Activity Report 2014

Project-Team RAP

Networks, Algorithms and Probability

RESEARCH CENTER
Paris - Rocquencourt

THEME
Networks and Telecommunications

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Project-Team RAP

Keywords: Markovian Model, Stochastic Algorithms, Distributed Algorithms, Optical Networks

Creation of the Project-Team: 2004 February 01.

1. Members

Research Scientists

Philippe Robert [Team leader, Inria, Senior Researcher, HdR]
Nicolas Broutin [Inria, Researcher, HdR]
Christine Fricker [Inria, Researcher]

PhD Students

Emanuele Leoncini [INRA,until May 2014]
Renaud Dessalles [INRA]
Sarah Eugene [Inria]
Wen Sun [Inria,from Sep 2014]
Guilherme Thompson [Inria,from Sep 2014]

Post-Doctoral Fellows

Jelena Pesic [Inria, until Mar 2014, granted by Min. du Redressement Productif]
Henning Sulzbach [Inria, until Aug 2014, granted by Fondation Sciences Mathématiques de Paris]

Administrative Assistant

Nelly Maloisel [Inria]

Others

Mohammadreza Aghajani [Inria,PhD, from Jun 2014 until Aug 2014]
Cédric Bourdais [Inria, from Apr 2014 until Aug 2014]
Yousra Chabchoub [ISEP,Associate Professor]
Hanène Mohamed [Univ. Paris X, Associate Professor]

2. Overall Objectives

2.1. Overall Objectives

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

At Orange Labs in 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 — Rocquencourt, the members of RAP have a recognized expertise in modeling methodologies applied to stochastic models of communication networks.

RAP 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. 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.

3.2. 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.

3.3. 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. Random Graphs

Participants: Nicolas Broutin, Henning Sulzbach.

4.1.1. Universality of scaling limits of random graphs

Random graphs are one of the most studied models of networks, and they turn out to be related to crucial questions in physics about the behaviour of matter at the phase transition, or in combinatorial optimization about the hardness of computation. In recent years, we have constructed the scaling limit of the classical Erdos-Renyi random graph model, and conjectured that this limit also happened to be universal.

The funding of the Associated Team RNA has permitted to invite Shankar Bhamidi. During his visit, we have worked and found a new way to construct the scaling limit of random graph processes in the critical window. This method is especially important since it is robust enough to prove universality of the limit, that is that many models have the same limit. The method relies on the dynamics of the coalescence of clusters as the edges are added, and allows us to hope for proofs that would be able to treat the more complex geometric models.

4.1.2. Cutting down random tree and the genealogy of fragmentations

The study of the internal structure of random combinatorial object such as graphs and trees led to question about whether such objects exhibit invariance by certain complex surgical operations (disconnect some pieces, and re-attach them somewhere else). In the context of graphs, this is related to the so-called self-organized criticality: certain distributions that yield fractal objects should naturally appear in nature because they are the fixed points of some recombination procedures. In the context of trees, it turns out that certain fragmentations arising when chopping off a random tree have a genealogy that has the same distribution as the original tree. We have investigated this with Minmin Wang, and obtained results about p-trees and the genealogy of the fragmentation on Aldous' celebrated continuum random tree. These may also be interpreted in terms of complex path transformations for Brownian excursions and other random processes with exchangeable increments, and hence relate to very classical questions in probability theory.

4.1.3. New encodings for combinatorial coalescent processes

In 2013, we had constructed the scaling limit of the minimum spanning tree of a complete graph using crucial information about the scaling limit of random graphs, and especially about the way the cluster merge as the edges are added in the graph. With J.-F. Marckert (LaBRI, Bordeaux) we have found a novel construction of the important multiplicative coalescent that describes how the connected components of a random graph coalesce as the edges are added. This unveils yet more interesting links between the minimum spanning tree and the random graph, since Prim's celebrated algorithm is used to construct a consistent ordering of the vertices that ensures that the connected components are intervals.

