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Comparison of Hemacytometer and HiRes Cell Counters Used in Potency Assays
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Background 3
Cell counting in potency assays

- Potency bioassays are used to measure the biological activity of a molecule.
- Bioassay performance depends on adding a target number of cells to the assay every time i.e. counting cells reproducibly.
- The current practice by most bioassay labs is to manually perform cell counting using a **Hemacytometer** to determine cell concentration and viability.
- Our bioassay lab recently acquired a new Roche Innovatis **HiRes** cell counter which is semi-automatic and reduces the time and labor considerably.
- A series of experiments using multiple cell lines was conducted to determine whether the HiRes could be a suitable alternative to counting cells using the Hemacytometer.

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Background 4
Two Instruments

Hemacytometer

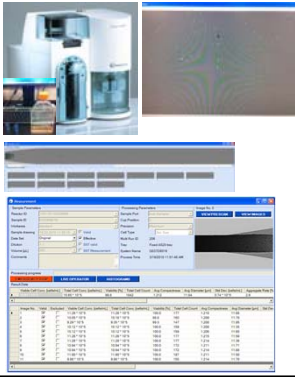
- Cells are harvested & loaded into the twin chambers A & B of the hemacytometer.
- The analyst counts the number of viable/live and non-viable/dead cells in quadrants 1, 2, 3 and 4 in each chamber.
- For count to be valid: the difference in the counts of two chambers A and B must be $\leq 10\%$; and each chamber must have ≥ 100 cells but ≤ 250 cells.
- The cell concentration is then calculated by adding the number of live cells in two chambers and adjusting for the dilution factor and number of quadrants.
- This method is labor-intensive, time-consuming and prone to high variability.

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Background
Two Instruments

Roche Innovatis HiRes

- Cells are harvested and 300 uL aliquot is put in a sample cup.
- The cup is loaded in the instrument, which adds the reagents and injects the sample into a chamber.
- 11 images are captured. Live & dead cells are counted for each image and the cell concentration is calculated.
- This method is semi-automated and fast.



Data
Experimental setup

- Variables

- Cell Line (1,...,11) (varying in size and type)
- Target concentration (7×10^5 cells/mL and 1.5×10^6 cells/mL)
- Method (Hemocytometer and HiRes)
- Analyst (A, ..., T – 19 different analysts)
- Replicate (1,...,8)

Cell Line	1	2	3	4	5	6	7	8	9	10	11
Analyst	A, L	I, J	C, Q	F, O	H, N	B, E	F, O	G, T	R, S	F, P	D, K

- We created a new variable:
 $Prep = Cell\ Line\ by\ Analyst\ (22\ levels)$

Prep describes the preparation effect when a specific analyst prepares a specific cell line. It is the sum of effects of the analyst and cell line; i.e. the variation of *Prep* is the sum of variations of analyst and cell line but we cannot estimate them individually due to confounding.

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Questions of Interest

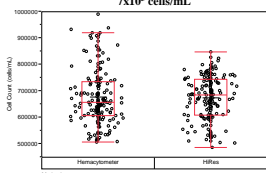
Primary

- 1) To assess the agreement between two methods in measuring cell count.
- 2) To estimate loss of precision in reducing the number of replicates from eight (in this study) to two or three.

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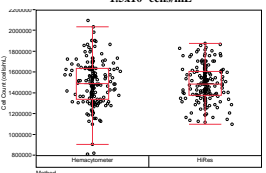
Raw Data Plots
Cell Counts by Method at low and high concentration

7×10^5 cells/mL



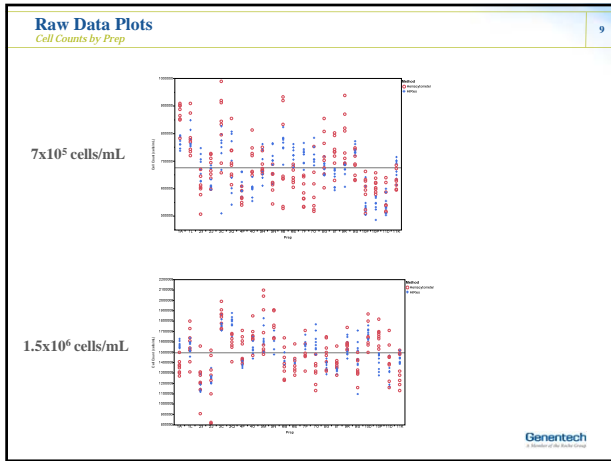
Method	Target	N	Min	Median	Max	Mean	Std Dev	CV
Hemocytometer	7×10^5 cells/mL	176	308,000	626,500	990,000	676,153	300,337	33.7%
HiRes	7×10^5 cells/mL	176	487,000	687,000	849,000	670,000	91,709	12.1%

