



Activity Report 2017

Team RAP2

Réseaux, algorithmes et probabilités

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

RESEARCH CENTER
Paris

THEME
Networks and Telecommunications

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Team RAP2

Creation of the Team: 2017 January 01, end of the Team: 2017 December 31

Keywords:

Computer Science and Digital Science:

A6.1.2. - Stochastic Modeling (SPDE, SDE)

A8.8. - Network science

A8.9. - Performance evaluation

Other Research Topics and Application Domains:

B6.3.2. - Network protocols

1. Personnel

Research Scientists

Nicolas Broutin [Inria, Researcher, until Aug 2017, HDR]

Christine Fricker [Inria, Researcher, HDR]

Philippe Robert [Team leader, Inria, Senior Researcher, HDR]

Post-Doctoral Fellow

Davit Martirosyan [Inria]

PhD Students

Renaud Dessalles [INRA, until Feb 2017]

Veronica Quintana Rodriguez [Telecom Bretagne]

Wen Sun [Inria]

Guilherme Thompson [Inria]

Intern

Othmane Safsafi [Ecole Normale Supérieure Paris, until Jul 2017]

Administrative Assistant

Nelly Maloysel [Inria]

Visiting Scientist

Ravi Rasendra Mazumdar [University of Waterloo, until Feb 2017]

External Collaborators

Yousra Chabchoub [ISEP]

Pierre Nicodeme [Université Paris XIII]

2. Overall Objectives

2.1. Overall Objectives

The research team RAP2 (Networks, Algorithms and Communication Networks) was created in 2004 on the basis of a long standing collaboration between engineers at Orange Labsin Lannion and researchers from Inria Paris. The initial objective was to formalize and expand this fruitful collaboration.

At Orange Labsin Lannion, the members of the team are experts in the analytical modeling of communication networks as well as on some of the operational aspects of network management concerning traffic measurements on ADSL networks, for example.

At Inria Paris, the members of RAP have a recognized expertise in modeling methodologies applied to stochastic models of communication networks.

RAP2 also has the objective of developing new fundamental tools to investigate *probabilistic* models of complex communication networks. We believe that mathematical models of complex communication networks require a deep understanding of general results on stochastic processes. The two fundamental domains targeted are:

1. Design and analysis of algorithms for communication networks.
2. Analysis of scaling methods for Markov processes: fluid limits and functional limit theorems.

From the very beginning, it has been decided that RAP would focus on a number of particular issues over a period of three or four years. The general goal of the collaboration with Orange Labs is to develop, analyze and optimize algorithms for communication networks. The design of algorithms to allocate resources in large distributed systems is currently investigated in the framework of this collaboration:

3. Research Program

3.1. Scaling of Markov Processes

The growing complexity of communication networks makes it more difficult to apply classical mathematical methods. For a one/two-dimensional Markov process describing the evolution of some network, it is sometimes possible to write down the equilibrium equations and to solve them. The key idea to overcome these difficulties is to consider the system in limit regimes. This list of possible renormalization procedures is, of course, not exhaustive. The advantages of these methods lie in their flexibility to various situations and to the interesting theoretical problems they raised.

A fluid limit scaling is a particularly important means to scale a Markov process. It is related to the first order behavior of the process and, roughly speaking, amounts to a functional law of large numbers for the system considered.

A fluid limit keeps the main characteristics of the initial stochastic process while some second order stochastic fluctuations disappear. In “good” cases, a fluid limit is a deterministic function, obtained as the solution of some ordinary differential equation. As can be expected, the general situation is somewhat more complicated. These ideas of rescaling stochastic processes have emerged recently in the analysis of stochastic networks, to study their ergodicity properties in particular.

3.2. Design and Analysis of Algorithms

Data Structures, Stochastic Algorithms

The general goal of the research in this domain is of designing algorithms to analyze and control the traffic of communication networks. The team is currently involved in the design of algorithms to allocate bandwidth in optical networks and also to allocate resources in large distributed networks. See the corresponding sections below.

