

This run implements an alternate model in order to understand the relation between the probability of lysogeny as a function the multiplicity of infection.

Theory: Dependent on the bacteria for survival, bacteriophages need to ensure a moderated approach to their growth so as to ensure a middle path between getting eliminated and eliminating the host bacteria. Numerically, if the Mol is consistently greater than 1, the phage population will eventually snowball and lead to the elimination of the host bacteria and vice versa. One possible coexistence strategy could be to move the environment towards an Mol of 1.

Approach: Instead of starting off with a constant initial Mol and following the progress to either of them is eliminated, we consider a single snapshot. The algorithm used has been elucidated below:

- for Mol values between 0 and 1 at intervals of 0.05
  - for Plyso values between 0 and 1 at intervals of 0.01
    - Run 1000 iterations of a single time step and note the resultant Mol in each case.
    - Calculate the average value of the Mol
  - Select the value of Plyso(=Plyso\_opt) that leads to the expected Mol value to be closest to 1
- Plot value of Plyso\_opt vs Mol

Shown below are plots comparing similar conditions in different environments and different conditions in the same environment.

Index:

1) alt\_run :  $\lambda_p = 1$ ,  $\lambda_b = 0.1$

2) alt\_run2 :  $\lambda_p = 2$ ,  $\lambda_b = 0.1$       3) alt\_run3 :  $\lambda_p = 2$ ,  $\lambda_b = 1.0$

4) alt\_run4 :  $\lambda_p = 3$ ,  $\lambda_b = 0.1$

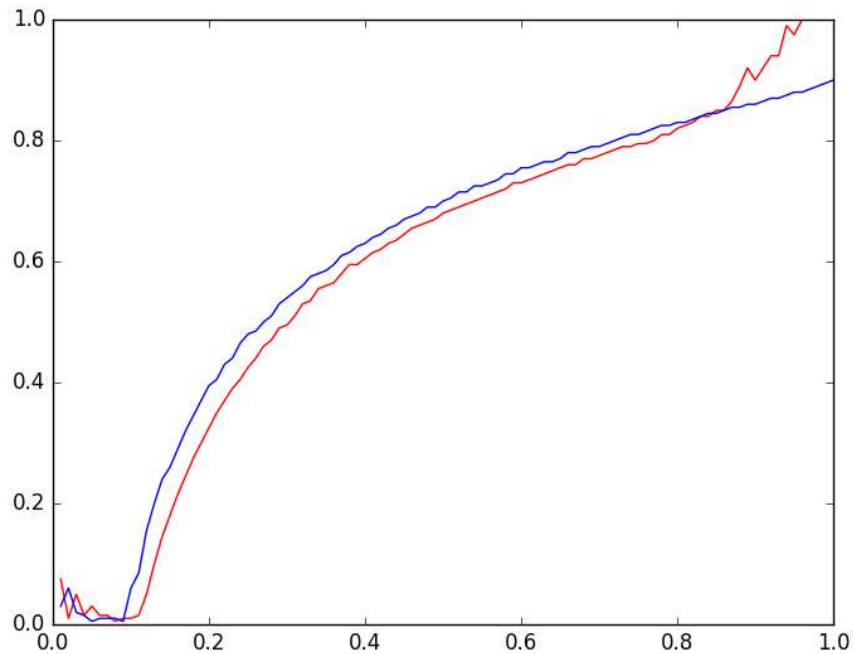
Thus, comparisons will be made among (1,2,4) and (2,3)

The following observations are made:

