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The five dimensions of the genome

Thursday, 8 September 2011 09:00 (40 minutes)

Thanks to large sequencing initiatives of the last 10 years we now have access to full genome sequences in digital form, in particular
for laboratory species such as the mouse whose genome is about 3.5 billion letters in size.
Recent high-throughput technologies allow to then probe the function of this genome in many different experimental conditions by
sampling the genome at the rate of 2-3 billion letters per experiment, distributed with strong bias towards particular
regions of the genome sharing a given biochemical property.
The analysis of these large datasets is a fascinating challenge.
I will illustrate this with two situations where time, space and chemical state of the DNA are interrelated:
I will first present data on the circadian (24h) rhythms in the mouse liver:
many biological functions must be activated synchronously at certain times of the day
and are coupled to an internal (biochemical) clock within each cell.
The second example comes from embryonic development, where the correct
body patterning relies on a complex network of interactions within the genome and in particular on a tight control of the 3D folding of the DNA molecule within the cell's nucleus.
I will show how we reconstruct such 5D configurations from the statistical analysis of the genome samples relative to the known full genome sequence,
and how we can make inferences about cellular machineries from these data.

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