4.1.4. Navigation in random Delaunay triangulations

Navigation or routing algorithms are fundamental routines: in order to solve many problems, one of the first steps consists in locating a node in a data structure. Unfortunately, the current algorithms are based on heuristics and very few rigorous results about the performance of such algorithms are known when the model for data is more realistic than the worst-case.

With O. Devillers and R. Hemsley, we have initiated a program that aims at finding rigourous estimates for the performance of routing algorithms in geometric structures such as Delaunay tesselations. So far we have managed to develop some tools that permitted us to analyse a simple algorithm. Although this algorithm has been designed for most of the analysis to work, this work paves the way towards the rigorous analysis of other more natural and widely used algorithms.

4.1.5. Connectivity and sparsification of sparse wireless networks

Many models of wireless networks happen to be connected only when the average degree is tending to infinity with the size of the network, more precisely when it is about the logarithm of the number of nodes. This raises questions about the potential issues in scaling such models. With L. Devroye (McGill) and G. Lugosi (ICREA and Pompeu Fabra), we have worked at analysing models in which we try to construct connected or almost connected networks in a distributed way (that is that no global optimization is allowed in designing the network, and every device should proceed in the same way to choose its neighbors). We have managed to analyse an algorithm for constructing such a network, and to obtain tight results about the number of links that a typical device should have in order for the global network to be connected. We further proved that this is asymptotically optimal when one only requires that most nodes should be in the same connected component.

4.2. Resource Allocation Algorithms in Large Distributed Systems

Participants: Christine Fricker, Philippe Robert, Guilherme Thompson.

This is a collaboration with Fabrice Guillemin from Orange Labs which started in February 2014.

4.2.1. Controlling impatience in cellular networks using QoE-aware radio resource allocation

Impatience of users when using a data service has a major impact on the quality of service offered by telecommunication networks, especially in cellular networks with scarce radio resources. Impatience is negative for users, it is due to many factors related to the performance of servers, customer devices, etc., but also to bandwidth sharing in the network.

While impatience can be seen as a negative phenomenon, it can also be used as a lever to discourage customers when the system becomes too much overloaded. This can be achieved in cellular networks by modulating the capacity available to customers being at a certain distance of the antenna. This general idea can be applied in several manners and can be viewed as a network optimization mechanism. In this paper, we reuse the general framework of α-fair scheduler in order to perform this control. This has the advantage of being easy to implement in realistic settings as α-fair schedulers (and especially the Proportional Fair (PF) one) are widely adopted in mobile networks. This also reduces the dimension of our problem as it narrows the optimization problem to the tuning of a single parameter α.

In order to achieve this goal, we first derive a model for reneging probabilities under a general α-fair scheduler. In particular, we consider a heavy load regime and develop a fluid flow analysis of impatience in cellular networks. We notably establish a fixed point formulation for the computation of the reneging probability and introduce a new metric, namely QoE perturbation, expressing how much a particular flow impacts the reneging probability in the system. We then use this QoE perturbation metric to design of a new radio resource management scheme that controls the parameter of the scheduler in order to reduce the global reneging in the system. For instance, recognizing that customers far from the base station degrade the global performance of the system, impatience and α-fair scheduling can be used to discourage those customers and in some sense to perform an implicit admission control in order to optimize the use of radio resources.

4.2.2. Resource Allocation in Large Data Centers

The goal of this study is to investigate the design of allocation algorithms of requests requiring different classes of quality of video streams as well as their performances. The class of algorithms considered may downgrade the quality of some of the transmission to maximize the utilization of the servers.

4.3. Stochastic networks: large bike sharing systems

Participants: Christine Fricker, Hanène Mohamed, Cédric Bourdais, Yousra Chabchoub.

Vehicle sharing systems are becoming an urban mode of transportation, and launched in many cities, as Velib' and Autolib' in Paris. 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 now the impact of stochasticity on the system behavior is commonly admitted. The problem is to understand their behavior and how to manage them in order to provide both resources to users.