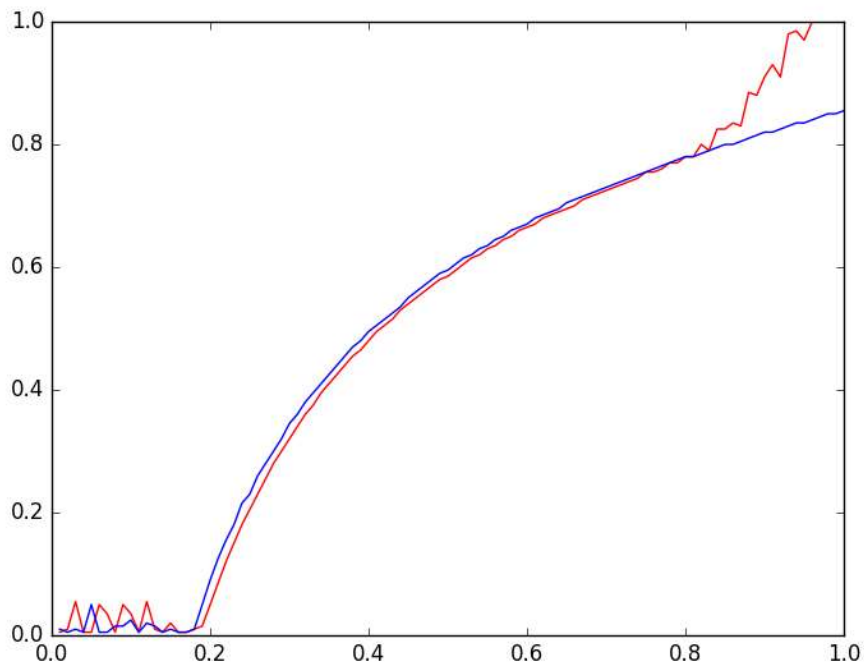
- For a given value of  $\lambda_b$  and  $\lambda_p$ ,

- for a bad phase environment ( $p_1 = 0.1$ ), bettering the bacterial environment ( $p_2 = 0.1$  to  $p_2 = 1.0$ ) does not change much

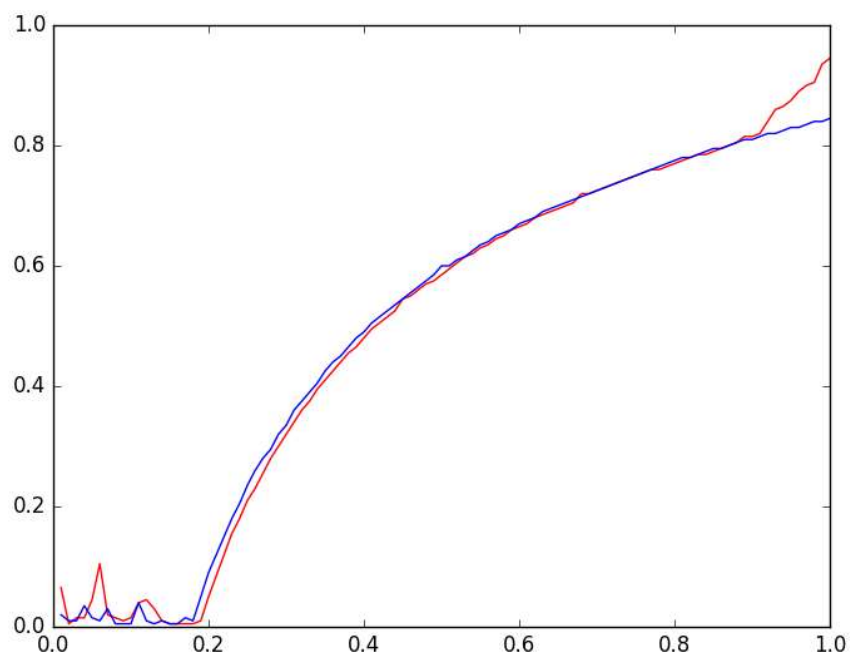
$r - \text{alt\_run}/p_1:0.1, p_2:0.1 = 0.589375$ ;  $b - \text{alt\_run}/p_1:0.1, p_2:1.0 = 0.6029$



