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agence d'évaluation de la recherche
et de l'enseignement supérieur

Department for the evaluation of
research units

AERES report on unit:

Computational and Quantitative Biology

CQB

Under the supervision of
the following institutions
and research bodies:

Université Paris 6 - Pierre et Marie Curie

Centre National de la Recherche Scientifique



February 2013



agence d'évaluation de la recherche
et de l'enseignement supérieur

Research Units Department

President of AERES

Didier Houssin

Research Units Department

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Pierre Glaudes



Grading

Once the visits for the 2012-2013 evaluation campaign had been completed, the chairpersons of the expert committees, who met per disciplinary group, proceeded to attribute a score to the research units in their group (and, when necessary, for these units' in-house teams).

This score (A+, A, B, C) concerned each of the six criteria defined by the AERES.

NN (not-scored) attached to a criteria indicate that this one was not applicable to the particular case of this research unit or this team.

Criterion 1 - C1 : Scientific outputs and quality ;

Criterion 2 - C2 : Academic reputation and appeal ;

Criterion 3 - C3 : Interactions with the social, economic and cultural environment ;

Criterion 4 - C4 : Organisation and life of the institution (or of the team) ;

Criterion 5 - C5 : Involvement in training through research ;

Criterion 6 - C6 : Strategy and five-year plan.

With respect to this score, the research unit concerned by this report and its in-house teams received the following grades:

- Grading table of the unit: **Computational and Quantitative Biology**

C1	C2	C3	C4	C5	C6
A	A	A	A	A	A+

- Grading table of the team: **Analytical Genomics**

C1	C2	C3	C4	C5	C6
A+	A+	A	NN	A+	A+

- Grading table of the team: **Structure, Dynamics and Evolution of Genetic Networks**

C1	C2	C3	C4	C5	C6
A	B	NN	NN	A	A

- Grading table of the team: **Biology of Genomes**

C1	C2	C3	C4	C5	C6
A	A	A	NN	A	A



- Grading table of the team: *Diatom Functional Genomics*

C1	C2	C3	C4	C5	C6
A	A+	A	NN	B	A

- Grading table of the team: *Genomic physics*

C1	C2	C3	C4	C5	C6
A+	A	NN	NN	B	A

- Grading table of the team: *Statistical Genomics and Biological Physics*

C1	C2	C3	C4	C5	C6
A	NN	NN	NN	NN	A

- Grading table of the team: *Computational Neuroscience Group (CNG)*

C1	C2	C3	C4	C5	C6
A	A	A	NN	A+	A



Evaluation report

Unit name:	Computational and Quantitative Biology
Unit acronym:	CQB
Label requested:	UMR CNRS
Present no.:	UMR 7238
Name of Director (2012-2013):	Ms Alessandra CARBONE
Name of Project Leader (2014-2018):	Ms Alesandra CARBONE

Expert committee members

Chair:	Mr Michael CHANDLER (Centre de Génétique Moléculaire, Toulouse)
Experts:	Ms Susan HOLMES (Stanford university , USA)
	Mr Daniel KAHN (Laboratoire de Biométrie et Biologie Evolutive, Lyon, representative of CoCNRS)
	Mr Peter KROTH (University of Konstanz, Germany)
	Mr Andrea PARMEGGIANI (University of Montpellier 2)
	Mr Vincent POIRRIEZ (Université de Valenciennes, representative of CNU)
	Mr Eduardo ROS (University of Granada, Spain)
	Mr Jacques VAN HELDEN (Université d'Aix-Marseille, Marseille-Luminy)

Scientific delegate representing the AERES:

Mr Jacques HAIECH

Representative(s) of the unit's supervising institutions and bodies:

Mr Thierry GRANGE (CNRS)

Mr Paul INDELICATO (UPMC-Paris 6)



1 • Introduction

History and geographical location of the unit

The unit was created in January 2009 as FRE 3214 (Génomique des Microorganismes) by the CNRS and the University Paris 6- Pierre and Marie Curie. It remained "virtual" for a full year since no space was allocated until January 2010 when it was installed on the Cordeliers Campus. In January 2011, the FRE3214 was transformed into UMR7238, an established unit managed by the CNRS and Paris VI. The unit became part of a larger project, the Paris-Seine Institute of Biology (IBPS) headed by Ms Catherine Jessus. A scientific advisory board evaluated this institute in February 2012 and UMR7238 was extremely well perceived.

The unit is still located at the Cordeliers Campus isolated from the main campus at Jussieu and one of the groups proposed to join in the near future is located elsewhere. Space has been reserved for the unit on the main campus and it will move when suitable renovations have been undertaken.

Management team:

UMR7238 is headed by Ms Alessandra CARBONE and during the period of this review was composed of 6 groups, 3 are computationally oriented and 3 experimentally oriented. It is proposed to integrate a seventh (theoretical) group in the new unit and to change the unit name to: Computational and Quantitative Biology.

AERES nomenclature:

SVE1_LS2

ST5

Unit workforce:

Unit workforce	Number as at 30/06/2012	Number as at 01/01/2014	2014-2018 Number of project producers
N1: Permanent professors and similar positions	8	10	10
N2: Permanent researchers from Institutions and similar positions	5	5	5
N3: Other permanent staff (without research duties)	3	4	
N4: Other professors (Emeritus Professor, on-contract Professor, etc.)			
N5: Other researchers from Institutions (Emeritus Research Director, Postdoctoral students, visitors, etc.)	5	8	8
N6: Other contractual staff (without research duties)			
TOTAL N1 to N6	21	27	23
Percentage of producers	100 %		



Unit workforce	Number as at 30/06/2012	Number as at 01/01/2014
Doctoral students	13	
Theses defended	6	
Postdoctoral students having spent at least 12 months in the unit*	5	
Number of Research Supervisor Qualifications (HDR) taken		
Qualified research supervisors (with an HDR) or similar positions	6	6



2 • Assessment of the unit

Strengths and opportunities:

At present the unit is well balanced and composed of three experimental and three theoretical teams. It was initially conceived as an entity in which experiment and theory could confront each other and provide a mutual synergism. This was not without risk but, after its first three years, this experiment seems to have been a true success with a growing interaction between the teams and approaches. The three experimental teams are addressing areas of gene expression networks and stress responses in yeast, the structure and evolution of yeast genomes and the biology of diatoms. The three theoretical teams are addressing protein structure and interactions, identification of small non-coding RNAs and more general genome annotation problems and microbial genome structure using computational approaches and the dynamics of microbial genomes using approaches derived from physics. This configuration has created a number of meaningful and very fruitful interactions between the theoretical and experimental groups. The unit is dynamic. It is composed of young energetic team leaders exploring new topics and approaches. Not surprisingly, some groups are already fully functional while other more recent arrivals have yet to build up their scientific "portfolios" in their areas of choice.

The unit will move to newly renovated space on the main Jussieu campus in the framework of the newly created Institut de Biologie Paris Seine (IBPS). This change of environment will provide significantly more space and also opportunities to foster collaborations with the other departments of the IBPS, in particular with the 'Evolution and Biodiversity' and 'Neurosciences' units and to a lesser extent with 'Developmental Biology'. It will change its name from 'Genomics of Microorganisms' to 'Computational and Quantitative Biology' to reflect an expansion in its themes to include Computational Neuroscience. The unit will also have access to a large number of platforms which are part of the IBPS.

Weaknesses and threats:

One of the major difficulties of the unit is its present isolation from the main campus but it should move into newly renovated space which is being prepared in the building which houses the IBPS. Other potential weaknesses are the very limited size of most teams, in particular, the Statistical Genomics and Biological Physics team and the Genophysics team. At present, each is composed of the PI and students (mainly masters students).

There is also a weakness in the packaging and distribution of the many software tools developed by various groups. Making the community aware of the availability of this software is important for recognition and impact of the unit as a whole. This weakness is partly explained by the difficulty for the unit to recruit permanent technical staff that would be dedicated to the packaging, maintenance, deployment and support for the software tool developed by the computer scientists of the unit.

The unit has already had to face delays in occupying and creating a functioning entity in its present space. It is now in a position where it is physically impossible to increase the number of students and faculty members. Integrating additional teams to strengthen areas of scientific interest is also unfeasible under these conditions. Any delays in the move to the main campus will have a serious negative effect on the development of the unit.

The inclusion of a computational neuroscience team will expand the interests of the unit but will present a challenge. There is a risk that the team, which has a strong track record, may be somewhat isolated thematically (although the committee understood that some mathematical tools it uses may overlap with those used in the established theoretical groups). Its interaction with the present neuroscience unit is not obvious.



Recommendations:

The committee feels that the major problem at this time centers around the move to the main campus. This should be expedited urgently and in a single step. This implies that both the wetbench labs (which are ready for occupation) and the space for the theoretical groups (which has yet to be renovated) must be ready before the final move.

It will be important to reinforce certain of the smaller groups with technical staff and young faculty members (or junior research staff). Even though the committee understood that two of the theoretical groups wish to remain small, the drain on the PI's time by high teaching loads must be compensated by additional staff.

Continuity must be maintained within the secretarial support of the unit by replacing the present administrator when she transfers to another post in the larger institute.

A system should be put in place to package the software produced by the unit and to rationalize computational resources. This could be readily undertaken by a central computing unit in the IBPS if this were to be envisioned. The committee understood that there is a post which has been open for several years but no suitable candidates have yet been found. This is possibly due to the wide profile requested and the non-attractiveness of academic positions in this area of expertise.

There are two requirements to assist in maintaining the computational infrastructure: a dedicated person (e.g. research engineer) to interact with researchers and to provide good practices for code engineering, code packaging, distribution, maintenance, user support and to ensure consistency between different projects; and a second position (e.g. an engineer or an assistant engineer which could be shared with the IBPS) to assume responsibility for transversal operations such as backup, computer maintenance, web site development and publication management. This structure would also provide the opportunity to acquaint incoming students with the available toolboxes and tools developed by the lab. The committee was surprised that such a basic informatics platform was not a priority of the IBPS.

