Identification of Regular Genes Demonstrating Insignificant Expression Changes

1. Introduction

1.1. Microarray is a cheap, high throughput, thus widely used to study expression.

1.2. However, microarray is unable to detect some upstream key regulations because of their low level expression changes.

1.3. Our PPMI can be used to identify these expression-insignificant regulators by retrieving the interactions between them and the expression-significant regulators detected by microarrays.

2.