Our stochastic model is the first studying the impact of the finite number of spots at the stations on the system behavior.

With Danielle Tibi, we use limit local theorems to obtain the asymptotic stationary joint distributions of several node (station or route) states when the system is large (both numbers of stations and bikes), also in the case of finite capacities of the stations. This gives an asymptotic independence preperty for node states. This widely extends the existing results on heterogeneous bike-sharing systems.

Second we investigate the impact of finite capacity of stations and reservation in car-sharing systems. The large-scale asymptotic joint stationary distribution of the numbers of vehicles and reserved parking places is given as the joint distribution in a tandem of queues with a constrained total capacity where rates are solutions of a system of two fixed point equations. Analytical expressions are given for performance in light and heavy traffic cases. As expected, reservation impact drastically increases with traffic. Even if the equilibrium is identified and analyzed, the question of convergence is still open.

JC Decaux provides us data describing Velib' user trips. These data are useful to measure the system behavior. With Yousra Chabchoub, we test clustering to obtain a typology of the stations. Then we focus on the resources availability (free docks and available bikes) and separate the Velib' stations into three clusters (balanced, overloaded and underloaded stations), using Kmeans clustering algorithm, along with the Dynamic Time Wraping (DTW) metric. We choose to update the centers of the clusters using the efficient Dtw Barycenter Averaging (DBA) method.

4.4. Scaling Methods

Participants: Philippe Robert, Wen Sun, Mohammadreza Aghajani.

4.4.1. Fluid Limits in Wireless Networks

This is a collaboration with Amandine Veber (CMAP, École Polytechnique). The goal is to investigate the stability properties of wireless networks when the bandwidth allocated to a node is proportional to a function of its backlog: if a node of this network has x requests to transmit, then it receives a fraction of the capacity proportional to $\log(1+x)$, the logarithm of its current load. A fluid scaling analysis of such a network is presented. We have shown that the interaction of several time scales plays an important role in the evolution of such a system, in particular its coordinates may live on very different time and space scales. As a consequence, the associated stochastic processes turn out to have unusual scaling behaviors which give an interesting fairness property to this class of algorithms. A heavy traffic limit theorem for the invariant distribution has also been proved. A generalization to the resource sharing algorithm for which the $\log$ function is replaced by an increasing function. This year we completed the analysis of a star network topology with multiple nodes. Several scalings were used to describe the fluid limit behaviour.

4.4.2. The Time Scales of a Transient Network

The Distributed Hash Table (DHTs) consists of a large set of nodes connected through the Internet. Each file contained in the DHT is stored in a small subset of these nodes. Each node breaks down periodically and it is necessary to have back-up mechanisms in order to avoid data loss. A trade-off is necessary between the bandwidth and the memory used for this back-up mechanism and the data loss rate. Back-up mechanisms already exist and have been studied thanks to simulation. To our knowledge, no theoretical study exists on this topic. With a very simple centralized model, we have been able to emphasise a trade-off between capacity and life-time with respect to the duplication rate. From a mathematical point of view, we are currently studying different time scales of the system with an averaging phenomenon.

4.5. Stochastic Models of Biological Networks

Participants: Renaud Dessalles, Sarah Eugene, Emanuele Leoncini, Philippe Robert.

4.5.1. 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 on December 2014.

In procaryots 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 85% 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. All molecules are supposed to move freely into the cytoplasm, it is assumed that the the encounter time between a given entity and its target is exponentially distributed.

4.5.1.1. Transcription-translation model for all proteins

The first model that has been studied integrates the production of all the proteins. Each gene has to be transcribed in mRNA and each mRNA has to be translated in protein. The transcription step needs a RNA-Polymerase molecule that is sequestered during the time of elongation. Likewise, each mRNA needs a ribosome in order to produce a protein. RNA-Polymerases/Ribosomes are present in limited amount and the genes/mRNAs sequester these molecules during the whole the time of elongation. Finally each mRNA has an exponentially distributed lifetime with an average value of 4 min and the proteins disappear at a rate of one hour, hence simulating the global dilution in the growing bacteria.