Integration of the computational neuroscience team could make sense for the IBPS and for the team itself, but an effort should be made to create a real interface and collaboration with the rest of the unit. The impression given by the team leader was that the unit would provide competence of large-system computing that would contribute to the research projects of the neuroscience team, but we were not convinced that this would be the case, beyond general considerations concerning the general sharing of methods and concepts related to mathematical analysis of complex systems. At present, this would clearly represent a general scientific policy decision since the added scientific value for the hosting unit is not yet clear. Perhaps the addition of other computational neuroscience teams or related areas in the future development of the unit would solve the potential problem of isolation. However, this implies that the Unit director will be obliged to defend two distinct subjects (the currently well-implemented genetics/genomics orientation, and the neurosciences) and balance the resources between the two.

Other significant components of the IBPS will be 'Developmental Biology' and 'Evolution and Biodiversity'. There will undoubtedly be opportunities to apply computational biology approaches in these areas. These should clearly be explored.



3 • Detailed assessments

Assessment of scientific quality and outputs

This is a truly multidisciplinary unit which, by its emphasis on the importance of combining both wet bench and theoretical approaches, is part of a paradigm shift in the study of biology. A reflection of this is the fact that the unit bridges two university departments: biology and engineering and is strongly supported by both in terms of faculty positions. The unit has a very good publication record in quantity and in quality. The different groups have published 66 peer reviewed articles in international journals and one patent since its creation in 2009. A number of these are in journals with strong impact factors (Cell, PNAS etc) and in journals which are important in the various fields of expertise represented here. Since 4 of the 6 team leaders are university professors and the majority of the junior members of the teams are junior faculty members with heavy teaching loads, this represents an excellent level of production. There are a number of joint publications between the theoretical and experimental groups indicating a strong and growing interactivity within the unit.

Eleven software packages have also been produced. These include tools to predict protein-protein interfaces (JET), genome-wide miRNA prediction (MIRENA), reconstruction of ancestral genomes (CHRONicle) and chromosome organization (NuST), protein remote homology detection (ILP-homology), Combination of Annotations by Species and pHMM CASH, Clusters AGgregation CLAG, miRNA Structural Clustering (MIRSTRuC), Maximal SubTrees (MST), Blocks In Sequences (BIS) some of which (e.g. ULYSSE for Automatic detection in clonal populations of rare genomic structural variations from next-gen sequencing data) have yet to be published.

Assessment of the unit's academic reputation and appeal

In spite of the fact that all constituent teams, except that of the unit director, were created at the time of the creation of the unit only three years ago, the individual PIs have already managed to build a solid academic reputation. Collectively they have been invited to more than 50 international and national meetings and an equivalent number of seminars. They have also made many contributions in the form of short communications and posters (this includes both the more junior research faculty members and various graduate students). All PIs and some of the more junior staff have fulfilled responsibilities as members of thesis and 'habilitation' juries and several group leaders are active on the editorial boards of various specialised journals. The majority of PIs have been involved in organising international meetings. The 21 meetings and 12 programme committees include Cross-Disciplinary Genomics, an EMBO meeting concerning diatoms and two workshops attached to the AMS (American Society of Microbiology) annual meeting.

An additional indication of the attractiveness of this unit is the fact that it has received nine visiting faculty from foreign institutions in the past three years.

Members of the unit have received a number of national and international awards including 2 highly competitive ATIPE grants (designed to support young and promising group leaders) from the CNRS, 2 Human Frontier Science Programme (HSFP) grants and two academic prizes from the Ministry of Research and the Académie des Sciences.

Finally, different teams in the unit are involved in a variety of national and international networks. These include a European Marine Biological Resource center, two European Marie Curie training programmes, a project with the Riken Institute (Jp), a LABEX for scientific modeling and two French research networks. There are a number of collaborations with groups in the USA (IBM, USCD, Scripps, Sloan-Kettering, Rice University and the University of Minnesota) as well as within Europe (MPI Berlin, University College London and the universities of Freiburg, Cambridge, Nottingham, Turin and Vienna), Japan (Osaka, Tokyo, RIKEN Institute), Brazil and India, and at the national level.

They have been able to attract a relatively large number of postdoctoral fellows and graduate students at both the thesis and masters levels.

This activity has resulted in successful grant applications amounting to over 2 million euros since 2010 compared with institutional funding of about 530 thousand euros (including an initial attribution of 330 thousand euros) over this period.



Assessment of the unit's interaction with the social, economic and cultural environment

Overall, the unit has a good interaction with the social, economic and cultural environment although this depends clearly on the nature of the research carried out by each team. This includes seven general public lectures in areas such as the role of women in science. Several teams are involved in collaboration with small industrial partners (a computer software company in the framework of an ANR "blanc"; three companies in the framework of the diatom programme). A technology transfer policy should be implemented within the expanded IBPS.

Assessment of the unit's organisation and life

The isolation of the unit from the main campus and the saturation of available space are both concerns which impact on the life and organisation of the unit. These must be addressed urgently. At present the unit is small enough that communication is less problematic than it could be. There is a critical lack of space for meetings. There are no dedicated seminar rooms. Those which exist belong to the Medical Faculty and must be reserved.

Faculty, staff and students are all aware and appreciative of the international and interdisciplinary culture that the unit has developed. However, as the laboratory grows, it will be necessary to circulate information more formally through a 'Conseil de Laboratoire'.

It will be necessary to develop some policies to pool and coordinate informatics resources.

It is also essential to replace secretarial staff to provide continuity in logistical support.

Assessment of the unit's involvement in training through research

Members of the unit are deeply involved in training at all levels (both undergraduate and graduate). Eleven PhD, eleven second year and ten first year Masters students have been hosted and seven PhD students have successfully defended their work. The unit is also involved in two European Training Networks. They have hosted 35 research students in 3 years. Their responsibilities include the direction of the genetics syllabus and of various Masters programmes including "Systems Biology" and "Bioinformatics and Modelling" and Molecular and Cellular Biology (the last program was created and are coordinated by the unit director). Different members of the unit are providing courses which offer new directions in biology involving both theoretical and experimental approaches. This will set the scene for a future generation of biologists comfortable with the disciplines required for the expanding field of systems biology and the increasing impact of computational biology, mathematics and physics.

Assessment of the five-year plan and strategy

The major part of the project will be to continue to develop the themes already present in the unit. Central to the success of next five year plan, however, is the integration of the unit into new space on the main Jussieu campus. This is strongly supported by both UPMC and the CNRS but must be accomplished rapidly. Localisation on the main campus will permit the unit to integrate into the new Institut de Biologie Paris Seine (IBPS) which is being organised around five research units with interests in neuroscience, evolution and biodiversity, biological adaptation and aging and developmental biology. The infrastructure of this institute will also include an extensive group of technological platforms several of which are directly relevant to members of the unit.

It is proposed that the unit, at present called 'Genomics of Microorganisms', will expand its areas of interest to enable it to interact with the other departments. The proposed change in name to 'Computational and Quantitative Biology Unit' (CQBU) reflects this opening. Clearly the move will reinforce interactions with natural partners such as certain groups in the Evolution department.

It is also proposed to introduce new themes. In particular the arrival of a computational neurosciences group (at present attached to the largely experimental neurosciences department) could provide a link between the neurosciences and the CQBU. This expansion is challenging. Although it appears that some of the theoretical tools used by the computational neuroscience group are similar to those already in use by the theoretical groups in the CQBU, integration of this group will necessitate a particular effort on the part of this rather small unit presently specialised in genome analysis. Such a move would need to be closely monitored by the direction to assure the CQBU retains a thematic (theoretical) coherence and to prevent isolation of the potential new group. The recruitment of several as yet undefined additional groups is also envisaged over the period of the next mandate.



Other preoccupations which must be addressed are the creation of a rational pipeline for publicizing the computational tools developed by the unit. Support should be provided to create 'packaged' software and databases with improved user interfaces and WebPages with clear examples and instructions. Although this requires logistic support, it will facilitate their use by the general community with a consequent positive impact on the visibility of the unit.

Another concern will be to reinforce several of the smaller groups which are of less than optimal size at present.



4 • Team-by-team analysis

Team 1 : Analytical Genomics

Name of team leader: Ms Alessandra CARBONE

Workforce

Team workforce	Number as at 30/06/2012	Number as at 01/01/2014	2014-2018 Number of project producers
N1: Permanent professors and similar positions	2	3	3
N2: Permanent EPST or EPIC researchers and similar positions			
N3: Other permanent staff (without research duties)		1	
N4: Other professors (PREM, ECC, etc.)			
N5: Other EPST or EPIC researchers (DREM, Postdoctoral students, visitors, etc.)	1	2	2
N6: Other contractual staff (without research duties)			
TOTAL N1 to N6	3	6	5

Team workforce	Number as at 30/06/2012	Number as at 01/01/2014
Doctoral students	3	
Theses defended	3	
Postdoctoral students having spent at least 12 months in the unit	1	
Number of Research Supervisor Qualifications (HDR) taken		
Qualified research supervisors (with an HDR) or similar positions	1	1



• Detailed assessments

Assessment of scientific quality and outputs

The focus of the team is applications of mathematical and algorithmic methods in the study of genomes. The quality and quantity of articles is high and are generally published in good journals and using a large spectrum of mathematical tools. The PI has a good vision of interesting problems where mathematics and theoretical computer science can make a difference. The PI is very highly regarded among the mathematical and mathematical biology community. The team is involved in several projects centred on understanding the evolution of molecular structures in the cell. This includes a large project which attempts to investigate protein-protein interactions of more than 2000 human proteins and is one of only seven international projects which use the powerful World Community Grid. However, the principal activities of the team centre around evolution to include the development and use of methods for: analysis of codon bias and related three dimensional gene positioning; detection of miRNAs; reconstruction of ancestral genomes; detection of distantly related proteins; detection of functional sites and protein partners; detection of co-evolving residues in proteins; and development of statistical methods for transcriptome analysis from deep sequencing.

