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# ABSTRACT

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# INTRODUCTION & PROBLEM STATEMENT

# Related work & Background

# Preliminary experiments & Results

This format is to be used for submissions that are published in the conference proceedings. We wish to give this volume a consistent, high-quality appearance. We therefore ask that authors follow some simple guidelines. You should format your paper exactly like this document. The easiest way to do this is to replace the content with your own material.

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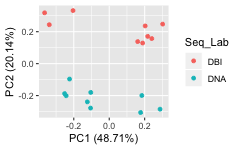
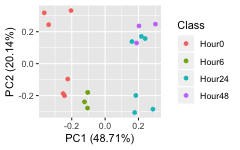
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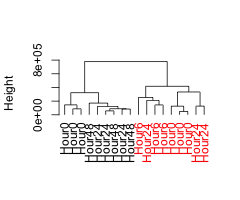
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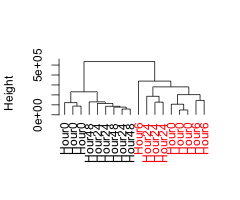
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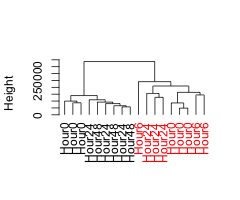
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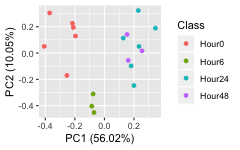
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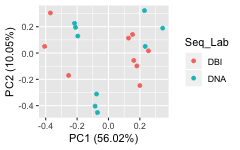
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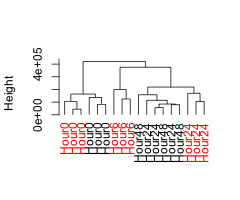
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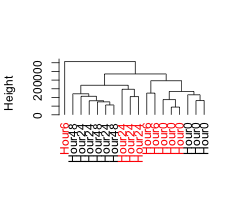
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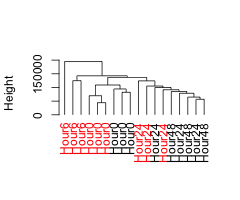
**Figure 1 Evaluation of TMM Normalized CPM for all samples using the top 200 genes (by overall variance). Principal components (A, B). Samples were clustered using agglomerative hierarchical clustering with either complete (C), average (D) or single(E) linkage and Manhattan distance. Leaves with red labels correspond to samples sequenced at DNA Link.**

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**Figure 2 Evaluation of Batch Corrected CPM for all samples using the top 200 genes (by overall variance). Principal Components (A, B). Samples were clustered using agglomerative hierarchical clustering with either complete (C), average (D) or single (E) linkage and Manhattan distance. Leaves with red labels correspond to samples sequenced at DNA Link.**

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| --- | --- | --- | --- |
| Number of Clusters, k = 2 | | | |
| Method | Rand Index | Mean Silhouette | Size (Mean Silhoute by cluster) |
| Euclidean, Complete | 1.000 | 0.739 | 9(0.82), 9(0.658) |
| Euclidean, Average | 1.000 | 0.739 | 9(0.82), 9(0.658) |
| Euclidean, Single | 1.000 | 0.739 | 9(0.82), 9(0.658) |
| Manhattan, Complete | 1.000 | 0.607 | 9(0.687), 9(0.526) |
| Manhattan, Average | 1.000 | 0.607 | 9(0.687), 9(0.526) |
| Manhattan, Single | 1.000 | 0.607 | 9(0.687), 9(0.526) |

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| Number of Clusters, k = 3 | | | |
| Method | Rand Index | Mean Silhouette | Size (Mean Silhoute by cluster) |
| Euclidean, Complete | 0.882 | 0.610 | 9(0.792), 6(0.518), 3(0.251) |
| Euclidean, Average | 0.948 | 0.633 | 9(0.808), 8(0.515), 1(0) |
| Euclidean, Single | 0.948 | 0.633 | 9(0.808), 8(0.515), 1(0) |
| Manhattan, Complete | 0.869 | 0.450 | 9(0.647), 5(0.291), 4(0.206) |
| Manhattan, Average | 0.948 | 0.467 | 9(0.672), 8(0.293), 1(0) |
| Manhattan, Single | 0.948 | 0.467 | 9(0.672), 8(0.293), 1(0) |

