.

This work has been published in Neural Computation, Massachusetts Institute of Technology Press (MIT Press), 2016 [16].

6.2.3. Retinal waves

6.2.3.1. Mathematical and experimental studies on retinal waves

Participants: Dora Karvouniari, Lionel Gil [INLN -Institut Non Linéaire de Nice Sophia-Antipolis], Olivier Marre [Institut de la Vision], Serge Picaud [Institut de la Vision], Bruno Cessac.

We reproduce the spontaneous intrinsic cell-autonomous rhythmic bursting in Starbust Amacrine Cells (SACs) and the slow After Hyperpolarisation Current (sAHP), which modulates the refractory process inbetween two consecutive bursts, observed experimentally in [85]. We describe the dynamical influence of cholinergic synapses, ensuring the level of SAC synchrony necessary for the emergence of waves. We obtain: a) a plausible generic mechanism generating spontaneous retinal waves in development, without any need for external stimulation as opposed to existing models and b) a mathematical characterization of retinal waves. Especially, a biophysical parameter controls the wave arousal and the corresponding shape. The model is accurate enough to reproduce existing experiments, but also to propose new ones.

This work has been presented in the workshop "Modelling the early visual system" [32], 2nd International Conference on Mathematical Neuroscience (ICMNS) [22], the AREADNE conference [34], the Bernstein conference [33]. Two papers are in preparation.

6.2.4. Trajectory anticipation, from retina to V1

This work is just starting. The main work has been done by Selma Souihel in her Master II instership supervised by Bruno Cessac [36]. The aim of the internship is to use and update the software VirtualRetina and Enas in order to reproduce the activity of the retina in response to the stimulus of a moving bar, observed By Mr Berry & al. A form of anticipation of the movement has been demonstrated experimentally by its authors in salamander, rabbit and goldfish retinas. This anticipation can be explained, in the case of a simple trajectory, by the gain control mechanism specific to the ganglion cells, implemented by Virtual-Retina-Enas.

6.2.5. Simulating and analysing retina's response to visual stimuli

6.2.5.1. ENAS: A new software for spike train analysis and simulation

Participants: Bruno Cessac, Pierre Kornprobst, Selim Kraria, Hassan Nasser, Daniela Pamplona, Geoffrey Portelli, Thierry Vieville [Mnemosyne - Mnemonic Synergy LaBRI - Laboratoire Bordelais de Recherche en Informatique, IMN - Institut des Maladies Neurodégénératives, [Bordeaux].

This work, presenting the Enas-Virtual Retina platform has been presented in [27] and submitted to Frontiers in Neuroinformatics [3].

6.2.5.2. Rank order coding: a retinal information decoding strategy revealed by large-scale multielectrode array retinal recordings

Participants: Geoffrey Portelli, John M. Barrett [Institute of Neuroscience, Medical School, Newcastle University, Newcastle UK], Gerrit Hilgen [Institute of Neuroscience, Medical School, Newcastle University, Newcastle UK], Timothée Masquelier [CERCO, Toulouse, France], Alessandro Maccione [NetS3 Lab - Neuro-Engineering & bio-arTificial Synergic SystemS Laboratory, Genova, Italy], Stefano Di Marco [NetS3 Lab - NeuroEngineering & bio-arTificial Synergic SystemS Laboratory, Genova, Italy], Luca Berdondini [NetS3 Lab - NeuroEngineering & bio-arTificial Synergic SystemS Laboratory, Genova, Italy], Pierre Kornprobst, Evelyne Sernagor [Institute of Neuroscience, Medical School, Newcastle University, Newcastle, UK].

