1. Aim of the visit

The aim of this visit was to start a long term collaboration between our labs in order develop quantification tools (cell tracking, segmentation) and a modeling framework (using the vertex model approach) in order to address the cell sorting mechanism at the Drosophila embryo. My team recently developed a modeling suite called PASTIS (PAtterning and Signaling in TISsues) that combines signaling (gene regulatory networks) and tissue dynamics including biomechanical inputs (elastic energy, cortical tension, actomyosin cables...). Thus, in the long term the plan is to implement this approach to the data from Dr. Sanson´s team about cell sorting in the Drosophila embryo (parasegmental boundaries formation and maintenance). Such implementation depends on the quantification of the cell sorting process and, to that end, we will also develop quantification tools.

2. Report of activities

1) By means of different meetings, I have interacted with Dr. Sanson team for getting familiar with the experimental tools they use in order to characterize the problem of interest (parasegmental compartmentalization).

2) In terms of the characterization of the actomyosin cable that separates different parasegmental boundaries, we have planned to compute double histograms in terms of the orientation of the cable with respect the DV axis as a function of the length of the cell edges that take part in the cable. This quantity will provide relevant information about possible correlations (orientation vs. length) and in addition will allow us to estimate the cable structure as a function of its individual constituents. Moreover, when the final experimental data is ready (upcoming months) we will also compute the so-called persistence length and relate the macroscopic structure of the cable (form) with its elastic properties.

3) I developed a computer program to extract a polygonal approximation from the experimental segmentation data. This step is critical for importing the real experimental data as the initial conditions of a vertex model simulation. At this point we still have to correct errors derived from T1/T2 recombination processes in the tissue.

4) I developed a mathematical model for describing the underlying gene regulatory network (GRN) that pattern the embryo at the stage of interest. I used a motif approach and reduce the number of elements to a minimum: Hh, Wg, and En

3. Conclusions and future work

This research stay has been really fruitful for our groups. I do believe that this collaboration will lead to a state-of-the-art research within the objectives of the Quantissue initiative. All in all, our initial plan to provide quantification tools for a deep understanding of the parasegmental boundaries formation and maintenance has truly started and is very promising. The future plans of our collaboration include:

1) Quantification of the cable properties as mentioned above (2) once the experimental data is available.

2) Numerical simulations of the GNR I develop under static situations (no tissue dynamics) to evaluate its reliability for maintaining the embryo patterning.

3) Once 2) has been fine-tuned, include the tissue dynamics using the initial experimental conditions (see 3) above) and couple the biomechanical properties of the tissue with the gene expression dynamics.

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