This global sharing of Ribosomes/RNA-Polymerases among all proteins induces a general regulation: each gene competing to each other to have access to these common resources. Because of the parameters of affinity (between gene and RNA-Poymerase and between mRNA and ribosome) are specific to each gene, it allows a large range of average protein production but induce some noise, especially for highly expressed proteins.

We developed a Python simulation, and using the biological experiments of Tanichuchi et al. (2010), and we have investigated a biologically coherent range of parameters. By making the simulations, we have been able to reproduce certain aspects of the biological measures, especially for the high amount of noise for well expressed proteins.

4.5.1.2. Simple feedback model

We have also investigated the production of a single protein, with the transcription and the translation steps, but we also introduced a direct feedback on it: the protein tends to bind on the promoter of its own gene, blocking therefore the transcription. The protein remains on it during an exponential time until its detachment caused by thermal agitation.

The mathematical analysis aims at understanding the nature of the internal noise of the system and to quantify it. We try to determine if, for instance, for the same average protein level, the feedback permits a noise reduction of protein distribution compared to the "open loop" model; or if it rather allows a better efficiency in case of a change of command for a new level of production (due, for example, to a radical change in the environment) by reducing the respond time to reach this new average.

4.5.2. Stochastic Modelling of Protein Polymerization

This is a collaboration with Marie Doumic, Inria MAMBA team.

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 a translation.

The first study we did proposed a simplified stochastic model to analyze this phenomenon. For this model, when the volume gets large, the quantity of polymers has the typical sigmoidal shape. A second order result has also been obtained for this model. We were able to compute the asymptotic distribution of the lag time and express its variance. The parameters of the model have been obtained by using data given by Wei-Feng Xue, University of Kent.

The current project concerns a more sophisticated mathematical model. Indeed, we have added a conformation step: before polymerizing, 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 follows the conformation step: this modelling leads to the study of averaging principles.

5. Bilateral Contracts and Grants with Industry

5.1. Contracts

- CELTIC-Plus Saser “Safe and Secure European Routing’. RAP participates in the section on optical networks. Participants include Orange labs, Alcaltel-Lucent, Telecom Institute, ENSSAT as well as a number of German laboratories. Duration three years.
- Contrat de recherche externalisé avec ORANGE SA "Scheduling Global OS”. Duration three years 2014-2016.
- PGMO project “Systèmes de véhicules en libre-service: Modélisation, Analyse et Optimisation” with G-Scop (CNRS lab, Grenoble) and Ifsttar. From 1 to 3 years. Starting at 1/10/2013.
- PhD grant CJS (Contrat Jeune Scientifique) Frontières du vivant of INRA for Emanuele Leoncini.
- 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.

5.2. Bilateral Grants

- The project RNA “Connectivity and distances in models of random networks and applications” is jointly funded by Inria through the Associate Team program, and Quebec's FQRNT team grant CARP. https://who.rocq.inria.fr/Nicolas.Broutin/aap-rna.html. Duration 2013-2014.

6. Partnerships and Cooperations

6.1. International Research Visitors

RAP team has received the following people:

- Louigi Addario-Berry (McGill)
- Shankar Bhamidi (University of North Carolina at Chapel Hill)
- Christina Goldschmidt (Oxford)
- Ross Hemsley (Inria Sophia)
- Stefan Langerman (UL Bruxelles)
- Gabor Lugosi (Pompeu Fabra)
- Ahmed Kharroubi (Casablanca, Marrocco)
- Juan Pablo Vigneaux (Santiago, Chile)
- Cecile Mailler (University of Bath)

6.2. National Research Visitors

RAP team has received the following people:

- Nicolas Gast (Inria Grenoble)
- Olivier Devillers (Inria Sophia)
- Marie Albenque (Ecole Polytechnique)

7. Dissemination

7.1. Leadership within scientific community

Nicolas Broutin is member of the steering committee of the international meeting on analysis of algorithms (AofA). He has been the referee for the PhD thesis of Elie de Panafieu (Paris 7) and a member of the committee for the PhD thesis of Ross Hemsley (U de Nice).

