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Menagerie of Viruses: Diverse Chemical Sequences or Simple Electrostatics?

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The genome packing in hundreds of viruses is investigated by analyzing the chemical sequences of the genomes and the corresponding capsid proteins, in combination with experimental facts on the structures of the packaged genomes. Based on statistical mechanics arguments and computer simulations, we have derived a universal model, based simply on non-specific electrostatic interactions. Our model is able to predict the essential aspects of genome packing in diversely different viruses, such as the genome size and its density distribution. Our result is in contrast to the long-held view that specific interactions between the sequenced amino acid residues and the nucleotides of the genome control the genome packing. Implications of this finding in the evolution and biotechnology will be discussed.