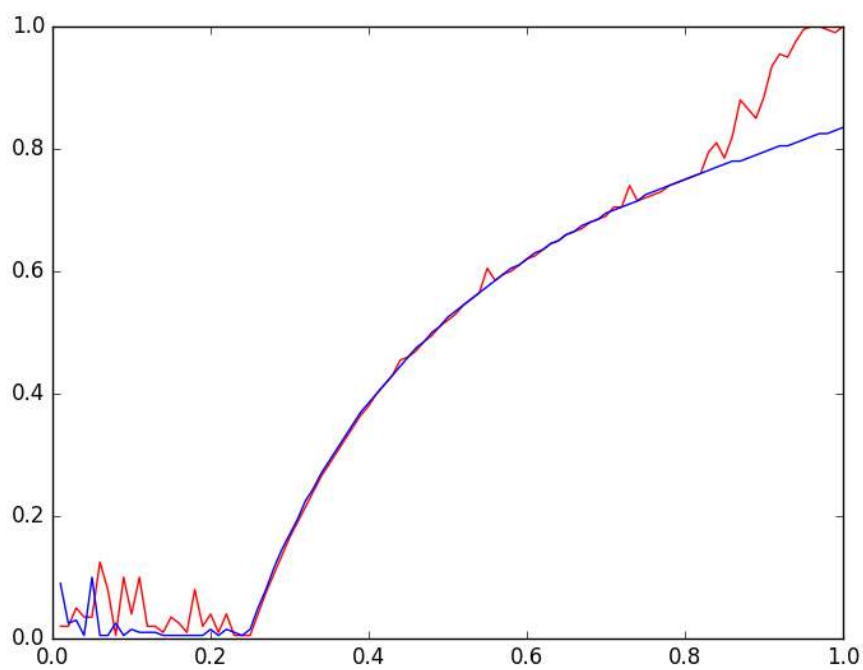
$r - \text{alt\_run2}/p_1:0.1, p_2:0.1 = 0.506175$ ;  $b - \text{alt\_run2}/p_1:0.1, p_2:1.0 = 0.495825$