Christine Fricker is member of the jury of agrégation. She is the leader of PGMO project "Systèmes de véhicules en libre-service: Modélisation, Analyse et Optimisation" with G-Scop (CNRS lab, Grenoble) and Ifsttar. From 1 to 3 years. Starting at 1/10/2013. *Christine Fricker* was member of Jury de recrutement de CR2 Inria-Saclay.

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". He is member of the scientific council of EURANDOM. He is also associate Professor at the École Polytechnique in the department of applied mathematics where he is in charge of lectures on mathematical modeling of networks. *Philippe Robert* has been a member of the technical programme committee of the conferences ACM Sigmetrics(2014) Performance(2014) and ICCCN (2014).

7.2. Teaching

Nicolas Broutin has taught at the Master Parisien de Recherche en Informatique (MPRI), in the course 2.15 on Analysis of Algorithms. He has also taught at NYU Shanghai during the fall of 2014.

Philippe Robert gives Master2 lectures in the laboratory of the Probability of the University of Paris VI. He is also giving lectures in the "Programme d'approfondissement de Mathématiques Appliquées et d'Informatique" on Networks and Algorithms at the École Polytechnique.

7.3. Conference and workshop committees, invited conferences

Nicolas Broutin has given lectures at the annual meeting of the GDR-IM and at the Journees de combinatoire de Bordeaux, the Workshop on New Frontriers in random geometric graphs at the Lorentz Center in Leiden. He has presented his results at seminars in Ecole Polytechnique (LIX and CMAP), Universite de Nice and at the East China Normal University in Shanghai. He has visited the mathematics department of the University of Bath and the NYU-ECNU institute for mathematical sciences at NYU Shanghai.

Sarah Eugene gave a talk at the Joint Annual Meeting of the Japanese Society for Mathematical Biology and the Society for Mathematical Biology on July 2014, Osaka, Japan.

Christine Fricker was invited at Tours University in a panel about “Trades of mathematics”, 20/11/2014. She gave a talk at ECQT (1rst European Conference on Queuing Theory), Ghent, 20-22/8/2014. Participation (co-author) at Workshop CluCo d’EGC 2014, Rennes, 28/01/2014, IWCIM, Paris, 1-2/11/2014.

Philippe Robert gave a keynote conference of “European Conference on Queueing Theory”, ECQT 2014, Ghent, August 2014. He gave a talk at the Lycee “Jeanne d’Albret” in Saint Germain en Laye in May, and for BTS students in April and also to maths teachers of option ISN (Informatique et sciences du numérique), académie de Versailles in April 2014.

8. Bibliography

Publications of the year

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[6] V. SIMON, S. MONNET, M. FEUILLET, P. ROBERT, P. SENS. *SPLAD: scattering and placing data replicas to enhance long-term durability*, May 2014, n° RR-8533, 23 p. , https://hal.inria.fr/hal-00988374

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[9] N. BROUTIN, L. DEVROYE, G. LUGOSI. *Almost optimal sparsification of random geometric graphs*, March 2014, https://hal.archives-ouvertes.fr/hal-01056127

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[12] N. BROUTIN, J.-F. MARCKERT. *A new encoding of coalescent processes. Applications to the additive and multiplicative cases*, September 2015, https://hal.inria.fr/hal-01092562

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[14] N. BROUTIN, M. WANG. *Reversing the cut tree of the Brownian continuum random tree*, August 2014, 24 pages, 5 figures, https://hal.archives-ouvertes.fr/hal-01056124

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