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## *30 years of PWMs: Where are we now and what comes next?*

Position weight matrices (also called just weight matrices or position specific scoring matrices, PSSMs) were introduced in a 1982 paper as a method to represent the specificity of a nucleic acid binding protein. After a few years it became the most commonly used representation while at the same time there became many alternative methods for determining PWMs, from fitting of experimental data to statistical analyses of collections of binding sites to the development of several motif discovery algorithms. Over the same period the limitations of PWMs became apparent and various alternatives were developed to provide better representations, although limiting data left PWMs as the primary model because of their relatively small number of parameters. Current high-throughput experimental methods allow us to address in detail and for many different factors the important questions of how accurate are their PWM representations and how to develop better representations. This talk will cover some history, some current work and some speculations about the future.