The team also pursues analysis of algorithms and data structures in the spirit of the former Algorithms team. The team is especially interested in the ubiquitous divide-and-conquer paradigm and its applications to the design of search trees, and stable collision resolution protocols.

3.3. Structure of random networks

This line of research aims at understanding the global structure of stochastic networks (connectivity, magnitude of distances, etc) via models of random graphs. It consists of two complementary foundational and applied aspects of connectivity.

RANDOM GRAPHS, STATISTICAL PHYSICS AND COMBINATORIAL OPTIMIZATION. The connectivity of usual models for networks based on random graphs models (Erdős–Rényi and random geometric graphs) may be tuned by adjusting the average degree. There is a *phase transition* as the average degree approaches one, a *giant* connected component containing a positive proportion of the nodes suddenly appears. The phase of practical interest is the *supercritical* one, when there is at least a giant component, while the theoretical interest lies at the *critical phase*, the break-point just before it appears.

At the critical point there is not yet a macroscopic component and the network consists of a large number of connected component at the mesoscopic scale. From a theoretical point of view, this phase is most interesting since the structure of the clusters there is expected (heuristically) to be *universal*. Understanding this phase and its universality is a great challenge that would impact the knowledge of phase transitions in all high-dimensional models of *statistical physics* and *combinatorial optimization*.

RANDOM GEOMETRIC GRAPHS AND WIRELESS NETWORKS. The level of connection of the network is of course crucial, but the *scalability* imposes that the underlying graph also be *sparse*: trade offs must be made, which required a fine evaluation of the costs/benefits. Various direct and indirect measures of connectivity are crucial to these choices: What is the size of the overwhelming connected component? When does complete connectivity occur? What is the order of magnitude of distances? Are paths to a target easy to find using only local information? Are there simple broadcasting algorithms? Can one put an end to viral infections? How much time for a random crawler to see most of the network?

NAVIGATION AND POINT LOCATION IN RANDOM MESHES. Other applications which are less directly related to networks include the design of improved navigation or point location algorithms in geometric meshes such as the Delaunay triangulation build from random point sets. There the graph model is essentially fixed, but the constraints it imposes raise a number of challenging problems. The aim is to prove performance guarantees for these algorithms which are used in most manipulations of the meshes.

4. New Results

4.1. Resource Allocation in Large Data Centres

Participants: Christine Fricker, Philippe Robert, Guilherme Thompson, Veronica Quintana Rodriguez.

With the emergence of new networking paradigms such as Cloud Computing and related technologies (Fog Computing, VNF, etc.) new challenges in understanding, modelling and improving systems relying on these technologies arise. Our research goal is to understand how the stochastic nature of the access to these systems affects their performance, and to design algorithms which can improve global performance using local information. This research is made in collaboration with Fabrice Guillemin, from Orange Labs.

Building up from the results previously obtained by this team, we have extend our research towards more complex systems, investigating the behaviour of multi-resource systems, which are globally stable but local congested, a problem that naturally arises from the decentralization of resources. We investigate a cooperation scheme between processing facilities, where congestion-maker clients, the one with the largest demand the locally congested resource are systematically forwarded to the another data centre when some threshold on the occupation level is reached. These thresholds are chosen to anticipate sufficiently in advance potential shortages of any resource in any data centre. After providing some convergence results, we are able to express the performance of the system in terms of the invariant distribution of an inhomogeneous random walk on the plane. We derive optimal threshold parameters, improving the performance of the distributed Cloud Computing system in such a way that it approaches the efficiency of a centralised system. Currently, a document is being prepared for publication, but the main results are presented in G. Thompson's PhD Document [2].

4.2. Ressource allocation in vehicle sharing systems

Participants: Christine Fricker, Yousra Chabchoub.

Vehicle sharing systems are becoming an urban mode of transportation, and launched in many cities, as Velib' and Autolib' in Paris. Managing such systems is quite difficult. One of the major issues is the availability of the resources: vehicles or free slots to return them. These systems became a hot topic in Operation Research and the importance of stochasticity on the system behavior leads us to propose mathematical stochastic models. The problem is to understand the system behavior and how to manage these systems in order to improve the allocation of both resources to users. This work is in collaboration with El Sibai Rayane (ISEP), Plinio Santini Dester (École Polytechnique), Hanène Mohamed (Université Paris-Ouest), and Danielle Tibi (Université Paris Diderot).