How a population of retinal ganglion cells (RGCs) encodes the visual scene remains an open question. Going beyond individual RGC coding strategies, results in salamander suggest that the relative latencies of an RGC pair encodes spatial information. Thus a population code based on this concerted spiking could be a powerful mechanism to transmit visual information rapidly and efficiently. Here, we tested this hypothesis in mouse by recording simultaneous light-evoked responses from hundreds of RGCs, at pan-retinal level, using a new generation of large-scale, high density multielectrode array consisting of 4096 electrodes. Interestingly, we did not find any RGCs exhibiting a clear latency tuning to the stimuli, suggesting that in mouse, individual RGC pairs may not provide sufficient information. We show that a significant amount of information is encoded synergistically in the concerted spiking of large RGC populations. Thus, the RGC population response

described with relative activities, or ranks, provides more relevant information than classical independent spike count- or latency- based codes. In particular, we report for the first time that when considering the relative activities across the whole population, the wave of first stimulus-evoked spikes (WFS) is an accurate indicator of stimulus content. We show that this coding strategy co-exists with classical neural codes, and that it is more efficient and faster. Overall, these novel observations suggest that already at the level of the retina, concerted spiking provides a reliable and fast strategy to rapidly transmit new visual scenes.

This work has been published in eNeuro [20].

6.2.5.3. Microsaccades enable efficient synchrony-based coding in the retina: a simulation study.

Participants: Timothée Masquelier [CERCO, Toulouse, France], Geoffrey Portelli, Pierre Kornprobst.

It is now reasonably well established that microsaccades (MS) enhance visual perception, although the underlying neuronal mechanisms are unclear. Here, using numerical simulations, we show that MSs enable efficient synchrony-based coding among the primate retinal ganglion cells (RGC). First, using a jerking contrast edge as stimulus, we demonstrate a qualitative change in the RGC responses: synchronous firing, with a precision in the 10 ms range, only occurs at high speed and high contrast. MSs appear to be sufficiently fast to be able reach the synchronous regime. Conversely, the other kinds of fixational eye movements known as tremor and drift both hardly synchronize RGCs because of a too weak amplitude and a too slow speed respectively. Then, under natural image stimulation, we find that each MS causes certain RGCs to fire synchronously, namely those whose receptive fields contain contrast edges after the MS. The emitted synchronous spike volley thus rapidly transmits the most salient edges of the stimulus, which often constitute the most crucial information. We demonstrate that the readout could be done rapidly by simple coincidence-detector neurons without knowledge of the MS landing time, and that the required connectivity could emerge spontaneously with spike timing-dependent plasticity.

This work has been published in Scientific Reports [17].

6.2.6. Mean-Field models in neuroscience

6.2.6.1. Perspectives on Multi-Level Dynamics

Participants: Fatihcan Atay [MPI-MIS - Max Planck Institute for Mathematics in the Sciences], Sven Banisch [MPI-MIS - Max Planck Institute for Mathematics in the Sciences], Philippe Blanchard [University of Bielefeld-Departement of physics], Bruno Cessac, Eckehard Olbrich [MPI-MIS - Max Planck Institute for Mathematics in the Sciences], Dimitri Volchenkov [University of Bielefeld, Departement of physics].

As Physics did in previous centuries, there is currently a common dream of extracting generic laws of nature in economics, sociology, neuroscience, by focalising the description of phenomena to a minimal set of variables and parameters, linked together by causal equations of evolution whose structure may reveal hidden principles. This requires a huge reduction of dimensionality (number of degrees of freedom) and a change in the level of description. Beyond the mere necessity of developing accurate techniques affording this reduction, there is the question of the correspondence between the initial system and the reduced one. In this paper, we offer a perspective towards a common framework for discussing and understanding multi-level systems exhibiting structures at various spatial and temporal levels. We propose a common foundation and illustrate it with examples from different fields. We also point out the difficulties in constructing such a general setting and its limitations.

This work has been published in The interdisciplinary journal of Discontinuity, Nonlinearity, and Complexity, 2016, 5 [15].

6.2.7. Motion perception

6.2.7.1. The relative contribution of noise and adaptation to competition during tri-stable motion perception

Participants: Andrew Isaac Meso [Institut de Neurosciences de la Timone, Team InVibe, France], James Rankin [Center for Neural Science, New York UniversityNew York, NY], Pierre Kornprobst, Olivier Faugeras [Université Côte d'Azur, Inria, MathNeuro team, France], Guillaume S. Masson [Institut de Neurosciences de la Timone, Team InVibe, France].