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| --- | --- | --- | --- |
| Number of Clusters, k = 4 | | | |
| Method | Rand Index | Mean Silhouette | Size (Mean Silhoute by cluster) |
| Euclidean, Complete | 0.765 | 0.427 | 3(0.423), 6(0.426), 6(0.518), 3(0.251) |
| Euclidean, Average | 0.869 | 0.561 | 9(0.792), 6(0.342), 2(0.462), 1(0) |
| Euclidean, Single | 0.850 | 0.499 | 9(0.785), 3(0.526), 5(0.067), 1(0) |
| Manhattan, Complete | 0.830 | 0.489 | 9(0.621), 3(0.68), 2(0.485), 4(0.051) |
| Manhattan, Average | 0.850 | 0.495 | 9(0.653), 5(0.387), 3(0.366), 1(0) |
| Manhattan, Single | 0.850 | 0.495 | 9(0.653), 5(0.387), 3(0.366), 1(0) |

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| Number of Clusters, k = 5 | | | |
| Method | Rand Index | Mean Silhouette | Size (Mean Silhoute by cluster) |
| Euclidean, Complete | 0.752 | 0.378 | 3(0.423), 6(0.426), 6(0.342), 2(0.462), 1(0) |
| Euclidean, Average | 0.817 | 0.515 | 9(0.782), 4(0.292), 2(0.262), 2(0.27), 1(0) |
| Euclidean, Single | 0.810 | 0.516 | 9(0.785), 3(0.41), 3(0.067), 2(0.399), 1(0) |
| Manhattan, Complete | 0.712 | 0.444 | 3(0.501), 6(0.546), 3(0.68), 2(0.485), 4(0.051) |
| Manhattan, Average | 0.732 | 0.434 | 3(0.501), 6(0.546), 5(0.387), 3(0.366), 1(0) |
| Manhattan, Single | 0.810 | 0.488 | 9(0.631), 3(0.574), 3(0.277), 1(0), 2(0.275) |

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| Number of Clusters, k = 6 | | | |
| Method | Rand Index | Mean Silhouette | Size (Mean Silhoute by cluster) |
| Euclidean, Complete | 0.699 | 0.337 | 3(0.423), 6(0.426), 4(0.292), 2(0.262), 2(0.27), 1(0) |
| Euclidean, Average | 0.699 | 0.337 | 3(0.423), 6(0.426), 4(0.292), 2(0.262), 2(0.27), 1(0) |
| Euclidean, Single | 0.758 | 0.279 | 8(0.349), 1(0), 3(0.41), 3(0.067), 2(0.399), 1(0) |
| Manhattan, Complete | 0.693 | 0.430 | 3(0.501), 6(0.546), 3(0.659), 2(0.443), 3(0.035), 1(0) |
| Manhattan, Average | 0.693 | 0.438 | 3(0.501), 6(0.546), 3(0.574), 3(0.277), 1(0), 2(0.275) |
| Manhattan, Single | 0.797 | 0.467 | 9(0.621), 3(0.574), 2(0.298), 1(0), 1(0), 2(0.248) |
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| **Table 1 Statistics for hierarchical clustering of TMM normalized counts. Samples were clustered using the top 200 genes (ranked by overall variance). No batch correction was applied prior to clustering. Rand indices were calculated using the categorical time point as the true class.** | | | |

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| Number of Clusters, k = 2 | | | |
| Method | Rand Index | Mean Silhouette | Size (Mean Silhoute by cluster) |
| Euclidean, Complete | 0.634 | 0.413 | 13(0.489), 5(0.217) |
| Euclidean, Average | 0.477 | 0.509 | 17(0.539), 1(0) |
| Euclidean, Single | 0.477 | 0.509 | 17(0.539), 1(0) |
| Manhattan, Complete | 0.471 | 0.312 | 6(0.514), 12(0.212) |
| Manhattan, Average | 0.477 | 0.325 | 17(0.344), 1(0) |
| Manhattan, Single | 0.477 | 0.325 | 17(0.344), 1(0) |

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| --- | --- | --- | --- |
| Number of Clusters, k = 3 | | | |
| Method | Rand Index | Mean Silhouette | Size (Mean Silhoute by cluster) |
| Euclidean, Complete | 0.608 | 0.341 | 13(0.385), 4(0.282), 1(0) |
| Euclidean, Average | 0.608 | 0.341 | 13(0.385), 4(0.282), 1(0) |
| Euclidean, Single | 0.490 | 0.289 | 16(0.325), 1(0), 1(0) |
| Manhattan, Complete | 0.529 | 0.388 | 6(0.496), 9(0.366), 3(0.238) |
| Manhattan, Average | 0.516 | 0.336 | 8(0.323), 9(0.386), 1(0) |
| Manhattan, Single | 0.516 | 0.132 | 15(0.112), 1(0), 2(0.349) |