4.2.1. Stochastic modelling of bike-sharing systems

The goal is to derive the stationary behavior of the state process in a quite general model: number of bikes in the stations and in routes between two stations. Our stochastic model is the first one taking into account the finite number of spots at the stations. The basic model for bike-sharing systems comes within the framework of closed networks with two types of nodes: single server/finite capacity nodes and infinite servers/infinite capacity nodes. The effect of local saturation is modeled by generalized blocking and rerouting procedures, under which, as a key argument, the stationary state is proved to have product-form. For a class of large closed Jackson networks submitted to capacity constraints, asymptotic independence of the nodes in normal traffic phase is proved at stationarity under mild assumptions, using a Local Limit Theorem. The limiting distributions of the queues are explicit. In the Statistical Mechanics terminology, the equivalence of ensembles - canonical and grand canonical - is proved for specific marginals. This widely extends the existing results on heterogeneous bike-sharing systems. The grand canonical approximation can then be used for adjusting the total number of bikes and the capacities of the stations to the expected demand. [12]

4.2.2. Local load balancing policies.

Recently we investigated some load balancing algorithms for stochastic networks to improve the bike sharing system behavior. We focus on the choice of the least loaded station among two to return the bike, the so called Power of choice. Nevertheless, in real systems, this choice is local. Thus the main challenge is to deal with the choice between two neighboring stations.

For that, a set of N queues, with a local choice policy, is studied. When a customer arrives at queue i , he joins the least loaded queue between queues i and $i + 1$. When the load tends to zero, we obtain an asymptotic for the stationary distribution of the number of customers at a queue. The main result is that, in equilibrium, queue lengths decay geometrically when ρ tends to 0, N fixed. It allows to compare local choice, no choice and Power of choice. The local policy changes the exponential decay with respect to no choice but does not lead to an improvement (double exponential tail decay) comparable to the random choice model. [19].

For a bike-sharing homogeneous model, we study a deterministic cooperation between the stations, two by two. Analytic results are achieved in an homogeneous bike-sharing model. They concern the mean-field limit as the system is large, and its equilibrium point. Results on performance mainly involve an original closed form expression of the stationary blocking probability and new tight bounds for the mean of the total number of customers in the classical join-the-shortest-queue model. These results are compared by simulations with the policy where the users choose the least loaded between two neighboring stations. It turns out that, because of randomness, the choice between two neighbours gives better performance than grouping stations two by two.

It relies on new results for the classical system of two queues under the join-the-shortest-queue policy. We revisited the study of the stationary distribution. A simple analytical solution is proposed. Using standard generating function arguments, a simple expression of the blocking probability is derived, which as far as we know is original. Furthermore, from the balance equations, all stationary probabilities are obtained as explicit combinations of those of states $(0, k)$ for $0 \leq k \leq K$. The blocking probability is also obtained for a variant with two queues under JSQ, where the constraint is on the total capacity of the system.

This extends to the infinite capacity and asymmetric cases, i.e., when the queues have different service rates. For the initial symmetric finite capacity model, the stationary probabilities of states $(0, k)$ can be obtained

recursively from the blocking probability. In the other cases, they are implicitly determined through some functional equation that characterizes their generating function. For the infinite capacity symmetric model, we provide an elementary proof of a result by Cohen which gives the solution of the functional equation in terms of an infinite product with explicit zeroes and poles. See [9].

