

Testing different strategies to compute a representative cluster profile (v2)

C1

```
In [320]: true_values <- c(-1.0102, -0.9091, -0.8081, 0.8081, 0.9091, 1.0102)
names(true_values) <- c("t1", "t2", "t3", "t4", "t5", "t6")
df <- read.table("Data/D1_C1.tsv", header = TRUE, row.names = 1)
df_scaled <- t(scale(t(df), center = TRUE, scale = TRUE))
eigengenes <- -svd(df_scaled)$v[,1]*(ncol(df_scaled)-1)^0.5
means <- apply(df_scaled, 2, mean)
trimmed_means <- apply(df_scaled, 2, mean, trim = 0.25)
medians <- apply(df_scaled, 2, median)
```

```
In [321]: sum(abs(eigengenes - true_values))
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0.0559107912943919

```
In [322]: sum(abs(means - true_values))
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0.784940472949121

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In [323]: sum(abs(trimmed_means - true_values))
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0.602575213783847

```
In [324]: sum(abs(medians - true_values))
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0.498337674586422

C2

```
In [325]: true_values <- c(1.0102, 0.9091, 0.8081, -0.8081, -0.9091, -1.0102)
names(true_values) <- c("t1", "t2", "t3", "t4", "t5", "t6")
df <- read.table("Data/D1_C2.tsv", header = TRUE, row.names = 1)
df_scaled <- t(scale(t(df), center = TRUE, scale = TRUE))
eigengenes <- -svd(df_scaled)$v[,1]*(ncol(df_scaled)-1)^0.5
means <- apply(df_scaled, 2, mean)
trimmed_means <- apply(df_scaled, 2, mean, trim = 0.25)
medians <- apply(df_scaled, 2, median)
```

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In [326]: sum(abs(eigengenes - true_values))
```

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0.0563707840974478
```

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In [327]: sum(abs(means - true_values))
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0.789153059039224
```

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In [328]: sum(abs(trimmed_means - true_values))
```

```
0.649745392255973
```

```
In [329]: sum(abs(medians - true_values))
```

```
0.560512280965099
```

C3

```
In [444]: true_values <- c(-0.9895, -0.2234, 1.2129, 1.2129, -0.2234, -0.9895)
names(true_values) <- c("t1", "t2", "t3", "t4", "t5", "t6")
df <- read.table("Data/D1_C3.tsv", header = TRUE, row.names = 1)
df_scaled <- t(scale(t(df), center = TRUE, scale = TRUE))
eigengenes <- -svd(df_scaled)$v[,1]*(ncol(df_scaled)-1)^0.5
means <- apply(df_scaled, 2, mean)
trimmed_means <- apply(df_scaled, 2, mean, trim = 0.25)
medians <- apply(df_scaled, 2, median)
```

```
In [445]: sum(abs(eigengenes - true_values))
```

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0.0659216634752623
```

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In [446]: sum(abs(means - true_values))
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```
0.709836147115349
```

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In [447]: sum(abs(trimmed_means - true_values))
```

```
0.542898857061318
```

```
In [448]: sum(abs(medians - true_values))
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0.452200429544802
```