Animals exploit antagonistic interactions for sensory processing and these can cause oscillations between competing states. Ambiguous sensory inputs yield such perceptual multistability. Despite numerous empirical studies using binocular rivalry or plaid pattern motion, the driving mechanisms behind the spontaneous transitions between alternatives remain unclear. In the current work, we used a tristable barber pole motion stimulus combining empirical and modeling approaches to elucidate the contributions of noise and adaptation to underlying competition. We first robustly characterized the coupling between perceptual reports of transitions and continuously recorded eye direction, identifying a critical window of 480 ms before button presses, within which both measures were most strongly correlated. Second, we identified a novel nonmonotonic relationship between stimulus contrast and average perceptual switching rate with an initially rising rate before a gentle reduction at higher contrasts. A neural fields model of the underlying dynamics introduced in previous theoretical work and incorporating noise and adaptation mechanisms was adapted, extended, and empirically validated. Noise and adaptation contributions were confirmed to dominate at the lower and higher contrasts, respectively. Model simulations, with two free parameters controlling adaptation dynamics and direction thresholds, captured the measured mean transition rates for participants. We verified the shift from noise-dominated toward adaptation-driven in both the eye direction distributions and intertransition duration statistics. This work combines modeling and empirical evidence to demonstrate the signal-strength–dependent interplay between noise and adaptation during tristability. We propose that the findings generalize beyond the barber pole stimulus case to ambiguous perception in continuous feature spaces.

This work is a a continuation of former paper [72], [12] and has been published in Journal of Vision [19].

6.2.7.2. Understanding the impact of recurrent interactions on MT population tuning: a simulation study.

Participants: Kartheek Medathati, Andrew Isaac Meso [Institut de Neurosciences de la Timone, Team InVibe, France], Guillaume S. Masson [Institut de Neurosciences de la Timone, Team InVibe, France], Pierre Kornprobst, James Rankin [Center for Neural Science, New York University, USA].

In sensory systems, different computational rules are often evident in different neuronal subpopulations. Most previous models of motion estimation by MT cells explain their specific tuning functions by having multiple feedforward inputs, largely ignoring the role of recurrent connectivity, a hallmark of cortical circuits. Therefore they fail to explain the dynamics of these tuning functions and the fact that different behaviour can be achieved by a single subpopulation when varying the spatiotemporal properties of the input. Here, using numerical simulations, we focus on a ring network that models visual motion processing at the level of MT cells. We show how excitatory and inhibitory recurrent connections shape motion direction tuning, thus resulting in different computational rules such as vector averaging, winner-take-all or bimodal representations. In particular, depending on the inhibition regime the ring network can switch from motion integration to motion segmentation, being able to compute either a single pattern motion or to superpose multiple inputs as in motion transparency. Such feature space centre-surround recurrent mechanisms may be widely applicable to explain context-modulation of sensory processing.

This work has been presented at AREADNE conference [35] and a paper is in preparation.

6.2.8. Bio-Inspired Computer Vision

6.2.8.1. Bio-Inspired Computer Vision: Towards a Synergistic Approach of Artificial and Biological Vision

Participants: Pierre Kornprobst, Guillaume S. Masson [Institut de Neurosciences de la Timone, Team InVibe], Kartheek Medathati [correspondent], Heiko Neumann [Ulm University, Germany].

Studies in biological vision have always been a great source of inspiration for design of computer vision algorithms. In the past, several successful methods were designed with varying degrees of correspondence with biological vision studies, ranging from purely functional inspiration to methods that utilise models that were primarily developed for explaining biological observations. Even though it seems well recognised that computational models of biological vision can help in design of computer vision algorithms, it is a non-trivial exercise for a computer vision researcher to mine relevant information from biological vision literature as very few studies in biology are organised at a task level.

In [26], we aim to bridge this gap by providing a computer vision task centric presentation of models primarily originating in biological vision studies. Not only we revisit some of the main features of biological vision and discuss the foundations of existing computational studies modelling biological vision, but also consider three classical computer vision tasks from a biological perspective: image sensing, segmentation and optical flow. Using this task-centric approach, we discuss well-known biological functional principles and compare them with approaches taken by computer vision. Based on this comparative analysis of computer and biological vision, we present some recent models in biological vision and highlight a few models that we think are promising for future investigations in computer vision. To this extent, this paper provides new insights and a starting point for investigators interested in the design of biology-based computer vision algorithms and pave a way for much needed interaction between the two communities leading to the development of synergistic models of artificial and biological vision.