We use data, trip data (trips collected in a month) obtained from JCDecaux and reports on station status collected as open data, to test local choice policy. Indeed we designed and tested a new method that globally improves the distribution of the resources (bikes and docks) among the stations. It relies on a local small change in user behaviors, by adapting their trips to resource availability around their departure and arrival stations. Results show that, even with a partial user collaboration, the proposed method increases significantly the global balance of the bike sharing system and therefore the user satisfaction. This is done using trip data sets. The key of our study is to detect spatial outliers, objects having a behavior significantly different from their spatial neighbors, in a context where neighbors are heavily correlated. Moran scatterplot is a well-known method that exploits similarity between neighbors in order to detect spatial outliers. We proposed an improved version of Moran scatterplot, using a robust distance metric called Gower similarity. Using this new version of Moran scatterplot, we identified many spatial outliers stations (often with much more available bikes, or with much more empty docks during the day) in Velib. For the occupancy data set obtained by modifying trips, the number of spatial outliers drastically decreases. See [18].

4.3. Scaling Methods

Participants: Davit Martirosyan, Philippe Robert, Wen Sun.

4.3.1. Large Unreliable Stochastic Networks

The reliability of a large distributed system is studied. The framework is a system where files are stored on servers. When one of these servers breaks down, all files on it are lost. We assume that these files could be retrieved immediately and re-allocated among other servers while the failed server restarts but empty. It is a reasonable assumption since the failure rate is quite small comparing to an effective recovery mechanism. It is also assumed that each server is connected with a subset of servers in the system. When it breaks down, files on it are re-allocated on the servers that in this subset, following a given policy. Our main interest is the influence on the loads due to two allocation algorithms: the “Random Choice” (RC) policy and the “Power of d Choices” (PoC) policy.

- (RC) Each copy join a server in the subset at random.
- (PoC) Each copy chooses d servers in the subset at random, and joins the least loaded one.

The asymptotic behaviors of these two policies are investigated through mean field models. We have show that when the number of servers getting large, the load of each server can be approached by a linear (resp. non-linear) Markov process for RC (resp. PoC) policy. The equilibrium distributions of these asymptotic processes are also given.

For the case $d = 2$ and all the servers are connected, see the paper [15]. This is a joint work with Inria/UPMC Team Regal. For a generalized case, there is a paper in preparation.

4.3.2. Bandwidth Allocation in Large Data Center

We are investigating a problem of efficient resource allocation in a large data center. In our model, the following is assumed. Each job that should be treated arrives to an $M/M/C$ queue and is placed in it if the latter is not exhausted. Otherwise, it is sent to another queue for the possible implementation with the help of a certain canal, whose size is finite. A mean-field or the so called chaoticity result is established. Informally speaking, we show that the stochastic process that describes the evolution of our system converges to a non-random limit. We then study the stability properties of this limiting process and prove that it has a unique equilibrium that attracts exponentially all solutions that are issued from its small neighborhood. Moreover, we also show that if the size of the canal is infinite (i.e., the jobs go freely to another queue when not served), the uniqueness for the fixed point problem is not guaranteed and, depending on some physical parameters, one can have no solution, a unique solution or two solutions. This phenomenon is quite surprising and it seems

that is was not observed before. We also investigate the stability of equilibrium points. Some techniques used in our proofs come from theories developed in the context of PDEs.

4.4. Stochastic Models of Biological Networks

Participants: Renaud Dessalles, Philippe Robert, Wen Sun.

4.4.1. Stochastic Modelling of self-regulation in the protein production system of bacteria.

This is a collaboration with Vincent Fromion from INRA Jouy-en-Josas, which started in December 2013.

In prokaryotic cells (e.g. E. Coli. or B. Subtilis) the protein production system has to produce in a cell cycle (i.e. less than one hour) more than 10^6 molecules of more than 2500 kinds, each having different level of expression. The bacteria uses more than 67% of its resources to the protein production. Gene expression is a highly stochastic process: bacteria sharing the same genome, in a same environment will not produce exactly the same amount of a given protein. Some of this stochasticity can be due to the system of production itself: molecules, that take part in the production process, move freely into the cytoplasm and therefore reach any target in the cell after some random time; some of them are present in so much limited amount that none of them can be available for a certain time; the gene can be deactivated by repressors for a certain time, etc. We study the integration of several mechanisms of regulation and their performances in terms of variance and distribution. As all molecules tends to move freely into the cytoplasm, it is assumed that the encounter time between a given entity and its target is exponentially distributed.