The team should be recommended for studying real biological problems in an honest way. In contrast to some current trends in the field of mathematical biology in which mathematics is the central driving force and possible biological applications appear secondary, this team actually starts with true biological questions and tries to answer them honestly.

The team has developed several pieces of software as tools in their analyses and has produced a number of good publications in specialised and reputable international scientific journals (NAR, PLoS ONE, PLoS Computational Biology). The PI has also received several prestigious national awards and prizes.

Assessment of the unit's academic reputation and appeal

Given the strength and number of publications and the importance of the methodology developed within the team, the group's work has not had as high an impact as might be hoped from the general use of their methods by other biologists. A possible reason for this is a limitation in the accessibility of these methods by the community at large. Although the published tools can be obtained by potential users, the work has not been currently implemented in practical platforms nor is there a unified web access to the computational resources developed by the team. This would certainly enhance the team's visibility.

However, the academic attractiveness of the team is also reflected in a number of national (LABEX, Research networks...) and international (Riken Institute, Japan) collaborations as well as in the number of invitations to national (14) and international (23) conferences, seminars and colloquia (14).

Assessment of the unit's interaction with the social, economic and cultural environment

The PI has been involved in public lecture programmes, for example, on "Women in Science" and other invited talks bringing mathematics and Information Science to more general audiences both in France and abroad.

Assessment of the unit's organisation and life

In view of its small size, assessment of co-ordination and organisation of the group is not relevant.

Assessment of the unit's involvement in training through research

As a professor at the University of Paris, the PI contributes significantly to teaching, mainly in mathematical modelling and bioinformatics. She has invested significant effort in creating an international level Master Program in Bioinformatics at UPMC and has successfully trained a number of PhD and Master students.



Assessment of the five-year plan and strategy

The research project is ambitious and addresses crucial challenges for the interpretation of genome data.

Conclusion

- Strengths and opportunities:

An important strength of the team is that it lies precisely at the intersection between several scientific disciplines for which everyone recognizes the need of inter-communication, namely mathematics, biology and computer science. The team leader has been very active in promoting effective inter-disciplinary interactions at all levels: within the team, in the structure of the unit, in teaching programs, and in collaborative research projects. There is a real opportunity for this team to bridge communities through training a new generation of biologists in the use of more mathematical tools and of mathematicians to understand more biology.

- Weaknesses and threats:

One weakness is the disparity between the scientific contributions of the team and its international recognition.

- Recommendations:

The "visibility" of the team could be greatly improved if tools and "advertising" were done effectively through the website. The development of a toolkit could also impact on enrolment in the Masters programme and provide the necessary skills for some students to go on to work in BioTech companies. Going forward, the integration of this team within a bigger 'biological sciences' infrastructure should have a positive effect on the scientific impact of the important scientific work done by this team. By educating and working with mainstream biologists the team should be able to have better access to the preoccupations in the biological community and participate in more of the conferences that biologists attend, thus increasing the overall impact of this very important work.

There needs to be more attention paid to pipelines. The area of analytic genomics moves very fast and using mainstream tools will enable the team to follow progress and build on other's progress as well as provide postdoctoral fellows for further collaboration in other cutting edge teams. For this to happen the PI needs to hire an engineer trained in the current packages and toolset, for instance R, Bioconductor, Cytoscape and Galaxy. Making the tools developed in the lab mesh with those from other teams will enhance the visibility. The team should also attend a few more mainstream biology meetings, (FEMS, ECV, SSB), these conferences would allow the team to distinguish which are the most important questions in the field being addressed and build more collaborations with the microbiologists, virologists who need their help.



Team 2 : Structure, Dynamics and Evolution of Genetic Networks

Name of team leader: Mr Frédéric DEVAUX

Workforce

Team workforce	Number as at 30/06/2012	Number as at 01/01/2014	2014-2018 Number of project producers
N1: Permanent professors and similar positions	2	2	2
N2: Permanent EPST or EPIC researchers and similar positions			
N3: Other permanent staff (without research duties)	1	1	
N4: Other professors (PREM, ECC, etc.)			
N5: Other EPST or EPIC researchers (DREM, Postdoctoral students, visitors, etc.)	1	1	1
N6: Other contractual staff (without research duties)			
TOTAL N1 to N6	4	4	3

Team workforce	Number as at 30/06/2012	Number as at 01/01/2014
Doctoral students		
Theses defended	1	
Postdoctoral students having spent at least 12 months in the unit		
Number of Research Supervisor Qualifications (HDR) taken		
Qualified research supervisors (with an HDR) or similar positions	1	1



• Detailed assessments

Assessment of scientific quality and outputs

The team was created in 2009, when the PI moved from his former position of leader of a technological platform at the Ecole Normale Supérieure. He has considerable expertise in the utilization of high-throughput technologies for characterizing transcriptional and post-transcriptional regulation at the genome level.

Current research projects are anchored on a long-term and fruitful collaboration with a colleague presently located in another research unit, and focuses on transcriptional regulation and post-transcriptional regulation of mitochondrial biogenesis in yeast and responses of these regulatory networks to chemical stress.

The team has a regular publication activity in good-quality journals of the field (including one co-authorship in PNAS in 2012). The PI generally appears as intermediate author, a position which can be understood in the context of his former position of platform leader, which stimulated participation in many collaborative projects. The current publication reflects a good capability of the team to establish and maintain collaborations with external teams. There is a current collaboration concerning *Candida* with a newly formed group in the Platforms and Technical Development Department of the future IBPS.

Assessment of the unit's academic reputation and appeal

The team has recruited a post-doctoral researcher and a junior faculty member ("Maître de conférences") since its formation. During that period, one PhD student successfully defended its thesis and a second was recruited. However, the team remains small..

Assessment of the unit's interaction with the social, economic and cultural environment

Interactions with social, economic and cultural environment are not of particular relevance to the activities of this team.

Assessment of the unit's organisation and life

NA

Assessment of the unit's involvement in training through research

Both permanent team members are heavily involved in teaching activities. The PI is director of the Genetics teaching programme and is responsible for a masters course in Evolutionary and Human Genetics. He also teaches a masters course in Functional Genomics and undergraduate courses in Biology and in Functional Genomics and Bioinformatics. The junior faculty member also undertakes a full teaching load.

Since 2010, the team has hosted 7 Master students and 4 students of technical schools (BTS, IUT) as well as numerous undergraduate research projects.

The strong involvement of the two permanent team members in teaching activities will certainly contribute to attracting PhD students in the future. This will probably be facilitated once the Unit will be installed on the teaching campus.

Assessment of the five-year plan and strategy

The group will extend their studies on *S.cerevisiae* to obtain information on single cell dynamic behaviour. They will then extend their studies on the dynamics and evolution of regulatory networks from the *S. cerevisiae* model to several additional yeast species. Yeast is at present a very attractive system since there are nearly 20 sequenced yeast genomes available. The research project is solid, anchored on the proved skills of the team members, and has a good feasibility. It is well-focused, and addresses precise biological questions, although not of exceptional originality.



Conclusion

- Strengths and opportunities:

The team has an excellent understanding of the analysis of the structure and dynamics of yeast stress regulatory networks with a constant cycling between experimental and computational analyses and prediction.

- Weaknesses and threats:

The team is very small at present. While it uses state-of-the art approaches, many of their studies have in the past been in collaboration with other groups. The team does not yet have a strong individual profile

- Recommendations:

The SWOT analysis should be enforced, in order to improve the identification of strengths and weaknesses. Efforts should be intensified in increasing the visibility of team-specific research activities. The team should make efforts to reinforce its activities by trying to attract junior research staff, postdoctoral fellows and PhD students.



Team 3 : Biology of Genomes

Name of team leader: Mr Gilles FISCHER

Workforce

Team workforce	Number as at 30/06/2012	Number as at 01/01/2014	2014-2018 Number of project producers
N1: Permanent professors and similar positions	1	1	1
N2: Permanent EPST or EPIC researchers and similar positions	1	1	1
N3: Other permanent staff (without research duties)	1	1	
N4: Other professors (PREM, ECC, etc.)			
N5: Other EPST or EPIC researchers (DREM, Postdoctoral students, visitors, etc.)	1	1	1
N6: Other contractual staff (without research duties)			
TOTAL N1 to N6	4	4	3

Team workforce	Number as at 30/06/2012	Number as at 01/01/2014
Doctoral students	2	
Theses defended		
Postdoctoral students having spent at least 12 months in the unit	2	
Number of Research Supervisor Qualifications (HDR) taken		
Qualified research supervisors (with an HDR) or similar positions	1	1



• Detailed assessments

Assessment of scientific quality and outputs

The Biology of Genomes (BG) group studies genome rearrangements on three different time scales (species, strains and populations) using an original yeast system. The reconstruction of ancestral yeast genomes required bioinformatics tools that were developed in collaboration with the Analytical Genomics team. Moreover the team was able to show the importance of structural genome variations within clonal yeast populations, a study which required careful statistical analysis undertaken in collaboration with the Genophysics team. They showed the importance of replication accidents in the formation of segmental chromosome duplications. The BG group also studies the relationships between mutation rates, nucleotide compositional skews and replication. In particular they were able to show that mutation rates (and GC%) correlate with replication timing and to measure mutation rate asymmetry between leading and lagging strands.

