

**Table 1.** Description of samples used for simulation study with  $S_{1,2,3}$ .

	Sample name	Treatment_time	Treatment_agent	Sample source	GEO sample (GSM) file Ids
1	Lm_Adult1	0 h	<i>Listeria monocytogenes</i>	Peripheral blood	GSM1467819
		2 h			GSM1467820
		6 h			GSM1467821
2	Lm_Adult2	0 h		Peripheral blood	GSM1467822
		2 h			GSM1467823
		6 h			GSM1467824
3	Lm_Adult3	0 h		Peripheral blood	GSM1467825
		2 h			GSM1467826
		6 h			GSM1467827

**Table 2.** Description of samples used for simulation study with  $S_{1,2,...,5}$ .

	Sample name	Treatment_time	Treatment_agent	Sample source	GEO sample (GSM) file Ids
1	Lm_Neonate3	0 h	<i>Listeria monocytogenes</i>	Umbilical cord blood	GSM1467816
		2 h			GSM1467817
		6 h			GSM1467818
2	Lm_Adult1	0 h		Peripheral blood	GSM1467819
		2 h			GSM1467820
		6 h			GSM1467821
3	Lm_Adult2	0 h		Peripheral blood	GSM1467822
		2 h			GSM1467823
		6 h			GSM1467824
4	Lm_OlderAdult 1	0 h		Peripheral blood	GSM1467828
		2 h			GSM1467829
		6 h			GSM1467830
5	Lm_OlderAdult 2	0 h		Peripheral blood	GSM1467831
		2 h			GSM1467832
		6 h			GSM1467833

## Results for $S_{1, 2, 3}$

Checking for genes expressed in all three samples and across all the three time points yielded 9429 genes. Genes with  $FPKM \geq 1$  at either 0 h or 2 h or 6 h were 8807 of which 7128 genes were found to meet the threshold of fold change ( $\geq 1.25$  or  $\leq 0.8$  for upregulation and downregulation, respectively for either 2 h / 0 h or 6 h / 2 h) in all the three samples.

**Table 4.** 'Cognizable' trends for dataset with three samples and three time points;  $m$  refers to number of samples

		No. of genes with 'cognizable' criteria ( $m$ )	
Trend	$\geq 2$	3	
T1		2142	653
T2		1812	411
T3		1022	251
T4		1176	231

**Table 5.** Summary of the results of bootstrapping; counts and probabilities of observing 'time-trends' with changing values of  $m$ .

Value of $m$ used for bootstrap	Time-trends							
	T1		T2		T3		T4	
	Counts out of 20000	Probability ( $P$ value)	Counts out of 20000	Probability ( $P$ value)	Counts out of 20000	Probability ( $P$ value)	Counts out of 20000	Probability ( $P$ value)
$m=3$	1788	0.0894	1157	0.05785	735	<b>0.03675</b>	645	<b>0.03225</b>
$m \geq 2$	6024	0.3012	5054	0.2527	2997	0.14985	3182	0.1591

Bold characters denote significant  $P$  values obtained on performing bootstrapping experiment.

## Results for $S_{1,2,\dots,5}$

Checking for genes expressed in all five samples and across all the three time points yielded 8974 genes. Genes with  $FPKM \geq 1$  at either 0 h or 2 h or 6 h were 8564 of which 6567 genes were found to meet the threshold of fold change ( $\geq 1.25$  or  $\leq 0.8$  for upregulation and downregulation, respectively for either 2 h / 0 h or 6 h / 2 h ) in all the five samples.

**Table 6.** 'Cognizable' trends for dataset with five samples and three time points;  $m$  refers to number of samples.

		No. of genes with 'cognizable' criteria ( $m$ )		
Trend	$\geq 3$	$\geq 4$	5	
T1	873	389	124	
T2	2268	1483	382	
T3	2151	1010	286	
T4	555	327	114	

**Table 7.** Summary of the results of bootstrapping; counts and probabilities of observing 'time-trends' with changing values of  $m$ .

Value of $m$ used for bootstrap	Time-trends							
	T1		T2		T3		T4	
	Counts out of 20000	Probability ( $P$ value)	Counts out of 20000	Probability ( $P$ value)	Counts out of 20000	Probability ( $P$ value)	Counts out of 20000	Probability ( $P$ value)
$m=5$	390	<b>0.0195</b>	1188	0.0594	880	<b>0.044</b>	338	<b>0.0169</b>
$m \geq 4$	1206	0.0603	4392	0.2196	3048	0.1524	1015	0.05075
$m \geq 3$	2603	0.13015	6898	0.3449	6546	0.3273	1704	0.0852

Bold characters denote significant  $P$  values obtained on performing bootstrapping experiment.