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A number of idealized models have been proposed to explain the long range organization of the DNA in bacteriophages. However few can account for the distributions of complex knots found when examining DNA extracted from bacteriophage P4 capsids. Furthermore these models do not consider possible chirality biases in the arrangement of the DNA molecule inside the capsid. In this talk we address these two issues by proposing a randomized version of one of the most popular models: the coaxially spooled model. We present analytical and numerical results for the properties of the random polygons (knots) generated using this model. We show that such model can easily generate complex knotted conformations and although it accounts for some chirality of the organization of the DNA molecules inside bacteriophage capsids does not fully explain the experimental data. (Received February 15, 2010)