Together the BG team's efforts are well focussed on fundamental issues addressing genome stability and evolution. The BG team has demonstrated its interdisciplinary commitment with successful collaborations with the Analytical Genomics and Genophysics teams, very much in the trans-disciplinary spirit of the unit. The team publishes in the very best journals in genome science, such as PLoS Genet., Genome Res., Genome Biol. and Molec. Biol. Evol.

Assessment of the unit's academic reputation and appeal

The BG team was initiated with a highly competitive ATIP grant in 2010. The team coordinates a major ANR grant (2011-2014). It has good connections with the national and international yeast community.

Assessment of the unit's interaction with the social, economic and cultural environment

The BG team collaborates with the Isoft company for genomic data analyses in the framework of an ANR grant. In collaboration with other teams, the BG team has developed useful pieces of software such as CHRONicle and ULYSSE that should be distributed after publication.

Assessment of the unit's organisation and life

In view of its small size, assessment of co-ordination and organisation of the group is not relevant.

Assessment of the unit's involvement in training through research

The BG team is very strongly involved in teaching and in laboratory training. The team is in charge of a Master program on 'Genetics, Genomes and Evolution' for computer science students and of a Bachelor program on 'Initiation to algorithmics and programming' for biology students.

Assessment of the five-year plan and strategy

The BG group's plans are well focussed. The team will address genome evolution and stability from 4 different perspectives, well in-line with the team's expertise and in collaboration with the Analytical Genomics and Genophysics teams. Most promising are the characterization of structural genome variations in clonal populations and the mapping of QTLs that should reveal the genetic bases of genome stability. This might also bridge with the proposed comparative analysis of replication origins and timing. Together with the reconstruction of ancestral genome rearrangements, the BG group is thus in a position to contribute significantly, perhaps decisively, to our understanding of genome stability and evolution in yeast.



Conclusion

- Strengths and opportunities:

The BG team is well focussed and has the appropriate connections to efficiently exploit NGS data to study yeast genome stability and evolution. The team collaborates effectively with theoreticians in the laboratory and has made substantial contributions to understanding the organisation and behaviour of yeast genomes.

- Weaknesses and threats:

It is essential for the future careers of the group members involved, to publish the software packages which have been developed.

- Recommendations:

The BG team is encouraged to strengthen its connections with international laboratories in order to increase its visibility, for instance by building upon the contacts that were made for the Marie Curie training Network. The team is also encouraged to popularize its bioinformatics tools by making them readily available and advertising them in the community.



Team 4 : Dlatom Functional Genomics

Name of team leader: Mr Angela FALCIATORE

Workforce

Team workforce	Number as at 30/06/2012	Number as at 01/01/2014	2014-2018 Number of project producers
N1: Permanent professors and similar positions	2	3	3
N2: Permanent EPST or EPIC researchers and similar positions	1	1	1
N3: Other permanent staff (without research duties)	1	1	
N4: Other professors (PREM, ECC, etc.)			
N5: Other EPST or EPIC researchers (DREM, Postdoctoral students, visitors, etc.)	1	1	1
N6: Other contractual staff (without research duties)			
TOTAL N1 to N6	5	6	5

Team workforce	Number as at 30/06/2012	Number as at 01/01/2014
Doctoral students	1	
Theses defended	1	
Postdoctoral students having spent at least 12 months in the unit	2	
Number of Research Supervisor Qualifications (HDR) taken		
Qualified research supervisors (with an HDR) or similar positions		1



• Detailed assessments

Assessment of scientific quality and outputs

The team has been very active while establishing themselves within the research unit. Their work is focused on the characterization of diatoms, unicellular algae, that are very peculiar regarding their evolution, their cell biology as well as their biochemical difference in comparison to well-studied green algae and land plants. The team has established new molecular tools and approaches for diatom studies. For example, they have provided evidence that RNA interference can be used as a strategy for undertaking functional genomics of these organisms.

In addition to contributions to the annotation of two diatom genomes - and the development with one of the theoretical groups of the UMR of the tools to identify small RNA-based regulatory systems, the group also studies how diatoms harvest light and deal with light stress. In particular they are studying blue light receptors with both transcription regulatory and DNA repair activities and their involvement in circadian rhythms. They have also identified a novel phytochrome which is a red light sensor and are investigating the role of this in the cell cycle.

The work shows a clear and positive development, since the team only started as independent group on arriving in the UMR. This is reflected by recent publications. Although the number of publications in the last two years is reasonable, publication output could be improved. However, data presented during the assessment clearly showed a large potential for a number of publications in the near future. The recent integration of new lab members should also contribute to increasing output. The research performed in the team deals with establishing up to date molecular tools in a diatom model system, which is highly appreciated by the international scientific community. The scientific manuscripts have been published in highly visible scientific journals (PNAS, NAR, Plant Physiol, EMBO rep).

Assessment of the unit's academic reputation and appeal

The group is internationally well connected. Team members have been invited to a number of workshops and congresses and collaborates with several groups outside France. The team is not yet the lead partner in the current research initiatives - which is not surprising in view of its recent founding - but for instance the role as main organizer of a large workshop on diatoms 2013 in Paris indicates that the PI is able to take leading positions. The numbers of visiting international PostDocs demonstrates that the lab is highly attractive for foreign scientists. One factor limiting the attractiveness of the group is the limited space available for research. The number of computer work stations as well as culturing facilities for microalgae should be improved. The PI has also received prestigious prizes such as the "Prime d'Excellence scientifique" CNRS in 2011, an ATIP grant in 2009, an HSFP grant in 2009 and a CDA_HSFP grant in 2006. The list of visited meetings indicate that the group is strongly focused on algal genomes and light sensing in Microalgae.

Assessment of the unit's interaction with the social, economic and cultural environment

The scientific work of the team is highly original since, not only a number of tools have to be developed but the algae of interest present new cellular functions to be explored. This research which is performed, clearly is at the cutting edge of current algal research and highly visible in the scientific community. Due to the biotechnological issues involved it is also interesting for economic purposes. Especially the role of microalgae for future energy supply is a topic that is discussed in the society and is regularly in the public media. The team has several contacts with biotechnological companies and is involved in biotechnological research groups. One patent on bioflocculation of algae has already derived from these interactions.

Assessment of the unit's organisation and life

In view of its small size, assessment of co-ordination and organisation of the group is not relevant.



Assessment of the unit's involvement in training through research

Although the team moved just recently to UPMC, it is already strongly involved in teaching, including lectures for bachelor and master students as well as tutoring of master students, PhD students and PostDocs. Furthermore the team is involved in one International Training Network (ITN) funded by the European Union. At this early stage it can be expected that the attractiveness of the group for students and postdocs alike will increase in the future, although, again, this will require improvements to the local working conditions.

Assessment of the five-year plan and strategy

The team has demonstrated its ability to perform original as well as risk-taking research. Although the different approaches and aims apparently are synergistic within the team, in view of the limited size of the group the high number of individual projects including photoreceptors, clock networks, regulation of photosynthesis, micro RNAs, genome engineering, screening of algal strains, characterization of transcription factors as well as biotechnological approaches appears extremely ambitious and raises the question how a group of this size (even with active collaborators) will be able to perform this research in detail instead of rather scratching at the surface of a number of projects. Therefore, in the absence of additional research staff it would be advisable to focus initially on a limited number of topics and questions. This would increase the chances of generating important results of high impact that could be generated within a feasible time and published in high-ranking journals.

This for instance could be the photoreceptors or the characterization of the diatom clock. However, all projects described seem attractive and have produced interesting results and the choice will be difficult. There are some reservations concerning too much involvement in biomass/biofuel projects, because this is currently a "trendy" scientific area pursued by a number of highly competitive large groups and companies, making it difficult for a small team to keep pace. It will be important that the team is seen as an independent group with an original topic rather than being mostly collaborators of other international teams. This does not mean of course that the number of international collaborations should be reduced, but rather that the profile of the research group should be sharpened to demonstrate independence. According to the present composition of the group it should not be too difficult to perform the suggested optimization of research foci.

Conclusion

- Strengths and opportunities:

This is a highly visible group, performing original interesting research with a strong potential for future findings, connections to biotechnological approaches.

- Weaknesses and threats:

Number of independent publication should rise in the near future, currently a clear focus on a feasible limited number of projects is missing. There is no clear strategy indicated about main and side projects. Biotechnology of diatoms may be a promising but also highly competitive field, where smaller groups like this unit may have difficulties to keep pace with larger groups.

- Recommendations:

It is recommended that the group focus its research activities and build in the areas in which its members have a budding reputation. In some sense this is an effort of consolidation.



Team 5 : Genomic physics

Name of team leader: Mr Marco Cosentino LAGOMARSINO

Workforce

Team workforce	Number as at 30/06/2012	Number as at 01/01/2014	2014-2018 Number of project producers
N1: Permanent professors and similar positions			
N2: Permanent EPST or EPIC researchers and similar positions	1	1	1
N3: Other permanent staff (without research duties)			
N4: Other professors (PREM, ECC, etc.)			
N5: Other EPST or EPIC researchers (DREM, Postdoctoral students, visitors, etc.)	2	0	1
N6: Other contractual staff (without research duties)			
TOTAL N1 to N6	3	1	2

Team workforce	Number as at 30/06/2012	Number as at 01/01/2014
Doctoral students	1	
Theses defended		
Postdoctoral students having spent at least 12 months in the unit	2	
Number of Research Supervisor Qualifications (HDR) taken		
Qualified research supervisors (with an HDR) or similar positions	1	1



• Detailed assessments

Assessment of scientific quality and outputs

The group works on physical modelling in quantitative biology with a focus on microorganisms. Different topics are studied such as genome organization and evolution, the biophysics of *E. coli* and the physical principles of swimming at microscopic scales. The team employs a variety of methods from statistical mechanics, bioinformatics and hydrodynamics and works in international collaborations with experimental groups, particularly on single cell experiments. Areas of interest include the use of statistical mechanics to describe the topology of regulatory networks, modeling population evolution by large-scale genome rearrangements and the development of new modeling approaches to understand the biophysics of the bacterial nucleoid as a complex polymer with a goal of understanding the dependency of gene expression on nucleoid conformation.