4.4.1.1. Models with Cell Cycle

Usually, classical models of protein production do not explicitly represent several aspects of the cell cycle: the volume variations, the division and the gene replication. Yet these aspects have been proposed in literature to impact the protein production. We have therefore proposed a series of “gene-centered” models (that concentrates on the production of only one type of protein) that integrates successively all the aspects of the cell cycle. The goal is to obtain a realistic representation of the expression of one particular gene during the cell cycle. When it was possible, we analytically determined the mean and the variance of the protein concentration using Marked Poisson Point Process framework.

We based our analysis on a simple model where the volume changes across the cell cycle, and where only the mechanisms of protein production (transcription and translation) are represented. The variability predicted by this model is usually assimilated to the “intrinsic noise” (i.e. directly due to the protein production mechanism itself). We then add the random segregation of compounds at division to see its effect on protein variability: at division, every mRNA and every protein has an equal chance to go to either of the two daughter cells. It appears that this division sampling of compounds can add a significant variability to protein concentration. This effect directly depends on the relative variance (Fano factor) of the protein concentration: this effect is stronger as the relative variance is low. The dependence on the relative variance can be explained by considering a simplified model. With parameters deduced from real experimental measures, we estimate that the random segregation of compounds can double the variability of the genes with the lowest relative variance.

Finally, we integrate the gene replication to the model: at some point in the cell cycle, the gene is replicated, hence doubling the transcription rate. We are able to give analytical expressions for the mean and the variance of protein concentration at any moment of the cell cycle; it allows to directly compare the variance with the previous model with division. We show that gene replication has little impact on the protein variability: an environmental state decomposition shows that the part of the variance due to gene replication represents only at most 2% of the total variability predicted by the model.

Finally, we have investigated other possible sources of variability by presenting other simulations that integrate some specific aspects: variability in the production of RNA-polymerases and ribosomes, uncertainty in the division and DNA replication decisions, etc. None of the considered aspects seems to have a significant impact on the protein variability.

In the end, these results are compared to the real experimental measure of protein variability. It appears that the models with cell cycle presented above tend to underestimate the protein variability especially for highly expressed proteins. See Dessalles [1] and Dessalles et al. [17]

4.4.2. Stochastic Modelling of Protein Polymerization

This is a collaboration with Marie Doumic, Inria MAMBA team. The first part of our work focuses on the study of the polymerization of protein. This phenomenon is involved in many neurodegenerative diseases such as Alzheimer's and Prion diseases, e.g. mad cow. In this context, it consists in the abnormal aggregation of proteins. Curves obtained by measuring the quantity of polymers formed in in vitro experiments are sigmoids: a long lag phase with almost no polymers followed by a fast consumption of all monomers. Furthermore, repeating the experiment under the same initial conditions leads to somewhat identical curves up to translation. After having proposed a simple model to explain this fluctuations, we studied a more sophisticated model, closer to the reality. We added a conformation step: before being able to polymerize, proteins have to misfold. This step is very quick and remains at equilibrium during the whole process. Nevertheless, this equilibrium depends on the polymerization which is happening on a slower time scale. The analysis of these models involves stochastic averaging principles.

We have also investigated a more detailed model of polymerisation by considering the the evolution of the number of polymers with different sizes ($X_i(t)$) where $X_i(t)$ is the number of polymers of size i at time t . By assuming that the transitions rates are scaled by a large parameter N , it has been shown that, in the limit, the process ($X_i^N(t)$) is converging to the solution of Becker-Döring equations as N goes to infinity. For another model including nucleation, we have given an asymptotic description of the lag time at the first and second order. These results are obtained in particular by proving stochastic averaging theorems.

