Oligonucleotide expression array technology has been adopted in many areas of biomedical research to measure simultaneously the level of messenger ribonucleic acid (mRNA) transcripts for thousands of genes. Affymetrix GeneChip arrays are the most popular amongst them. In this technology each gene is represented by a set of 11 to 20 pairs of oligonucleotides that we refer to as probes. Each probe pair is composed of a perfect match (PM) probe, a section of mRNA molecule of interest, and a mismatch (MM) probe that is created by changing the middle base of the PM. To define a measure of the expression level associated to each gene, it is necessary to summarise the probe intensities for each probe set. The analysis of such experiments is not trivial because the probe signals are affected by many levels of variation introduced at different stages of the experiments. A further difficulty is represented by the large differences that may exist among different probe sets used to interrogate the same gene. In literature there are several model-based approaches used to derive the gene expression level form oligonucleotide arrays, but there is no standard to compare and test summaries of probe level data. In this work we propose a novel approach that makes use of probabilistic models for the PM and MM samples. We use these models to summarise and extract a level of uncertainty associated with each probe set. We evaluated our approach both on benchmark data and on epithelial oviduct cell oligonucleotide data, we compared the results with the expression measure provided by the default Affymetrix microarray suite.