The output is original and the work bridging approaches from statistical physics and bioinformatics. The team has an excellent and abundant publication record, including several in high impact journals (Phys Rev Lett, Phys Rev E Stat Nonlin Soft Matter Phys, Nucleic Acids Res. Genome Biol Evol.). A website offering tools for genomic analysis is available to the scientific community.

Assessment of the unit's academic reputation and appeal

The team is building an international reputation with excellent worldwide connections in biology, bioinformatics and physics. It has been supported by the Human Frontier Science Program (HFSP) on the study of the bacterium nucleoid. The team has also been very active in organizing international workshops.

Assessment of the unit's interaction with the social, economic and cultural environment

NA

Assessment of the unit's organisation and life

In view of its small size, assessment of co-ordination and organisation of the group is not relevant.

Assessment of the unit's involvement in training through research

The team is involved in teaching at the University of Paris and abroad, mainly in mathematical-physics modelling of biological systems. The team is involved in training a number of Master and PhD students in quantitative and computational biology.

Assessment of the five-year plan and strategy

The team is young and the future research themes are adapted to the environment of the future unit of "Computation and Quantitative Biology" within the "Institute of Biology Paris-Seine". The team aims to continue developing its current nucleoid project and the study of large-scale rearrangements in genome evolution, using methods from statistical physics, bioinformatics and in close collaboration with experimental teams. In doing so, the team is in the process of growing in number for non-permanent and permanent positions. This is a growing and important area of research.



Conclusion

- Strengths and opportunities:

The team has excellent ongoing international collaborations with groups in France and abroad. In perspective, these collaborations will be very useful for future recruitments of permanent and non-permanent members. The team is actively involved in promoting interdisciplinary research via teaching, training for research activity and organizing schools and conferences.

- Weaknesses and threats:

Despite the team's excellent publication record, there is a risk that the large number of different topics may weaken the team's impact in the future. Indeed, the team currently counts only one permanent member while it will be facing strong international competition. The team also needs access to students from different training programs such as statistical physics, biological physics and computer science (bioinformatics). While the latter category can be easily recruited due to the Laboratory's involvement in the "Bioinformatics and Modeling" master program, the former category might require more involvement of the team in local master programs for mathematical and physical approaches of biology and complex systems.

- Recommendations:

The team is young and needs to be reinforced with permanent positions and to establish a stronger connection with local master programs in order to attract students from physics and mathematics that are acquainted with bioinformatics and biology. A Maitre de Conférence position would be ideal in this respect.

In conclusion, to improve the impact of the team, it is recommended: 1) to avoid the risk of potential thematic dispersion, especially in this early phase of team growth; 2) to hire permanent personnel with expertise in biological physics and knowledge of bioinformatics tools and language; 3) to explore opportunities for local teaching and training of students in mathematics and physics applied to genomics and quantitative biology.



Team 6 : Statistical Genomics and Biological Physics

Name of team leader: Mr Martin WEIGT

Workforce

Team workforce	Number as at 30/06/2012	Number as at 01/01/2014	2014-2018 Number of project producers
N1: Permanent professors and similar positions	1	1	1
N2: Permanent EPST or EPIC researchers and similar positions			
N3: Other permanent staff (without research duties)			
N4: Other professors (PREM, ECC, etc.)			
N5: Other EPST or EPIC researchers (DREM, Postdoctoral students, visitors, etc.)		1	1
N6: Other contractual staff (without research duties)			
TOTAL N1 to N6	1	2	2

Team workforce	Number as at 30/06/2012	Number as at 01/01/2014
Doctoral students	1	
Theses defended		
Postdoctoral students having spent at least 12 months in the unit		
Number of Research Supervisor Qualifications (HDR) taken		
Qualified research supervisors (with an HDR) or similar positions	1	1



- Detailed assessments

Assessment of scientific quality and outputs

The focus of the group is statistical inference in computational biology, bioinformatics and structural biochemistry. In particular, the PI has worked on the development of statistical mechanics methods for inference in biology complexity. The work has been published in international journals of good impact for the scientific community, mostly in biological and physical sciences (PNAS- 5 in the last 5 years, Phys Rev E Stat Nonlin Soft Matter Phys., Nucleic Acid Research, Plos one).

Assessment of the unit's academic reputation and appeal

The team PI has an international reputation as a physicist with good connections to applications in biology and bioinformatics. The team has been formed very recently and it is just now in the process of growing in size.

Assessment of the unit's interaction with the social, economic and cultural environment

NA

Assessment of the unit's organisation and life

In view of its small size, assessment of co-ordination and organisation of the group is not relevant.

Assessment of the unit's involvement in training through research

There is a high investment of the PI in teaching as a professor at the University of Paris, mainly in mathematical modelling and bioinformatics. The team is involved in training through research by recruiting some new non-permanent members such as Master and PhD students.

Assessment of the five-year plan and strategy

The team is very young and its future themes are naturally adapted to the environment of the future unit of "Computation and Quantitative Biology" within the "Institute of Biology Paris-Seine".

The team aims at developing topics inherent to statistical inference, reverse engineering and combinatorial optimization at the interface between statistical physics, computational biology and bioinformatics. The team PI expects to develop parallel research lines on theoretical and more applied topics and in particular stronger collaborations with experimental groups. In doing so the team is in the process of growing in number for non-permanent and permanent positions.



Conclusion

- Strengths and opportunities:

The team PI has strong international collaborations with first rate bio-physics groups. To date, an effort has been made to make Matlab code publicly available to popularize implementation.

The PI participates actively in the teaching component of the Masters at University Pierre and Marie Curie and has an important opportunity to collaborate with bioinformatics and experimental teams within the same research unit, but also outside. In perspective, the PI good collaborations can be very useful to develop the team for future recruitments of permanent and non-permanent members.

- Weaknesses and threats:

Due also to its recent formation, the team has not yet really exploited opportunities for PhD training, in particular in statistical genomics. This is one of the areas where students very easily find jobs and postdoctoral fellowships if they are trained to analyze big data effectively. It is important to stress the big data component in modern statistics and provide students with the tools that enable them to see the link to real world situations, even further than biology. Moreover, the team has not yet established a clear pipeline with statisticians (especially on research ground), fact that could weaken its scientific impact in perspective.

- Recommendations:

The focus of the group is mainly statistical inference, so it would improve the visibility of the group to compare the methods developed with existing methods published in statistical journals. It would be important to enhance future impact to create bridges with the statistical language of exponential families and Exponential Random Graph Models (ERGM) through collaboration with teams such as those at INRA or in Oxford who specialize in such techniques.

This process would be even more effective, given the lively job market in Statistics, if the team could train students also in data mining and practical statistics. To this effect, it would be beneficial to hire an assistant professor, possibly, with expertise in big data science, applied machine learning and related methods. This would ensure the success of this team with a statistical focus in providing much needed trainees.

In conclusion, to improve the impact of the team, it is recommended to invest energy in: 1) learning the vocabulary and buzzwords of modern statistics to create bridges to well established pipelines of statisticians; 2) publishing in machine learning and statistics journals by collaborating with bioinformaticians and statisticians; 3) hiring permanent personnel with expertise in big data science and related methods; 4) exploring opportunities for local teaching and training of students in mathematics, physics and statistics applied to genomics and quantitative biology.



Team 7 : Computational Neuroscience Group (CNG)

Name of team leader: Mr Angelo ARLEO

Workforce

Team workforce	Number as at 30/06/2012	Number as at 01/01/2014	2014-2018 Number of project producers
N1: Permanent professors and similar positions			1
N2: Permanent EPST or EPIC researchers and similar positions	2	2	2
N3: Other permanent staff (without research duties)			
N4: Other professors (PREM, ECC, etc.)			
N5: Other EPST or EPIC researchers (DREM, Postdoctoral students, visitors, etc.)	2	1	2
N6: Other contractual staff (without research duties)			
TOTAL N1 to N6	4	3	5

Team workforce	Number as at 30/06/2012	Number as at 01/01/2014
Doctoral students	5	
Theses defended	3	
Postdoctoral students having spent at least 12 months in the unit	1	
Number of Research Supervisor Qualifications (HDR) taken		
Qualified research supervisors (with an HDR) or similar positions	1	1



• Detailed assessments

Assessment of scientific quality and outputs

The scientific production is of high quality with articles published in highly ranked journals (such as Neural Computation and PLoS Comput Biol). Their impact (in terms of citations) is also significant. Within the neuroscience field there are a number of joint publications with experimentalist groups. Although the team is still rather small, the recent arrival of another permanent researcher may lead to an even more active and sustainable scientific activity. Other researchers in the team, including Masters and PhD students and post-doc researchers also contribute significantly to this output.

The external collaboration network is very significant at national and international level. The team has been involved in different international research initiatives (2 EU research grants) and is very active in international collaborations (roughly 20 collaborations with other groups even sharing PhD students). It is worth indicating how the group has established collaborations with both theoretical driven groups and also with experimentalist groups. It should be noted that these are almost entirely with groups outside the Jussieu site. Many of these collaborations are supported by joint publications and shared projects. This intensive exchange dynamic is very fruitful and allows the young members of the group to easily access other collaborating labs for complementing their training or even for continuing their research career. The group is exploring a number of topics that are related but allow different synergies with different experimental groups (mainly neurophysiological labs). This also validates the expertise of the group in actively collaborating with neurophysiological and neuroscience groups and should be an excellent starting point for initiating collaborations with the largely experimentalist Neuroscience Unit which will be also integrated in the Institut de Biologie Paris Seine (IBPS).

