ID de Contribution: **51** Type: **Non spécifié**

A minimal in vivo model to quantify the interplay between transcription and DNA supercoiling

In bacteria, genetic context can have significant impact on gene expression but is currently not integrated in quantitative models of gene regulation despite known biophysical principles and quantitative *in vitro* measurements. Conceptually, the simplest genetic context consists of a single gene framed by two topological barriers, also known as the twin transcriptional-loop model, which illustrates how transcription both affects and is affected by DNA supercoiling. *In vivo*, DNA supercoiling is additionally modulated by topoisomerases whose modus operandi remains to be quantified.

In this talk, I will first present an experimental realisation of the twin transcriptional-loop model in *Escherichia coli*. I will then show how a first-principle biophysical model of DNA transcription accounts quantitatively for all the data and makes predictions on topoisomerase activity *in vivo*.

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