1.5×10^6 cells/mL



Method	Target	N	Min	Median	Max	Mean	Std Dev	CV
Hemocytometer	1.5×10^6 cells/mL	176	814,000	1,493,000	2,300,000	1,493,522	213,366	14.3%
HiRes	1.5×10^6 cells/mL	176	1,300,000	1,490,000	1,580,000	1,491,623	173,525	11.6%

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Results

Random Effects Model

Regression Model: To assess relationship between *Prep* and *Cell Count*, following random effects model was used (it was fit to each method and cell concentration separately),

$$Y_{ij} = \mu + \alpha_i + \varepsilon_{ij} \quad (1)$$

where,

Y_{ij} is the j -th ($j = 1, \dots, r = 8$) observation in the i -th preparation ($i = 1, 2, \dots, 22$)

μ is the mean cell count across the population of *Preps* sampled

$\alpha_i \sim N(0, \sigma_{prep}^2)$ is a random variable representing *Prep* effect (deviation of mean cell count for j -th *Prep* from the population mean); σ_{prep}^2 represents the between-*Prep* variability.

$\varepsilon_{ij} \sim N(0, \sigma^2)$ is a random variable representing unexplained noise (deviation of cell count from the mean cell count for *Prep* i); σ^2 represents the within-*Prep* variability.

Then, coefficient of variation is calculated as,

$$CV(\%) = \frac{\sqrt{\sigma_{prep}^2 + \sigma^2}}{\hat{\mu}} \times 100\% \quad (2)$$

where values on the right hand side are estimated from the data.

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Method Comparison

CVs from the fitted regression model

Target	Hemocytometer	HiRes
7 x 10 ⁵ cells/mL	12.59%	10.52%
1.5 x 10 ⁶ cells/mL	11.59%	10.74%

- In each case, about 60-80% variation was explained by *Prep*.

HiRes is at least as good as Hemocytometer.

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Replicate Analysis

CVs from the regression model

- CVs are computed using the random effects model for different number of replicates

- For both target concentrations, the CV with $r = 2$ (-11%) was comparable to the CV obtained using $r = 8$ replicates; i.e. the gain in precision by increasing the number of replicates was minimal.

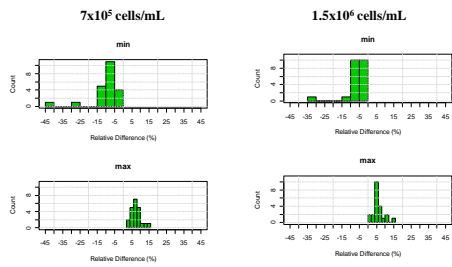
Target	Replicates	HiRes
7 x 10 ⁵ cells/mL	2	11.31%
	3	10.96%
	8	10.52%
1.5 x 10 ⁶ cells/mL	2	11.19%
	3	10.99%
	8	10.74%

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Sensitivity Analysis

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A relative difference was calculated using the worst case values (min or max) for each *Prep*, where,
- Old Reported Value = mean of 8 replicates for a given *Prep*
- New Reported Value = min or max of 8 replicates
- Relative Difference = $100\% \times (\text{New Reported Value} - \text{Old Reported Value}) / \text{New Reported Value}$



Summary of Results

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- There is a good agreement between the manual Hemacytometer versus the automated HiRes cell counting method with percent difference <1% regardless of cell line.
- Loss of precision in reducing the number of replicates from eight to two was acceptable.
- HiRes is a suitable alternative to the current manual counting. It is more efficient and provides improvement in ergonomics.