Assessment of the unit's academic reputation and appeal

The reputation of the group at the academic level is good. The PI has maintained teaching activities in Italy, coordinates a Master Technical Module at university Pierre and Marie Curie and teaches at Master and Bachelor levels.

Though rather young, the team has already been involved in several international and national projects raising significant research funds (roughly 800 Keuros).

It participates in numerous collaborative networks (>10 international collaborations). 17 invited talks to international conferences /institutions.

Assessment of the unit's interaction with the social, economic and cultural environment

Collaborations with both local and national industrial partners have been established. The team is applying for specific industrial driven initiatives including two main industrial companies. The team makes also efforts towards exploiting (with industrial partners) their results and models developed in the framework of more general basic science. Thus, these industry collaboration activities can be seen as part of a more global exploitation plan, beyond the basic science which is the main focus of the group. This may have an impact on the social, economical and cultural environment. The team is also active in the organization of international science events that may also have an impact in their environment.

Assessment of the unit's organisation and life

The group is too small for this to be relevant.



Assessment of the unit's involvement in training through research

The team is involved in training (masters and PhD students). This involvement is significant for a group with a dominant CNRS profile of members. The interest of the team for training is noteworthy as the permanent CNRS researchers are involved in several masters at UPMC with a significant number of lectures.

They are deeply involved in teaching and supervising students and young researchers (2 pots-docs, 8 Phd Students, 13 master students and engineer trainees).

The team members who have developed scientifically within the framework of the team have gained expertise in interdisciplinary approaches which include both experimentalists and theorists. This natural environment enhances interdisciplinary capabilities seldom acquired in the majority of research centers and institutions where approaches are less transversal.

Assessment of the five-year plan and strategy

The team is addressing three relevant targets focusing on: further development of the peripheral processing and impact of aging on temporal coding, spatio-temporal coding of behavioural adaptation and neural coding of contextual representations. The team has a comprehensive command of the required methods and the appropriate collaborations.

The five-year plan and strategy pursues feasible but ambitious scientific goals, strongly supported and enriched by an international collaboration network. The project is based on previous expertise and developments in this field undertaken by the research group and collaborators. This makes the plan feasible and also worthwhile for consolidating different collaborations with other relevant international groups.

Conclusion

- Strengths and opportunities:

One of the main strengths of the team is its natural interaction between experimental and theoretical researchers and its national and international collaboration network. This has even led to sharing students with relevant researchers in different countries (in particular to reinforce the experimental aspects of the work). The group has established strong interdisciplinary collaborations with different researchers, which have resulted in shared scientific production and joint participation in international initiatives (EU grants).

The group will be integrated in the Unit of Computational and Quantitative Biology in the framework of a larger institution (the newly created Institut of Biologie Paris Seine, IBPS). Though this integration is seen as a challenge in itself, if driven properly, it certainly represents an opportunity for the group to collaborate with other researchers in an interdisciplinary environment (stretching beyond computational neuroscience). With this integration, the group will also have access to a number of platforms, equipment and specialized technical personnel which will also be integrated in this new IBPS.

Finally, another opportunity is the potential of the team for collaboration with industry, since the topics of the team may allow commercial exploitation actions.

- Weaknesses and threats:

The main weakness may be the fact that this would be the only computational neuroscience group in the Unit which is at present composed of groups concerned with problems in genomics and bioinformatics. This may be seen as a threat of becoming isolated within the Unit, an outcome which could be overcome if the unit integrates new groups of computational neuroscience specialists or can attract groups from other disciplines in its new wider scope of Computational and Quantitative Biology Unit. An additional concern is the current lack of collaborations within the neurobiology unit which will be a component of the future IBPS. Such collaborations are not explicit in the current documentation (which is related to the new unit and not to the former neurobiology unit).



- Recommendations:

Clearly, if this group is integrated into the CQB, a significant effort must be made to integrate the discipline. Perhaps there will be room for exploring the possibility of joint research actions to bridge the research of the Unit to the Neuroscience Unit, in the framework of Institute IBPS.

The integration of the computational neuroscience group into the Computational and Quantitative Biology Unit is seen as a challenge. Thus it needs to be driven carefully and the group should take great care in monitoring the integration process.



5 • Conduct of the visit

Visit dates:

Start: February 6th 2013 at 8:30 AM

End: February 7th 2013 at 1:30 PM

Visit site(s):

Institution: Les Cordeliers

Address: Campus des Cordeliers 15, rue de l'école de médecine 75006 Paris

Conduct or programme of visit:

Lundi 5 février : Dîner de rencontre du comité

Mercredi 6 Février

8h30 -9h00 Huis clos - Présentation de l'AERES au comité par le Délégué

9h00 -9h15 Devant l'unité, présentation du Comité de visite et Présentation de l'AERES par le Délégué

9h15-10h Présentation de l'unité, bilan et projet

AUDITION DES EQUIPES

(y compris la moitié du temps pour la discussion, et 5 mn en tête à tête avec le chef d'équipe, si demandé par le président ou les chefs d'équipe)

10h-10h45 Bilan et projet équipe Frédéric DEVAUX

10h45-11h Pause

11h-11h45 Bilan et projet équipe Angela FALCIATORE

11h45-12h30 Bilan et projet équipe Gilles FISCHER

12h45-14h Déjeuner de travail et rencontre avec les tutelles

14h-14h45 Bilan et projet équipe Angelo ARLEO

14h45-15h30 Bilan et projet équipe Alessandra CARBONE

15h30-16h : Pause

16h-16h45 Bilan et projet équipe Marco COSENTINO-LAGOMARSINO

16h45-17h30 Bilan et projet équipe Martin WEIGT

17h30-20h Réunion à huis clos du comité

20h30 : Dîner comité



Jeudi 7 Février

SESSION RENCONTRE AVEC LE PERSONNEL PERMANENT ET NON PERMANENT

Le comité se répartit en trois sous-groupes

- 9h-10h **Rencontre avec les ITA titulaires , CDD**
Auditoire : membres du Comité, Délégué AERES, sans les Tutelles, ni la Direction
- Rencontre avec les doctorants et post-doctorants et/ou CDD « chercheurs », Ingénieurs**
Auditoire : membres du Comité, Délégué AERES, sans les Tutelles, ni la Direction
- Rencontre avec les chercheurs et enseignants chercheurs titulaires**
Auditoire : membres du Comité, Délégué AERES, sans les Tutelles, ni la Direction, ni les responsables d'Equipes
- 10h-11h **Rencontre avec la direction de l'unité**
Auditoire : membres du Comité, Délégué AERES
- 11h-13h **Réunion du comité à huis clos**
Présence : membres du Comité, délégué AERES



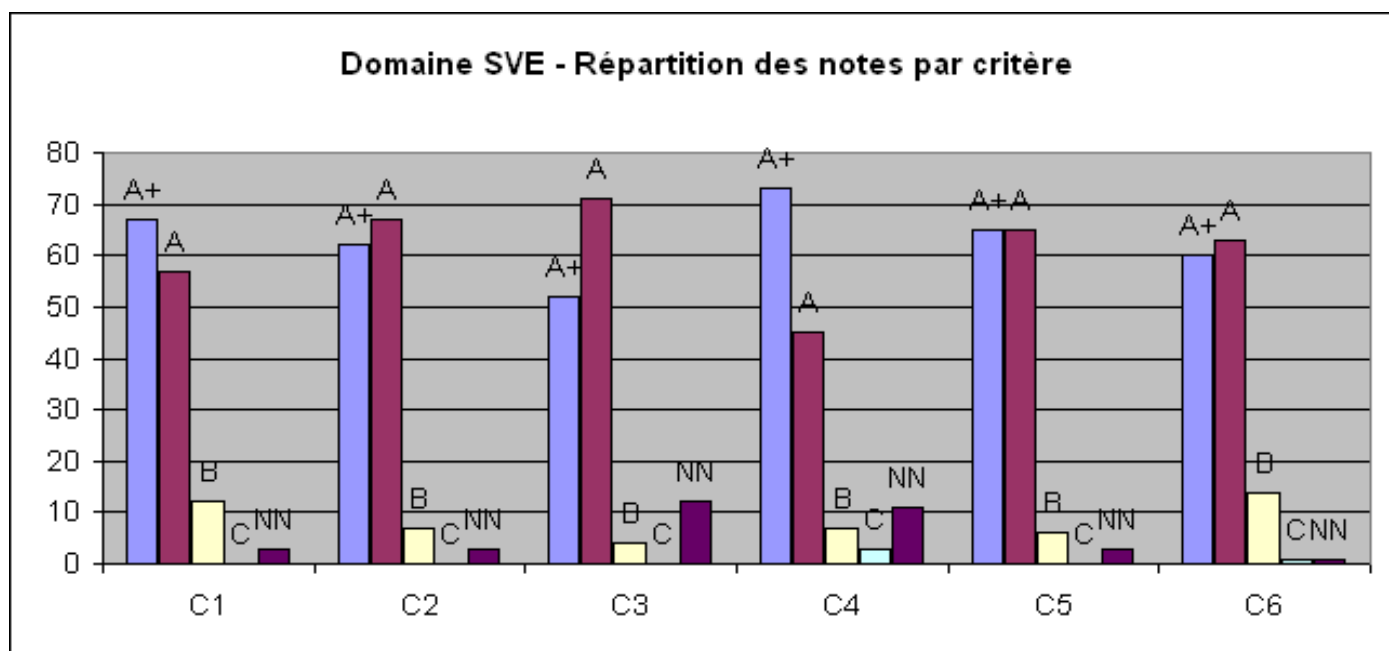
6 • Statistics by field: SVE au 10/06/2013

