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Imaging Membrane traffic at the pertinent scale. The group develops a workflow of optics, biophysical and mathematic approaches mainly devoted to high spatio-temporal studies of molecular dynamics and mechanisms in membrane traffic. His main focus is on the quantitative and temporal deciphering of the very late steps of vesicle recycling at the plasma membrane. In this context a particular attention is paid to the coordination of the Rab11A platform (Rab11A/Rab11FIP2/myosinVB) (**Fig 1**) and its interaction with cytoskeleton elements.

We already adapted or developed diverse photonic approaches aimed to determine the dynamic and topological characterization of Rab domains in conjunction with both a cargo specificity study (Langerine/TfR) and of multi-Rab complexes (Rab11A/RCP/Rab4; Rab6A or A'/Rab6IP1/Rab11A), in living cells. Our work is now fully dedicated to decipher the dynamic coordination and organization of molecular complexes at the single cell level. Dedicated "hybrid" technologies have been developed to perform this task. These techniques (i.e. High res SIM+ Q-scanTIRFM; Boulanger et al. 2014) are used to define the spatial positioning (3D high res) of a molecule or a group of molecules within the living cell at the best temporal regime and we are now classifying the 3D dynamical behavioral of exocytic vesicles, in diverse conditions (Basset et al. TPI, submitted).

Modelling dynamics in single cell biology: toward integrated analysis. Together with the **SERPICO Team at Inria, Rennes**, we have proposed original formalisms and user-friendly algorithms for intracellular traffic estimation (Network Tomography, image denoising (bias-variance trade-off), space-time object detection and background subtraction). We shall pursue this research in 2 complementary directions:

-From the experimental view point, molecular (RNA interference), mechanical (micro-patterning) and optical (FRAP, photoactivation) perturbations combined with multi-parametric image acquisition (TIRF, 4D, FLIM) allow one to quantify the molecular interactions in the cell. The issue we now wish to address is to link this type of information with meaningful events and signals as they are detected in space and time in order to evaluate correlations (ICS, RICS, optical flow... [P. Roudot et al., (in preparation)])

-Another aspect is to analyse and compare these events using original metrics (e.g. geodesics

metrics from valuated Network Tomography-based graphs) and simulation methods (e.g. Monte-Carlo methods, “Cross-Entropy”). We have now built a dynamic model able to statistically mimic observed processes (Pécot *et al.* 2014 Epub ahead; and **Fig. 2**). Ideally, the simulation and real data should be “similar” as much as possible, both statistically and visually. From simulations, we determined meaningful features to be matched to real image data. Iteratively, we use description parameters from the simulation to extract statistical information, from larger sets of real data with the ultimate goal to predict intracellular behaviours.

Key publications

Year of publication 2014

Thierry Pécot, Patrick Bouthemy, Jérôme Boulanger, Anatole Chessel, Sabine Bardin, Jean Salamero, Charles Kervrann (2014 Dec 12)

Background fluorescence estimation and vesicle segmentation in live cell imaging with conditional random fields.

IEEE transactions on image processing : a publication of the IEEE Signal Processing Society : 667-80 : [DOI : 10.1109/TIP.2014.2380178](https://doi.org/10.1109/TIP.2014.2380178)

Jérôme Boulanger, Charles Gueudry, Daniel Münch, Bertrand Cinquin, Perrine Paul-Gilloteaux, Sabine Bardin, Christophe Guérin, Fabrice Senger, Laurent Blanchoin, Jean Salamero (2014 Nov 17)

Fast high-resolution 3D total internal reflection fluorescence microscopy by incidence angle scanning and azimuthal averaging.

Proceedings of the National Academy of Sciences of the United States of America : 17164-9 : [DOI : 10.1073/pnas.1414106111](https://doi.org/10.1073/pnas.1414106111)

Carine Rossé, Catalina Lodillinsky, Laetitia Fuhrmann, Maya Nourieh, Pedro Monteiro, Marie Irondelle, Emilie Lagoutte, Sophie Vacher, François Waharte, Perrine Paul-Gilloteaux, Maryse Romao, Lucie Sengmanivong, Mark Lynch, Johan van Lint, Graça Raposo, Anne Vincent-Salomon, Ivan Bièche, Peter J Parker, Philippe Chavier (2014 Apr 21)

Control of MT1-MMP transport by atypical PKC during breast-cancer progression.

Proceedings of the National Academy of Sciences of the United States of America : E1872-9 : [DOI : 10.1073/pnas.1400749111](https://doi.org/10.1073/pnas.1400749111)

Year of publication 2013



Space-time Imaging of Organelles and Endomembranes Dynamics UMR144 - Cell biology and cancer

Pedro Monteiro, Carine Rossé, Antonio Castro-Castro, Marie Ironnelle, Emilie Lagoutte, Perrine Paul-Gilloteaux, Claire Desnos, Etienne Formstecher, François Darchen, David Perrais, Alexis Gautreau, Maud Hertzog, Philippe Chavrier (2013 Dec 18)

Endosomal WASH and exocyst complexes control exocytosis of MT1-MMP at invadopodia.

The Journal of cell biology : 1063-79

Xavier Heiligenstein, Jérôme Heiligenstein, Cédric Delevoye, Ilse Hurbain, Sabine Bardin, Perrine Paul-Gilloteaux, Lucie Sengmanivong, Gilles Régnier, Jean Salamero, Claude Antony, Graça Raposo (2013 Aug 28)

The CryoCapsule: simplifying correlative light to electron microscopy.

Traffic (Copenhagen, Denmark) : 700-16 : [DOI : 10.1111/tra.12164](https://doi.org/10.1111/tra.12164)

Year of publication 2014

Sofia Traikov, Christoph Stange, Thomas Wassmer, Perrine Paul-Gilloteaux, Jean Salamero, Graça Raposo, Bernard Hoflack (1970 Jan 1)

Septin6 and Septin7 GTP binding proteins regulate AP-3- and ESCRT-dependent multivesicular body biogenesis.

PloS one : e109372 : [DOI : 10.1371/journal.pone.0109372](https://doi.org/10.1371/journal.pone.0109372)