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Statistical Characterization of a 1D Random Potential Problem– with applications in score statistics of MS-based peptide sequencing[1] GELIO ALVES, YI-KUO YU, National Center for Biotechnology Information/NIH — We provide a complete thermodynamic solution of a 1D hopping model in the presence of a random potential by obtaining the density of states. Since the partition function is related to the density of states by a Laplace transform, the density of states determines completely the thermodynamic behavior of the system. We have also shown that the transfer matrix technique, or the so-called dynamic programming, used to obtain the density of states in the 1D hopping model may be generalized to tackle a long-standing problem in statistical significance assessment for one of the most important *proteomic* tasks - - peptide sequencing using tandem mass spectrometry data.

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