Notes

Critères	C1 Qualité scientifique et production	C2 Rayonnement et attractivité académiques	C3 Relations avec l'environnement social, économique et culturel	C4 Organisation et vie de l'entité	C5 Implication dans la formation par la recherche	C6 Stratégie et projet à cinq ans
A+	67	62	52	73	65	60
A	57	67	71	45	65	63
B	12	7	4	7	6	14
C	0	0	0	3	0	1
Non Noté	3	3	12	11	3	1

Pourcentages

Critères	C1 Qualité scientifique et production	C2 Rayonnement et attractivité académiques	C3 Relations avec l'environnement social, économique et culturel	C4 Organisation et vie de l'entité	C5 Implication dans la formation par la recherche	C6 Stratégie et projet à cinq ans
A+	48%	45%	37%	53%	47%	43%
A	41%	48%	51%	32%	47%	45%
B	9%	5%	3%	5%	4%	10%
C	0%	0%	0%	2%	0%	1%
Non Noté	2%	2%	9%	8%	2%	1%





7 • Supervising bodies' general comments

Paris le 17 04 2013

Le Président
Didier Houssin
Agence d'évaluation de la recherche
et de l'enseignement supérieur
20 rue Vivienne - 75002 PARIS

M. le Président,

Nous avons pris connaissance avec le plus grand intérêt de votre rapport concernant le projet du Laboratoire de Biologie computationnelle et quantitative, porté par Mme. Carbone. Nous tenons à remercier l'AERES et le comité pour l'efficacité et la qualité du travail d'analyse qui a été conduit.

Ce rapport a été transmis à la directrice du laboratoire qui nous a fait part en retour de ses commentaires que vous trouverez ci-joint. Nous espérons que ces informations vous permettront de bien finaliser l'évaluation du laboratoire.

Restant à votre disposition pour de plus amples informations, je vous prie de croire, M. le Président, à l'expression de mes salutations respectueuses.

Le Vice -Président Recherche et Innovation

Paul Indelicato



Answer of the Laboratory “Computational and Quantitative Biology”

by Alessandra Carbone

We thank the committee for all the work done and wish to state here that all members of the laboratory highly appreciated the sensibility of the committee towards our multidisciplinary laboratory, its aims, results and efforts in realizing it. There are two main points that we want to reply to :

1. the opening of the new scientific direction of computational neuroscience in the laboratory.
2. the report on Martin Weigt’s team.

1. On the future integration of the Computational Neuroscience Group in CQB

The CQB laboratory will open up new research directions in the next few years. One main aim is to create scientific exchanges and collaborations with other laboratories at IBPS. In particular, CQB will enlarge its scientific scope by encompassing and developing the computational neuroscience axis. The team by Angelo Arleo will be integrated in CQB starting from January 2014 and will be instrumental to bridge the (otherwise unlikely) interaction between CQB and both the Neuroscience unit and the Adaptive Biology and Aging unit.

The committee, even if supportive about the integration of the Computational Neuroscience group, appears concerned with the risk of isolation of the team within CQB. As stated during the visit and in the documents, we would like to underlie that CQB’s policy during the next period will aim at attracting other computational neuroscience groups. Notably, a Professor position is currently open at the Faculty of Life Sciences of UPMC (N. PR 46.3) and one of the candidates wishes to join (if selected) the CQB unit to lead a 2nd team in theoretical neuroscience.

Also, the integration of this Computational Neuroscience team in the lab is grounded on common methodological approaches (e.g. biophysics and biostatistics) shared with several theoretical groups in the unit. Martin Weigt, for instance, has expertise and is interested in the statistical models of network dynamics and in the information theoretical tools developed by the Computational Neuroscience team. As a consequence, he will be exchanging, and possibly collaborating, with Angelo Arleo’s team.

Concerning the interaction of the Computational Neuroscience team with the Neuroscience laboratory (P5: *“Its interaction with the present neuroscience unit is not obvious.”*), we wish to highlight two facts:

- During the period 2007-2013, the team shared 5 journal papers (plus 1 in preparation), 2 peer-reviewed proceeding papers, 1 software license, and 4 conference abstracts with members of the former and future neurobiology unit.
- During the period 2007-2013, the team was involved in 1 ANR and 1 UPMC-funded project with teams of the former and future neurobiology unit.

This information (concerning publications and projects) was both reported in the Scientific Report of the team and mentioned during the oral presentation. Details on the shared publications and collaborative projects with the neuroscience unit can be found in the section “Answer of the Team “Computational Neuroscience”” of this document.

2. On the recent integration of the team by M.Weigt in CQB

We believe the **scientific quality and the output of Martin Weigt’s team** have not been appreciated enough in the report. For this, we would like to report facts that can help to evaluate properly the team and understand correctly the comments reported in the AERES document.

The focus of this new team (established Sept. 2011) is in statistical inference in computational biology, bioinformatics and structural biology, the works are based methodologically on the background of the PI in theoretical statistical physics, but they are driven by biological questions. Results have been published in high-impact journals (e.g. PNAS - 5 in the last 5 years, Phys Rev E, PLoS One, Bioinformatics, BMC Bioinformatics, J Stat Mech...).

The central focus of the PI over the last years has been the detection of residue coevolution in proteins. In particular a global statistical inference method, called direct-coupling analysis, has been proposed, which infers residue contacts from sequence and guides 3D protein structure prediction. This work has reached very high visibility in the scientific community (Weigt et al. PNAS 2009 - 140 citations on google scholar, Schug et al. PNAS 2009 - 27 citations, Morcos et al PNAS 2011 - 32 citations, selected Faculty of 1000), the web site

dca.upmc.fr makes source code publicly available.

For what it concerns the assessment of the team's academic reputation and appeal, we want to highlight that the PI has an international reputation as a physicist with good connections to applications in biology and bioinformatics. He has excellent international connections with collaborations in physics, bioinformatics and biology, and a good record of invitations to international conferences / institutions. The team has been formed very recently and it is just now in the process of growing in size.

Answer of the Team “Analytical Genomics” by Alessandra Carbone

We thank the committee for the work done. We completely agree with the committee that the visibility of the software developed by the team is insufficient and should be increased. We are aware of it and, as mentioned by the committee, the solution asks for the opening of an engineer position that can appropriately valorize the work done.

In this respect, we believe that the sentence highlighted as a unique weakness of the team:

“One weakness is the disparity between the scientific contributions of the team and its international recognition”

is pertinent. Indeed we should work on promoting our software and data further in the community of biologists, as suggested in the recommendations. The committee highlighted on the one hand the quality and the importance of the work realized by the team by referring to it as a “very important scientific work”, and on the other hand the international recognition, testified by the numerous international invitations to meetings at the interface of mathematics, computer science and, at some extent, physics with biology. **What appears to be missing is a strong impact within the community of biologists at the international level.** In France, this impact is witnessed by several invitations to give talks in biology laboratories and conferences, and by the projects that have been developed in the past and are run right now.

Details on the production of the team have been indirectly pointed out in the general document praising the work done within the laboratory, but missed in the team evaluation. These values, for the period 2007-2012 are:

- 20 original research articles - in multidisciplinary (Molecular System Biology-Nature/EMBO, PLoS ONE, Nucleic Acids Research), computational biology (PLoS Computational Biology, Bioinformatics, BMC Bioinformatics), microbiology (Journal of Clinical Microbiology), and computer science (Theoretical Computer Science, Journal of Logic and Computation) journals. Two more invited publications appeared in Springer books at the interface of computer science with biology.
- 2 edited books;
- 8 software packages have been produced and published, and 3 more are under publication process;
- 23 invitations in international meetings at several interfaces: mathematics-biology, computer science-biology, physics-biology; 14 invitations in national meeting; 14 invitations to seminars and colloquia.
- the PI has been program committee member of 17 international meetings and organized 5 international meetings and 1 summer school.

Answer of the Team “Structure, Dynamics and Evolution of Genetic Networks” by Frédéric Devaux

A number of incorrect and important facts need to be amended.

“The team was created in 2009, when the PI moved from his former position of leader of a technological platform at the Ecole Normale Supérieure.”

This is a surprising and wrong statement. The PI stopped participating to the management of the ENS platform at the end of 2004 to develop his own research projects... 8 years ago! There was no ambiguity on this point in the documents provided to the committee.

“The PI generally appears as intermediate author, a position which can be understood in the context of his former position of Platform leader, which stimulated participation in many collaborative projects.”

This statement is not in accordance with the publication records provided to the committee. Since 2008, 12 publications out of 16 directly arose from the specific projects of the PI (6 articles since 2010). The PI was the first, last or co-last author of 8 of these 12 publications (3 since 2010).

“many of their studies have in the past been in collaboration with other groups. The team does not yet have a strong individual profile”

This is a very ambiguous statement that suggests that our publication record on our own projects is poor. Again, the PI published 8 articles as main investigator (1 as first, 4 as last and 3 as co-last author) since 2008 (3 publications since 2010). So, what does a “strong individual profile” mean?

Answer of the Team “Diatoms Genomics” by Angela Falciatore

Despite a few errors in describing the recent team composition, the team leader appreciates and validates the conclusions and suggestions of the AERES committee.

