第 18回 RcMcD 融合研究セミナー
（5研究科共同セミナー）

演　題：Using single particle trajectory statistics and polymer simulations to analyze and predict changes in chromatin structure

講演者：Andrew Seeber
（Friedrich Miescher Institute for Biomedical Research, Basel, Switzerland）

日　時：平成２８年１１月２８日（月）１４：３５～１６：０５

場　所：広島大学先端科学総合研究棟　３０２S 会議室

【Abstract】

Biological implications of chromatin movement can be analyzed by polymer models. Here we present an analysis workflow that consists of an improved imaging regime employing high spatial and temporal resolution microscopy coupled with a statistical analysis to extract biophysical parameters from trajectories. The last step of the method is the construction of a polymer model from data to explore in simulations the chromatin condensation state and the interactions the locus experiences. Our approach allows us to differentiate between extrinsic forces from the cytoskeleton and intrinsic chromatin alterations. We have applied this to a yeast inducible double-strand break system and used the extracted parameters to predict chromatin expansion near a break. Super resolution microscopy confirms this prediction and shows that expansion depends on the INO80 nucleosome remodeler. The present method is not limited to yeast and can be used for trajectories generated from any model organism.

References

1) Amitai, A., and Holcman, D. (2013b). Polymer model with long-range interactions: analysis and applications to the chromatin structure. Phys Rev E Stat Nonlin Soft Matter Phys 88, 052604.
2) Amitai, A., Toulouze, M., Dubrana, K., and Holcman, D. (2015). Analysis of Single Locus Trajectories for Extracting In Vivo Chromatin Tethering Interactions. PLoS Computational Biology 11.
3) Seeber, A., Dion, V., and Gasser, S.M. (2013). Checkpoint kinases and the INO80 nucleosome remodeling complex enhance global chromatin mobility in response to DNA damage. Genes Dev 27, 1999-2008.

お問い合わせ先：クロマチン動態数理研究拠点事務局
082-424-7898（内線 7898）　E-mail：rcmcd@hiroshima-u.ac.jp