This work has been published in Computer Vision and Image Understanding Journal (CVIU) [9].

6.2.8.2. Retina-inspired tone mapping

Participants: Marco Benzi, Maria-Jose Escobar [Universidad Técnica Federico Santa María, Valparaíso, Chile], Adrien Bousseau [Inria, GraphDeco project-team], Pierre Kornprobst [correspondent].

Real-world radiance values span several orders of magnitudes which have to be processed by biological and artificial systems in order to maintain high visual sensitivity.

In biological systems, process starts at the retina level, where adaptation is absolutely crucial since retinas must maintain high contrast sensitivity over a very broad range of luminance, from starlight to direct sunlight. Adaptation is both global through neuromodulatory feedback loops and local through adaptive gain control mechanisms so that retinal networks can be adapted to the whole scene luminance level while maintaining high contrast sensitivity in different regions of the image, despite their considerable differences in luminance. Adaptation is present at different levels, e.g., at the photoreceptor level where sensitivity is a function of the recent mean intensity, and at the bipolar level where slow and fast contrast adaptation mechanisms are found. These multiple adaptational mechanisms act together, with lighting conditions dictating which mechanisms dominate.

In artificial systems, the process of compressing the range of intensities in High-Dynamic Range (HDR) images is know as tone mapping. It is a necessary step to properly visualize captured natural scenes as common displays are Low-Dynamic Range, spanning up to two orders of magnitude. There is a large body of literature in this area on static images, with approaches which combine luminance adaptation (using empirical laws such as the Naka-Rushton equation) and local contrast enhancement sometimes closely inspired from retinal principles [43], [61]. Recent developments concern video-tone mapping where a few approaches have been developed [49].

In this work, we investigate if the Virtual Retina simulator [14] could serve as a goof basis to develop a new tone mapping operator for videos. One strength of this simulator is its model of fast contrast gain control which has been validated on experimental data. However this model was not designed to deal with color and HDR images. This requires some pre- and post-processing but also changes in the Virtual Retina to account for other adaptation phenomena. Preliminary encouraging results have been obtained and we plan to continue that project in 2017.

7. Partnerships and Cooperations

7.1. National Initiatives

7.1.1. ANR

7.1.1.1. Trajectory

Title: Encoding and predicting motion trajectories in early visual networks

Programm: ANR

Duration: October 2015 - September 2020

Coordinator: Invibe Team, Institut des Neurosciences de la Timone, Frédéric Chavane,

Partners:

AMU INT Aix-Marseille, Université Institut de Neurosciences de la Timone

INSERM IDV INSERM Institut de la Vision

USM UV U Santa Maria & U Valparaiso

Inria contact: Bruno Cessac

Global motion processing is a major computational task of biological visual systems. When an object moves across the visual field, the sequence of visited positions is strongly correlated in space and time, forming a trajectory. These correlated images generate a sequence of local activation of the feed-forward stream. Local properties such as position, direction and orientation can be extracted at each time step by a feed-forward cascade of linear filters and static non-linearities. However such local, piecewise, analysis ignores the recent history of motion and faces several difficulties, such as systematic delays, ambiguous information processing (e.g., aperture and correspondence problems) high sensitivity to noise and segmentation problems when several objects are present. Indeed, two main aspects of visual processing have been largely ignored by the dominant, classical feed-forward scheme. First, natural inputs are often ambiguous, dynamic and non-stationary as, e.g., objects moving along complex trajectories. To process them, the visual system must segment them from the scene, estimate their position and direction over time and predict their future location and velocity. Second, each of these processing steps, from the retina to the highest cortical areas, is implemented by an intricate interplay of feed-forward, feedback and horizontal interactions. Thus, at each stage, a moving object will not only be processed locally, but also generate a lateral propagation of information. Despite decades of motion processing research, it is still unclear how the early visual system processes motion trajectories. We, among others, have proposed that anisotropic diffusion of motion information in retinotopic maps can contribute resolving many of these difficulties. Under this perspective, motion integration, anticipation and prediction would be jointly achieved through the interactions between feed-forward, lateral and feedback propagations within a common spatial reference frame, the retinotopic maps. Addressing this question is particularly challenging, as it requires to probe these sequences of events at multiple scales (from individual cells to large networks) and multiple stages (retina, primary visual cortex (V1)). “TRAJECTORY” proposes such an integrated approach. Using state-of-the-art micro- and mesoscopic recording techniques combined with modeling approaches, we aim at dissecting, for the first time, the population responses at two key stages of visual motion encoding: the retina and V1. Preliminary experiments and previous computational studies demonstrate the feasibility of our work. We plan three coordinated physiology and modeling work-packages aimed to explore two crucial early visual stages in order to answer the following questions: How is a translating bar represented and encoded within a hierarchy of visual networks and for which condition does it elicit anticipatory responses? How is visual processing shaped by the recent history of motion along a more or less predictable trajectory? How much processing happens in V1 as opposed to simply reflecting transformations occurring already in the retina? The project is timely because partners master new tools such as multi-electrode arrays and voltage-sensitive dye imaging for investigating the dynamics of neuronal populations covering a large segment of the motion trajectory, both in retina and V1. Second, it is strategic: motion trajectories are a fundamental aspect of visual processing that is also a technological obstacle in computer vision and neuroprostheses design. Third, this project is unique by proposing to jointly investigate retinal and V1 levels within a single experimental and theoretical framework. Lastly, it is mature being grounded on (i) preliminary data paving the way of the three different aims and (ii) a history of strong interactions between the different groups that have decided to join their efforts.

7.2. European Initiatives

7.2.1. FP7 & H2020 Projects

7.2.1.1. RENVISION

Title: Retina-inspired ENcoding for advanced VISION tasks

Programm: FP7

Duration: March 2013 - February 2016

Coordinator: Instituto Italiano di Tecnologia_Pattern Analysis and Computer vision) Vittorio Murino

Partners:

PAVIS,NET3 Fondazione Istituto Italiano di Tecnologia (Italy)

Institute for Adaptive and Neural Computation, The University of Edinburgh (UK)

Institute of Neuroscience, University of Newcastle Upon Tyne (UK)

Inria contact: Bruno Cessac

The retina is a sophisticated distributed processing unit of the central nervous system encoding visual stimuli in a highly parallel, adaptive and computationally efficient way. Recent studies show that rather than being a simple spatiotemporal filter that encodes visual information, the retina performs sophisticated non-linear computations extracting specific spatio-temporal stimulus features in a highly selective manner (e.g. motion selectivity). Understanding the neurobiological principles beyond retinal functionality is essential to develop successful artificial computer vision architectures. RENVISION's goal is, therefore, twofold: i) to achieve a comprehensive understanding of how the retina encodes visual information through the different cellular layers; ii) to use such insights to develop a retina-inspired computational approach to high-level computer vision tasks. To this aim, exploiting the recent advances in high-resolution light microscopy 3D imaging and high-density multielectrode array technologies, RENVISION will be in an unprecedented position to investigate pan-retinal signal processing at high spatio-temporal resolution, integrating these two technologies in a novel experimental setup. This will allow for simultaneous recording from the entire population of ganglion cells and functional imaging of inner retinal layers at near-cellular resolution, combined with 3D structural imaging of the whole inner retina. The combined analysis of these complex datasets will require the development of novel multimodal analysis methods. Resting on these neuroscientific and computational grounds, RENVISION will generate new knowledge on retinal processing. It will provide advanced pattern recognition and machine learning technologies to ICTs by shedding a new light on how the output of retinal processing (natural or modelled) allows solving complex vision tasks such as automated scene categorization and human action recognition.

