RECONSTRUCTION OF MULTILEVEL DYNAMICS FROM BIOLOGICAL 3D+TIME IMAGING DATA

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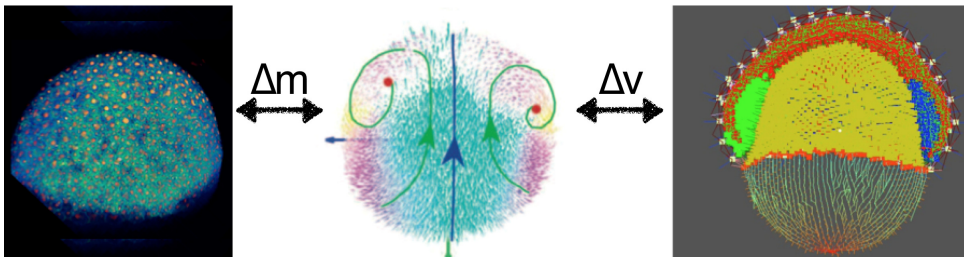
Biology and especially embryology, investigating the development of an egg to an embryo on its way to an adult organism, has long been going from observations, hypotheses, perturbation of the biological system, interpretation and conclusions, without quantitative data except for statistical analysis to decide about the significance of the observations. The quantification and the estimation of measurement precision and accuracy are always a challenge. If strategies to quantify the concentration or the number of molecules are quite well established, strategies to define and calculate quantitative descriptors of shapes and patterns, their changes, similarities and differences from one individual to the other largely remain to be explored. Microscopy 3D optical sectioning repeated at time intervalles with the simultaneous acquisition of different types of signals revealing biological structures and biological activities, opens the way to the quantitative description of biological complexity. We developed and validated in the context of European projects and of the France BioImaging National Infrastructure, a methodology for the integrative modeling of living systems morphogenesis based on multiscale measurements. The three pictures below illustrate our concepts with the biomechanical modeling of the zebrafish early embryogenesis: imaged live specimen (left panel), reconstructed specimen based on algorithmic methods to extract measurements from 3D+time images (middle panel) [1], and simulated specimen with the MecaGen platform (right panel) [2]. Measuring the differences (Delta: measures m and validation v) between the multiscale raw data, the phenomenological data and the virtual data is the way to biological insights.



References

[1] E. Faure et al. A workflow to process 3D+time microscopy images of developing organisms and reconstruct their cell lineage. *Nature Comms*, 7:8674–8683, 2016. doi:10.1038/ncomms9674.

[2] J. Delile et al. A cell-based computational model of early embryogenesis coupling mechanical behaviour and gene regulation. *Nature Comms*, 8:13929–13938, 2017. doi:10.1038/ncomms13929.