She most particularly appreciates the evaluation on the quality and originality of her current projects and on the important efforts invested for installing a new diatom team in the Research Unit. A. Falciatore also acknowledges that publication record in the last two years is only "reasonable" but will be improved by a series of manuscripts in preparation. This delay originates from the intense activity for building the team and seeking additional funding that were necessary to initiate the team activity in the context of a new laboratory, and also from the decision to initiate novel research axes aimed at integrating her scientific questions with the objectives of the Quantitative Biology unit. She fully agrees with the suggestion that, considering the actual size of team and the limited lab space available, clear priorities need to be established in order to finalize several projects. In spite of an apparent lack of focus, **all current projects are strongly interconnected and positioned within a central theme, the diatom light response adaptative strategies**, and have the potentiality of generating resources and data that can fuel each other within the team. Novel financial support from national and international grants will be used for recruiting two PhDs and one additional post-doc in 2013, possibly even before the move to a new building. Finally, the group leader would like to clarify that she associated her activity with two research projects with biotechnological purposes with the clear intention to improve genetic engineering tools in diatoms. The planned activity in the context of these project provides molecular foundation for industrial applications (exploited by other partners in the networks) and strongly support her own scientific questions through the development of novel genetic resources, thereby providing a significant contribution in the establishment of diatoms as novel molecular model species. On a longer term, further development of these genetic resources will necessitate the recruitment of a permanent staff member, which has recently been requested to both the CNRS and the UPMC, as well as the centralization of the mutated diatom strains in *ad hoc* genetic stock centers within the frame of the European Molecular Biology Marine Biological Resource Center (EMBRC) project.

Answer of the Team “Genomic Physics” by Marco Cosentino-Lagomarsino

1) Statements on the research themes of the group are not very clear / focused. I refer to page 5 "the dynamics of the microbial genomes...", and to the first paragraph of page 23.

We would like to clarify that the team works on the organization of microbial genomes, on quantitative aspects of bacterial physiology, and on low Reynolds-number swimming and synchronization

2) The list of journals seems incomplete: we would like it to be clear that the output is interdisciplinary and includes physics (e.g. prl, pre, ropp, soft matter), bioinformatics (e.g. bioinformatics, molecular biosystems) and (systems/evolutionary) biology (NAR, genome biology, GBE, BMC systems biology) and also one interdisciplinary journal (PNAS).

3) The point on the potential thematic dispersion of the genomic physics group is well taken, but we would like it to be clear that there is a priority in establishing a reputation in the next five years, in the community that works on the quantitative laws of bacterial genomics and physiology.

Answer of the Team “Statistical Genomics and Biological Physics” by Martin Weigt

A number of incorrect / incomplete statements in the assessment of the group has been listed in the general answer of the Unit, and is not replicated here. Here we mainly discuss a number of unclear issues in the evaluation of the team's work. The review lists mainly two weaknesses of the team, whereas the main strength and scientific achievements of the team (and its PI shortly before the creation of the team) are hardly recognized:

"...the team has not yet really exploited opportunities for PhD training, in particular in statistical genomics..."

It has to be mentioned, that the team was created in Sept. 2011 with the recruitment of the PI as a professor at the UPMC. In this time, the PI has been heavily involved in the master program in Bioinformatics and Modeling in particular with statistics-related courses (Statistical sequence analysis, Population genetics), and has supervised two Master theses (one M2 thesis, the candidate is currently IE (CDD) at INRA, one M1 currently ongoing), and a PhD student started in Sept. 2012. A new PhD student is expected to start in Sept. 2013.

"Moreover, the team has not yet established a clear pipeline with statisticians (especially on research ground), fact that could weaken its scientific impact in perspective."

It has to be mentioned that the team PI is a statistical physicist by training, working on problems in computational biology; he is not a statistician. In consequence an elevated number of international collaborations with world-wide recognized groups in statistical and biological physics, in bioinformatics and in experimental biology have been established (University of California at San Diego, US; The Scripps Research Institute La Jolla, US; Rice University Houston, US; Human Genetics Foundation, Turin, Italy; Karlsruhe Institute for Technology, Germany; Ecole Normale Supérieure, Paris, France; Memorial Sloan-Kettering Cancer Center, New York, US; Harvard Medical School Boston, US). The team PI has, in the evaluated period 2007-12, published 19 original research articles - in multidisciplinary (PNAS, PLoS ONE), physics (Phys Rev E, Europhysics Letters, J Stat Mech) and bioinformatics journals (Bioinformatics, BMC Bioinformatics) - and a number of proceedings and book chapters, many of them as first or last author. He has been invited as a speaker in 31 international conferences or institutions. The five most cited papers during this period are (source Google scholar)

- Weigt et al. PNAS 2009 - 140 citations
- Leone et al. Bioinformatics 2007 - 65 citations
- Morcos et al. PNAS 2011 - 32 citations, selected by Faculty of 1000
- Schug et al. PNAS 2009 - 27 citations
- Bailly-Bechet et al. BMC Bioinformatics 2010 - 15 citations

These numbers, which are steadily growing in time, show the good impact of the team in computational biology research. Seen the multi-disciplinary effort in the team's research work, it is not clear at all, how the publication in mono-disciplinary statistics journals (instead of e.g. PNAS, PLoS) - as recommended in the report - could improve the impact of the team, in particular how they could reach a biology audience as is the aim of the team.

We recognize the concern of the reviewer concerning the development of a common language for interdisciplinary research, and a number of joint research papers with colleagues from other disciplines illustrates well that the team is dedicating energy towards the scientific communication beyond traditional borders between disciplines, in full coherence with the leading principles of the Computational and Quantitative Biology Unit.

Answer of the Team "Computational Neuroscience" by Angelo Arleo

Overall, the team leader acknowledges the analysis and suggestions made by the AERES committee. Notwithstanding, he has identified some inconsistencies and misjudgments that require rectification:

P29, *"Although the team is still rather small, the recent arrival of another permanent researcher may lead to an even more active and sustainable scientific activity."*

The team has actually recruited 2 permanent members (1 CNRS researcher in 2012, 1 Maître de Conference in 2013). The latter was mentioned during the audition.

P29, *"It should be noted that these are almost entirely with groups outside the Jussieu site"*

This sentence does not account for the fact that the team was involved in the 4 collaborative projects within the Jussieu site:

- 1 ANR (2009-13) in collaboration with B. Girard (ISIR-UPMC Jussieu) & L. Rondi-Reig (NPA-UPMC);
- 1 UPMC Emergence (2011-12), coordinated by the team, in collaboration with V. Hayward (ISIR-UPMC);
- 1 collaborative postdoctoral project (2008-9, funded by UPMC) in collaboration with S. Otani (NPA-UPMC).
- 1 EU Integrated Project, 6th FP, EU IST-027819-IP, (2007-10) in collaboration with J-A. Meyer (ISIR-UPMC).

Ever since 2007, these collaborations gave rise to a series of shared papers in 8 journals and 3 peer-reviewed proceedings (as indicated in the Scientific Report of the team).

P30, *"[...] this would be the only computational neuroscience group in the Unit which is at present composed of groups concerned with problems in genomics and bioinformatics."*

As stated in the Project of the unit, both the team leader and the unit leader have already set forth a policy to attract other theoretical neuroscience groups during the next period. For instance, already in 2013 a candidate to a Professorship at the Faculty of Life Science of UPMC wish to join (if selected) the CQB unit to found a 2nd computational neuroscience group.

P29 & 30, “ [...] for initiating collaborations with the largely experimentalist Neuroscience Unit which will be also integrated in the Institut de Biologie Paris Seine (IBPS).” “[...] the current lack of collaborations within the neurobiology unit which will be a component of the future IBPS.”

These statements are misleading and do not take into account actual facts:

- During the period 2007-2012, the team shared a series of publications (3 journals, 2 peer-reviewed proceedings, 4 conference abstracts) with members of the former and future neurobiology unit:
 - o Martinet L-E, Sheynikhovich D, Benchenane K, Arleo A (2011) *PLoS Comput Biol*, 7 (5):e1002045.
 - o Sheynikhovich D, Otani S, Arleo A (2011) *J Physiol P*, 105(1-3):45-52.
 - o Arleo A, Rondi-Reig L (2007) *J Integr Neurosci*, 6(3):327-66.
 - o Sheynikhovich D, Otani S, Arleo A (2010) *Proc 5th French Conf Comput Neurosci*, 77-81.
 - o Passot JB, Rondi-Reig L, Arleo A (2009) *Proc European Symposium Artif Neural Network*, 17:287-92.
 - o Sheynikhovich D, Otani S, Arleo A (2012) *FENS Abstracts*, Spain.
 - o Martinet LE, Sheynikhovich D, Benchenane K, Arleo A (2011) *French Society Neurosci Abs*, France.
 - o Passot JB, Sheynikhovich D, Rondi-Reig L, Arleo A (2011) *French Society Neurosci Abs*, France.
 - o Sheynikhovich D, Otani S, Arleo A (2011) *French Society Neurosci Abs*, France.
- In 2013, the team shared already 4 productions with members of the former and future neurobiology unit:
 - o Sheynikhovich D, Otani S, Arleo A (2013) *J Neurosci* (conditionally accepted).
 - o Jarlier F & Arleo A, Petit G, Fouquet C, Burguière E, Rondi-Reig L. (2013) *J Neurosci Methods*, (in press).
 - o 1 Software CeCILL licence with L. Rondi-Reig (2013).
 - o 1 journal paper in preparation shared with L. Rondi-Reig.
- Note that the collaboration with L. Rondi-Reig actually started in 2005:
 - o Burguière E, Arleo A, [...], Rondi-Reig L (2005) *Nat Neurosci*, 8(10):1292-4.
- During the period 2007-2013 the team was involved in 2 collaborative projects with the neuroscience unit:
 - o 1 ANR project (2009-2013) in collaboration with L. Rondi-Reig's team;
 - o 1 UPMC project (2008-2009) in collaboration with S. Otani's team.

Most of this information (notably concerning publications and projects during the 2007-2012 period) was reported in the Scientific Report of the team. In addition, the first section of the Scientific Project clearly stated that the mission of the Computational Neuroscience within the CQB unit will be to promote a number of inter-unit collaborations, particularly between CQB and Neuroscience, and between CQB and Adaptive Biology and Aging.