4.4.3. Central Limit Theorems

We have investigate the fluctuations of the stochastic Becker-Döring model of polymerization when the initial size of the system converges to infinity. A functional central limit problem is proved for the vector of the number of polymers of a given size. It is shown that the stochastic process associated to fluctuations is converging to the strong solution of an infinite dimensional stochastic differential equation (SDE) in a Hilbert space. We haveproved that, at equilibrium, the solution of this SDE is a Gaussian process. The proofs are based on a specific representation of the evolution equations, the introduction of a convenient Hilbert space and several technical estimates to control the fluctuations, especially of the first coordinate which interacts with all components of the infinite dimensional vector representing the state of the process. See Sun [21]

4.4.4. Study of the Nucleation Phenomenon

We have investigated a new stochastic model describing the time evolution of a polymerization process. The initial state of the system consists only of isolated monomers. We study the *lag time* of the polymerization process, that is, the first instant when a fraction of the initial monomers is polymerized, i.e. the fraction of monomers used in the polymers. The mathematical model includes a *nucleation property*: polymers with a size below some threshold n_c , the size of the nucleus, are quickly fragmented into smaller polymers. For a size greater than n_c , the fragmentation still occurs but at a smaller rate. A scaling approach is used, by taking the volume N of the system as a scaling parameter. If $n_c \geq 3$, under quite general assumptions on the way polymers are fragmented, we prove a limit theorem for the instant T^N of creation of the first "stable" polymer, i.e. a polymer of size n_c . It is proved that the distribution of T^N/N^{n_c-3} converges to an exponential distribution. We also show that, if $n_c \geq 4$, then the lag time has the same order of magnitude as T^N and, if $n_c = 3$, it is of the order of $\log N$. An original feature of our model is the significant variability (asymptotic exponential distribution) proved for the instants associated to polymerization. This is a well known phenomenon observed in the experiments in biology but it has not been really proved in appropriate mathematical models up to now. The results are proved via a series of (quite) delicate technical estimates for occupations measures on fast time scales associated to the first n_c coordinates of the corresponding Markov process. Extensive Stochastic calculus with Poisson processes, several coupling arguments and classical results from continuous branching processes theory are the main ingredients of the proofs.

5. Bilateral Contracts and Grants with Industry

5.1. Bilateral Contracts with Industry

- Contrat de recherche externalisé avec ORANGE SA "Scheduling Global OS". Duration three years 2014-2017.
- PhD grant CJS (Contrat Jeune Scientifique) Frontières du vivant of INRA for Renaud Dessalles.
- PhD grant from Fondation Sciences Mathématiques de Paris for Wen Sun.
- PhD grant from Brazilian Government for Guilherme Thompson.
- CELTIC+ Contract "SENDATE".

6. Partnerships and Cooperations

6.1. International Research Visitors

6.1.1. Visits of International Scientists

- Louigi Addario-Berri (McGill)
- Gabor Lugosi (ICREA and Pompeu Fabra)
- Cyril Marzouk (Paris Sud)
- Minmin Wang (Buenos Aires)
- S. Foss (Heriot-Watt University, UK)
- V. Gupta (University of Chicago, USA)

6.1.2. Visits to International Teams

- *Nicolas Broutin* visited the computer science department of McGill University (Canada), the CRM in Montreal, the mathematics institute in Nice and the university Aix-Marseille.
- *Wen Sun* has visited the Division of Applied Mathematics in Brown University to work with Kavita Ramanan, 07-16 Nov. 2017.

7. Dissemination

7.1. Promoting Scientific Activities

7.1.1. Journal

7.1.1.1. Member of the Editorial Boards

- *Nicolas Broutin* is member of the steering committee of the international meeting on analysis of algorithms (AofA).
- *Philippe Robert* is Associate Editor of the Book Series "Mathématiques et Applications" edited by Springer Verlag and Associate Editor of the journal "Queueing Systems, Theory and Applications".

7.1.1.2. Member of the Conference Program Committees

- *Philippe Robert* has been in the TPC of Performance'2017, Caching and Delivery in Wireless Networks Workshop (CCDWN)'2017 and Stochastic Networks'2018.

7.1.2. Conferences

- *Nicolas Broutin* has given lectures at the probability seminar in Marseille on Jan 9, the probability seminar in Nice on March 21, and the annual days of the ANR project GRAAL on May 10.

