

UNIVERSITY OF CALIFORNIA

DEPARTMENT OF BACTERIOLOGY

Garber

Address Reply to:
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Dear Joshua,

This makes the second letter this week but the information herein may be worth your while. Streptomycin-resistance mutation rates are so low in my problem that the L&D graph is useless. Also, the methods of approximation are sort of cumbersome. I had our physicist prepare both a table and graph which permits rapid calculation of "a" from the second of L&D's methods. The table requires the following data:

r - mean number of mutant colonies
C - number of cultures
N - mean number of viable cells/ml

$X = 1.443 CNa$

| r | C | rC | X |
|------|-----|----|------|
| 0.01 | 100 | 1 | 1.78 |
| 0.02 | " | 2 | 2.35 |
| 0.03 | " | 3 | 2.88 |
| 0.04 | " | 4 | 3.33 |
| 0.05 | " | 5 | 3.80 |
| 0.06 | " | 6 | 4.20 |
| 0.07 | " | 7 | 4.60 |
| 0.08 | " | 8 | 5.00 |
| 0.09 | " | 9 | 5.40 |
| 0.10 | " | 10 | 5.80 |

We have altered the L&D graph so that "rC" and "X" represent the coordinates. They have separate curves and the the intercept with the specific curve (C) represents the desired value. In this way we could handle any value of "rC" and could extend the graph. Should you want a copy of the graph, I'll send one along.

Sincerely -
Ed