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Employing Statistics in Systems Microscopy

As the role of metastasis is fundamental in the progression of breast cancer, it is of paramount significance to study cell adhesion and cell migration, mechanisms tightly related to the machinery of metastasis, in closer details. Yet, cell adhesion and cell migration result from a series of dynamic procedures in space on a sub-cellular level, namely the organization of cell-matrix adhesion complexes (CMACs) [1].

Using techniques of high-throughput microscopy and post-acquisition image quantification, large sets of data representing cell and CMAC properties are made available for statistical analysis. Such analysis is an essential component of what is now termed as Systems Microscopy: systems biology analysis of living cells using a coalition of automated microscopy, image quantification, data mining and statistical analysis [2].

The nature of the statistical analysis in Systems Microscopy includes unsupervised as well as supervised statistical learning. The unsupervised learning approaches are employed for purposes such as visualization using dimension reduction, and detection of sub-populations using mixture models. The focus of the supervised learning methodologies is on between-population tests, spatial point pattern analysis, and predictive modeling using various techniques of classification. Naturally, given that the self-organization of living cells is a spatio-temporal process, all of the aforementioned statistical procedures are intended to interrogate static as well as dynamic (time-series) data.

Thus, by employing the necessary data and various statistical methodologies, the processes of cell adhesion and cell migration may receive further elucidation and potentially advance our understanding of the underlying causes as well as the progression of metastasis.

The aim of this talk is to give a brief description of some of the employed methods in the statistical analysis.

REFERENCES

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