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Acknowledgements

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BT group

- Ingrid Lesaca
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NCB Group

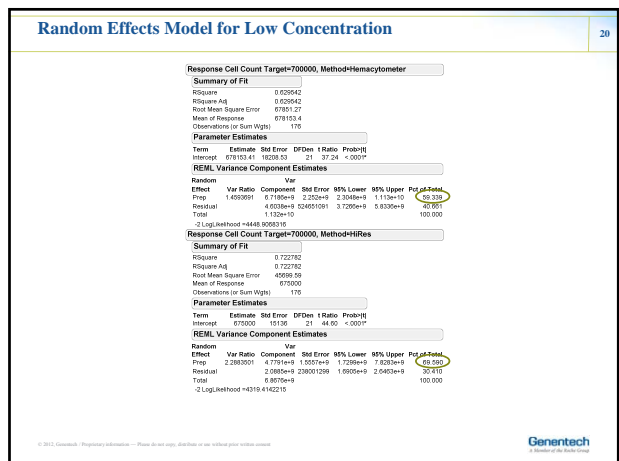
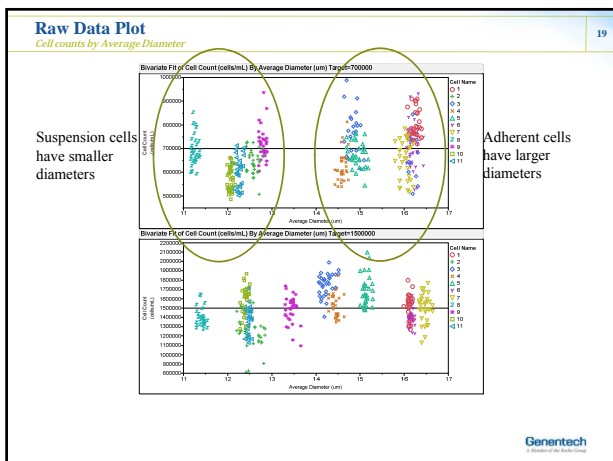
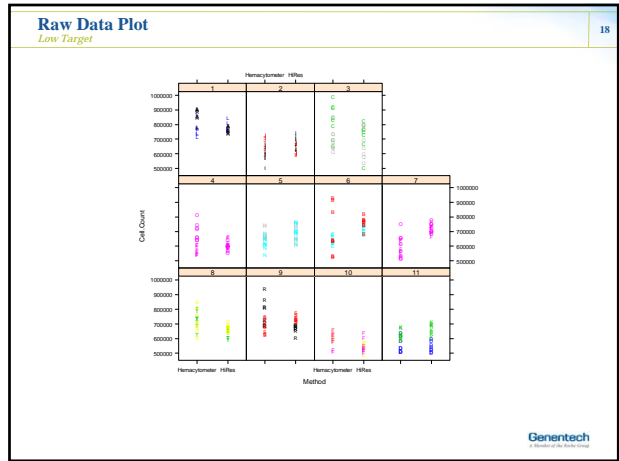
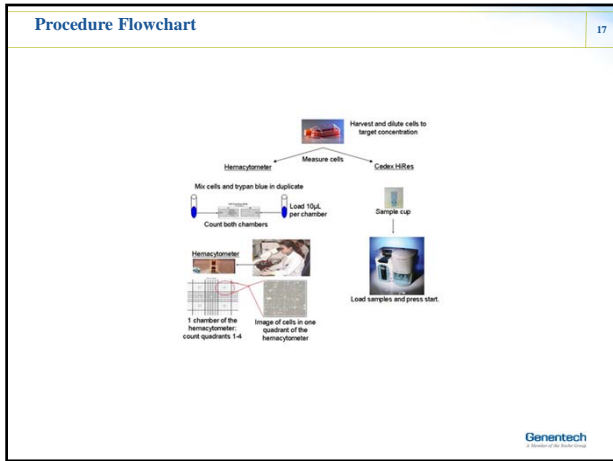
- Imola Fodor

Thanks!

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BACKUP

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Random Effects Model for High Concentration

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Response Cell Count Target=1500000, Method=Hemocytometer

Summary of Fit

R-Square 0.82573
 R-Square Adj 0.82573
 Root Mean Square Error 149972.6
 Mean of Response 1499722
 Observations (or Sum Wgts) 170

Parameter Estimates

Term	Estimate	Std Error	DF Den	t Ratio	Prob> t
Intercept	1499722.0	30900.47	21	49.17	<.0001*

REML Variance Component Estimates

Effect	Var Ratio	Component	Std Error	95% Lower	95% Upper	P(Chi-Square)
Prop	1.44112	2.705e+10	0.2785e+9	0.4635e+9	4.294e+10	20.035
Residual		1.819e+10	0.1869e+9	1.523e+10	2.432e+10	20.995
Total		4.654e+10				100.000

-2 Log Likelihood = 188.4705945

Response Cell Count Target=1500000, Method=HiRes

Summary of Fit

R-Square 0.82573
 R-Square Adj 0.82573
 Root Mean Square Error 75992.47
 Mean of Response 1499925
 Observations (or Sum Wgts) 170

Parameter Estimates

Term	Estimate	Std Error	DF Den	t Ratio	Prob> t
Intercept	1499925.0	34236.59	21	43.88	<.0001*

REML Variance Component Estimates

Effect	Var Ratio	Component	Std Error	95% Lower	95% Upper	P(Chi-Square)
Prop	4.2251193	2.505e+10	0.5095e+9	0.4467e+9	4.564e+10	20.982
Residual		0.8275e+10	0.7504e+9	4.788e+9	7.5114e+9	78.155
Total		3.097e+10				100.000

-2 Log Likelihood = 4514.303827