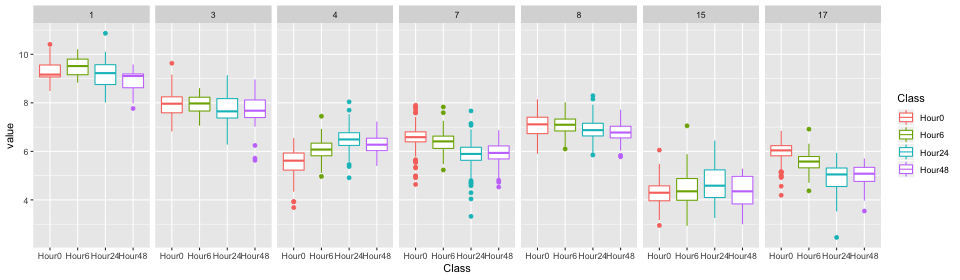
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| Number of Clusters, k = 4 | | | |
| Method | Rand Index | Mean Silhouette | Size (Mean Silhoute by cluster) |
| Euclidean, Complete | 0.608 | 0.301 | 6(0.28), 7(0.398), 4(0.238), 1(0) |
| Euclidean, Average | 0.582 | 0.244 | 1(0), 12(0.278), 4(0.264), 1(0) |
| Euclidean, Single | 0.484 | 0.068 | 15(0.082), 1(0), 1(0), 1(0) |
| Manhattan, Complete | 0.647 | 0.355 | 6(0.444), 6(0.42), 3(0.186), 3(0.215) |
| Manhattan, Average | 0.516 | 0.346 | 6(0.397), 9(0.353), 1(0), 2(0.34) |
| Manhattan, Single | 0.516 | 0.346 | 6(0.397), 9(0.353), 1(0), 2(0.34) |

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| Number of Clusters, k = 5 | | | |
| Method | Rand Index | Mean Silhouette | Size (Mean Silhoute by cluster) |
| Euclidean, Complete | 0.582 | 0.257 | 6(0.262), 7(0.36), 2(0.186), 2(0.078), 1(0) |
| Euclidean, Average | 0.562 | 0.174 | 1(0), 11(0.191), 1(0), 4(0.258), 1(0) |
| Euclidean, Single | 0.497 | 0.108 | 14(0.139), 1(0), 1(0), 1(0), 1(0) |
| Manhattan, Complete | 0.634 | 0.336 | 6(0.386), 6(0.42), 3(0.179), 1(0), 2(0.34) |
| Manhattan, Average | 0.634 | 0.336 | 6(0.386), 6(0.42), 3(0.179), 1(0), 2(0.34) |
| Manhattan, Single | 0.510 | 0.246 | 6(0.336), 9(0.268), 1(0), 1(0), 1(0) |

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| Number of Clusters, k = 6 | | | |
| Method | Rand Index | Mean Silhouette | Size (Mean Silhoute by cluster) |
| Euclidean, Complete | 0.556 | 0.254 | 6(0.235), 1(0), 6(0.445), 2(0.169), 2(0.078), 1(0) |
| Euclidean, Average | 0.536 | 0.133 | 1(0), 11(0.163), 1(0), 2(0.225), 2(0.078), 1(0) |
| Euclidean, Single | 0.549 | 0.156 | 12(0.205), 1(0), 2(0.172), 1(0), 1(0), 1(0) |
| Manhattan, Complete | 0.621 | 0.305 | 6(0.386), 6(0.354), 2(0.188), 1(0), 1(0), 2(0.334) |
| Manhattan, Average | 0.621 | 0.305 | 6(0.386), 6(0.354), 2(0.188), 1(0), 1(0), 2(0.334) |
| Manhattan, Single | 0.536 | 0.234 | 6(0.336), 8(0.275), 1(0), 1(0), 1(0), 1(0) |
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| **Table 2 Statistics for hierarchical clustering of Batch Corrected, TMM normalized counts. Samples were clustered using the top 200 genes (ranked by overall variance). Surrogate variable analysis was used to correct for variation introduced by sequencing of samples at different labs. Rand indices were calculated using the categorical time point as the true class.** | | | |

## References and Citations

Use a numbered list of references at the end of the article, ordered alphabetically by last name of first author, and referenced by numbers in brackets [1,3,4].



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**Figure: Intersection between gene lists for pairwise contrasts in samples analyzed at DBI Only**

**Figure: Intersection between gene lists for pairwise contrasts in samples analyzed at DNA Link Only**

**Figure: Intersection between gene lists for pairwise contrasts in samples analyzed at both sequencing labs.**

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# METHOD

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# Preliminary experiments & Results

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