Analyzing the Information Processing Capabilities of Gene Expression based Logic

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Abstract—**We present the information processing capabilities in simple biological systems with gene expression based logic. Analogy with binary computer structures is made. In order to design such systems *in silico* approaches can be used. Different models can be established and their analysis can be made before *in vivo* realization. Here we present a sample computer model of such system and its analysis from information processing viewpoint.**

Keywords—synthetic biology; unconventional computing; transcription based logic; gene regulatory networks
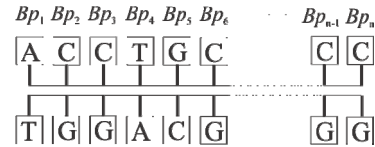

Figure 1. Genome as a sequence of complementary base pairs.

double DNA (sometimes also on RNA) strand. DNA strand is composed of sequentially bounded *nucleotides*, namely *Cytosine (C)* , *Guanine (G)*, *Thymine (T)* and *Adenine (A)*. Length of the strand is measured with the