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## Weighted Sum Computation *In Vitro* Using Differentially Labeled Molecular Beacon Mixture

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DNA computing is a computing system that embodies massive parallelism as information storage media and information processing operators using DNA or RNA. The power of DNA computing as information processing shows the possibility as applications to diverse biological problems like gene expression pattern analysis and disease diagnosis. In the previous work, we developed a DNA-based weighted sum computation method as a primitive operation for a molecular pattern classifier and demonstrated the classification of synthetic oligonucleotide mixtures patterns [1]. The previous weight-encoding scheme was based on differentially labeled linear probe pairs, so the unbound probes needed to be eliminated before final output detection. Here, we propose an improved method of the weighted sum computation using a molecular beacon mixture. Because molecular beacons emit fluorescence only upon hybridization with target molecules, the elimination step can be skipped and the overall experimental protocol can thus be simplified. We verified the weight-encoding scheme and the weighted sum method using synthetic oligonucleotide targets encoding input values and differentially labeled molecular beacons. First, we performed a series of competitive hybridization reactions between single input and corresponding molecular beacon mixture under various input levels and mix ratios to verify the proposed weighted encoding scheme. Second, we computed the weighted sum of two inputs with various weight values *in vitro*. Finally, molecular pattern classification *in vitro* was demonstrated. The experimental results showed reasonable correlations (>0.95) between the computation results detected as relative fluorescence unit and the predicted computation results calculated from the experimental settings. Being a primitive operation for molecular pattern classification *in vitro*, our weighted sum method has the potential as a gene expression-based disease diagnosis tool. The detailed experimental results will be presented in the presentation.

### References

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