- *Christine Fricker* has given a talk “Analysis of large scale closed networks with reservation” at the 2017 INFORMS 19th Applied Probability Conference, Northwestern University, USA on 10-12 July, 2017. *Christine Fricker* gave a talk at the day “Filles et math: une équation lumineuse” for 100 high school girls organised by Animath and Femmes et maths (19/12/2017).
- *Wen Sun* has given a talk “A Large Scale Network with Moving Servers” on 5-9 June 2017 at the Sigmetrics workshop MAMA in Urbana-Champaign, Illinois, USA and a talk “An asymptotic study of allocation policies in a large balls and bins model” at the 2017 INFORMS 19th Applied Probability Conference, Northwestern University, USA on 10-12 July, 2017.
- *Guilherme Thompson* has given a talk “Studying an offloading policy for multi-resource Cloud services under Kelly’s Regime” at the 2017 INFORMS 19th Applied Probability Conference, Northwestern University, USA on 10-12 July, 2017. *Philippe Robert* has given a talk “Asymptotics of Stochastic Protein Assembly Models” at the PDMP workshop in Seillac, France, June 2017. He has given a talk “Analysis of a Stochastic Model of Replication in Large Distributed Storage Systems: A Mean-Field Approach” at the ACM Sigmetrics conference, Urbana-Champaign, USA on 5-9 June 2017, and also a talk “A Large Scale Analysis of Unreliable Stochastic Networks” at the 2017 INFORMS 19th Applied Probability Conference, Northwestern University, USA on 10-12 July, 2017. He has given a talk “Stochastic Models of Gene Expression” at the SBF-Kolloquium, Institut für Mathematik, Universität Potsdam, October 2017. He gave a seminar “Asymptotic Studies of Large Distributed systems with Failures” at Inria Rhône-Alpes (Polaris team).

7.1.3. Scientific Expertise

- *Christine Fricker* is member of the jury of agrégation

7.2. Teaching - Supervision - Juries

7.2.1. Teaching

- Master : *Nicolas Broutin* Master Parisien de Recherche en Informatique (MPRI), in the course 2.15 on Analysis of Algorithms.
- *Philippe Robert* Master, Probabilités et Applications, UPMC

7.2.2. Supervision

- *Renaud Dessalles* [17] (January 2017) and *Guilherme Thompson* [2] (December 2017) have defended their PhD thesis.
- *Christine Fricker* got her habilitation to supervise research on 20/11/2017. The manuscript is entitled “Stochastic Networks”. Reviewers: Alexandre Proutière (professor, KTH Stockohlm), Isi Mitrani (professor, Newcastle University), Laurent Massoulié (research position, Inria-Microsoft Research leader). Jury: Alexandre Proutière (professor, KTH Stockohlm), Laurent Massoulié (Inria-Microsoft Research leader), reviewers, Irina Kurkova (professor, UPMC), Laurent Decreusefond (professor, Telecom Paristech), Carl Graham (research position, CNRS, Ecole Polytechnique).

7.2.3. Juries

Philippe Robert has been a member of the juries of PhD defenses by R. Dessalles (Ecole Polytechnique, January 2017), Y. Petot (Nancy, October 2017), G. Thompson (UPMC< December 2017) and V. Bœuf (Saclay, December 2017).

8. Bibliography

Publications of the year

Doctoral Dissertations and Habilitation Theses

- [1] R. DESSALLES. *Stochastic models for protein production: the impact of autoregulation, cell cycle and protein production interactions on gene expression*, École Polytechnique, January 2017, <https://hal.inria.fr/tel-01482087>

- [2] G. R. THOMPSON. *Stochastic Models for Resource Allocation in Large Distributed Systems*, Université Pierre et Marie Curie, December 2017, <https://hal.inria.fr/tel-01661815>

Articles in International Peer-Reviewed Journals

- [3] L. ADDARIO-BERRY, N. BROUTIN, C. GOLDSCHMIDT, G. MIERMONT. *The scaling limit of the minimum spanning tree of the complete graph*, in "Annals of Probability", 2017, vol. 45, pp. 3075–3144, <https://arxiv.org/abs/1301.1664>, <https://hal.inria.fr/hal-00773360>
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