7.3. International Initiatives

7.3.1. Informal International Partners

- Maria-Jose Escobar, University Santa-Maria, Valparaiso;
- Adrian Palacios, Centro de Neurociencia, Valparaiso

7.4. International Research Visitors

7.4.1. Visits of International Scientists

7.4.1.1. Internships

- Marco Benzi (grant: Stage Master Transverse Biovision–GraphDeco), Retina-inspired tone mapping. Supervisors: Pierre Kornprobst and Adrien Rousseau (GraphDeco), in collaboration with Maria-Jose Escobar (Universidad Técnica Federico Santa María, Valparaíso, Chile)

- Alberto Patino (grant: CONACYT), Studying image transforms at neuronal level and in Virtual Reality. Supervisors: Pierre Kornprobst (Biovision) and Fabio Solari (University of Genoa, Italy)

8. Dissemination

8.1. Promoting Scientific Activities

8.1.1. Scientific Events Organisation

8.1.1.1. Member of the Organizing Committees

- Bruno Cessac: "Neural Network Dynamics in Health and Disease", 12-14 October 2016, Institut de Neurosciences de la Timone (INT), Marseille, France, http://www.gdr-neuralnet.cnrs.fr/en.
- Bruno Cessac: "Neurostim2016", http://neurostim2016.inria.fr/ 22 November 2016.

8.1.2. Scientific Events Selection

8.1.2.1. Member of the Conference Program Committees

- Pierre Kornprobst was a member of the program committee of the 24th European Signal Processing Conference (EUSIPCO 2016).

8.1.2.2. Reviewer

Pierre Kornprobst has been a reviewer for SIGGRPAH 2016.

8.1.3. Journal

8.1.3.1. Member of the Editorial Boards

Pierre Kornprobst is associate editor for the Computer Vision and Image Understanding Journal (CVIU).

8.1.4. Invited Talks

- Bruno Cessac, Toulon, March 2016.
- Bruno Cessac, Theoretical Physics lab, Geneve, March 2016.

8.1.5. Research Administration

- Pierre Kornprobst is an elected member of the Conseil Académique d'Université Côte d'Azur (UCA).
- Pierre Kornprobst leads the project UCAGate to provide UCA a new tool aiming at (i) giving a clear view of skills and competences of UCA for internal and external users, (ii) facilitate the emergence of new transdisciplinary synergies between UCA partners, (iii) provide UCA tools to show the transformation effect from the IDEX for the next evaluation. A first prototype is expected in February 2017.
- Pierre Kornprobst is member of the editorial committee of the Sophia Antipolis internal letter SAM & YOU.
- Pierre Kornprobst has been appointed by Inria Direction representative of the administration in the advisory committee of Inria contractual doctoral candidates [4] (on July 16, for two years).

[4] Représentant de l'administration suppléant au sein de la Commission consultative des doctorants contractuels d'Inria

8.2. Teaching - Supervision - Juries

8.2.1. Teaching

Licence : Theodora Karvouniari, "Transmissions numériquese , 1ere année de l' IUT, Departement Réseaux et Telecommunications, 64h/ an, 50 students.

Master 2: Bruno Cessac, *Neuronal dynamics*, 36 hours, Master 2 of Computational Biology and Biomedicine, Université Nice Sophia Antipolis, France.

8.2.2. Supervision

- PhD in progress: Selma Souihel, "Generic and specific computational principles for the visual anticipation of motion trajectories". Started in November 2016. Supervisor B. Cessac
- PhD in progress: Theodora Karvouniari, "Retinal waves in the retina: theory and experiments". Started in October 2014. Supervisor, B. Cessac.
- PhD defended: Kartheek Medathati, "Towards synergistic models of motion information processing in biological and artificial vision", co-supervised by Pierre Kornprobst and Guillaume S. Masson (Institut de Neurosciences de la Timone, Marseille, France), December 13, 2016.

8.2.3. Juries

Bruno Cessac, member of the Jury's thesis: "Vers des modèles synergiques de l'estimation du mouvement en vision biologique et artificielle", by Kartheek Medathati.

Bruno Cessac, member of the Jury's thesis: "Structuration temporelle de la mémoire de travail dans les réseaux de neurones récurrents" by Guillaume Rodriguez.

8.3. Popularization

- Rencontre avec le public à la suite de la projection du film "La nuit qu'on suppose" de Benjamin d'Aoust, Médiathèque d'Antibes, 16 Janvier 2016.
- Bruno Cessac. Cafe In Sophia. La rétine, fonctionnement et thérapie, 28 Janvier 2016.

9. Bibliography

Major publications by the team in recent years

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Publications of the year

Articles in International Peer-Reviewed Journals

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