r - alt\_run3/p1:0.1,p2:0.1= 0.49315;    b - alt\_run3/p1:0.1,p2:1.0= 0.492675

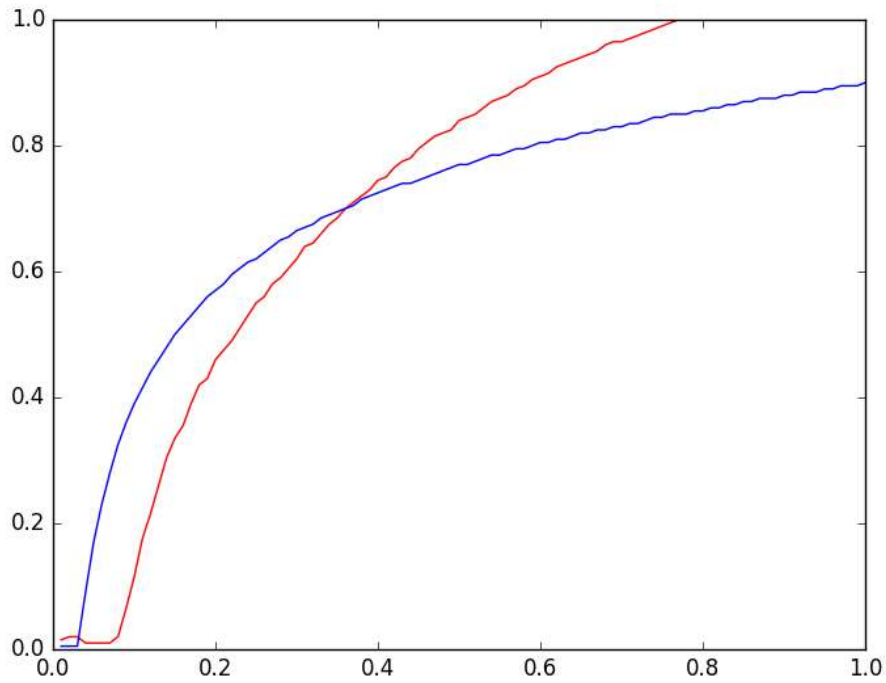


r - alt\_run4/p1:0.1,p2:0.1= 0.4619;    b - alt\_run4/p1:0.1,p2:1.0= 0.437325

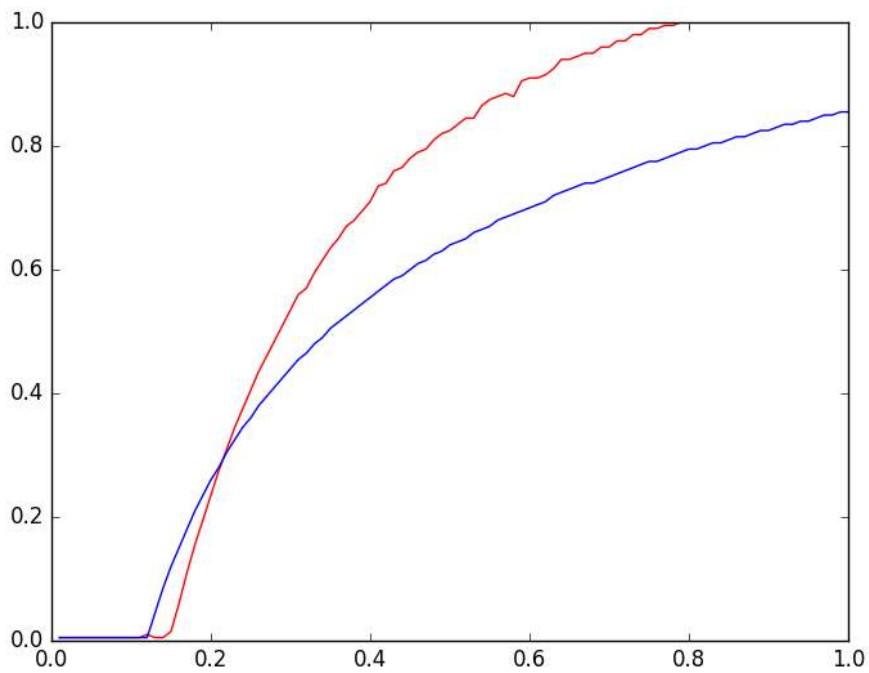


- for a good phage environment ( $p_1 = 1.0$ ), bettering the bacterial environment ( $p_2 = 0.1$  to  $p_2 = 1.0$ ) makes the curve flatter and smaller

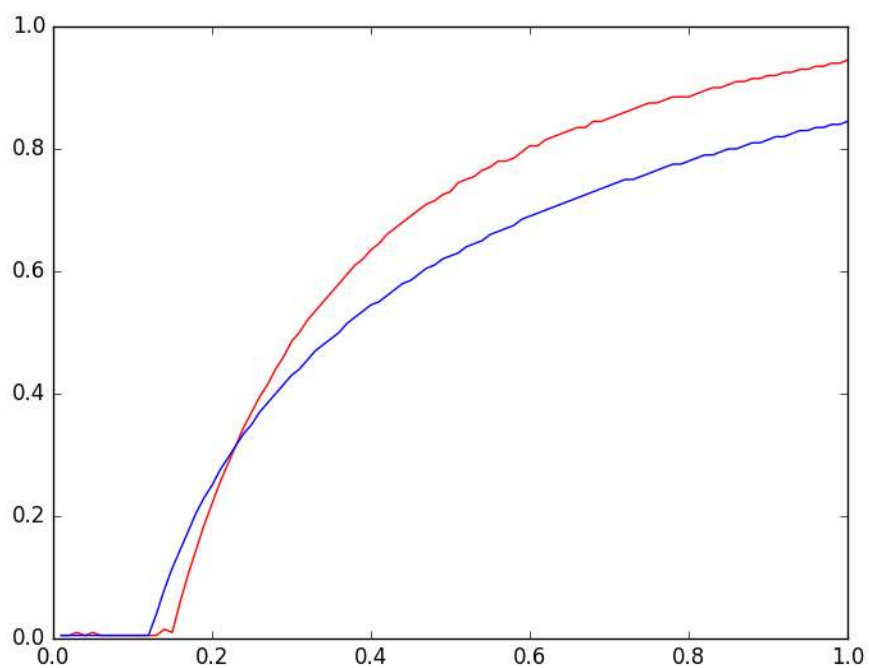
$r - \text{alt\_run}/p_1:1.0, p_2:0.1 = 0.716275$ ;  $b - \text{alt\_run}/p_1:1.0, p_2:1.0 = 0.692725$



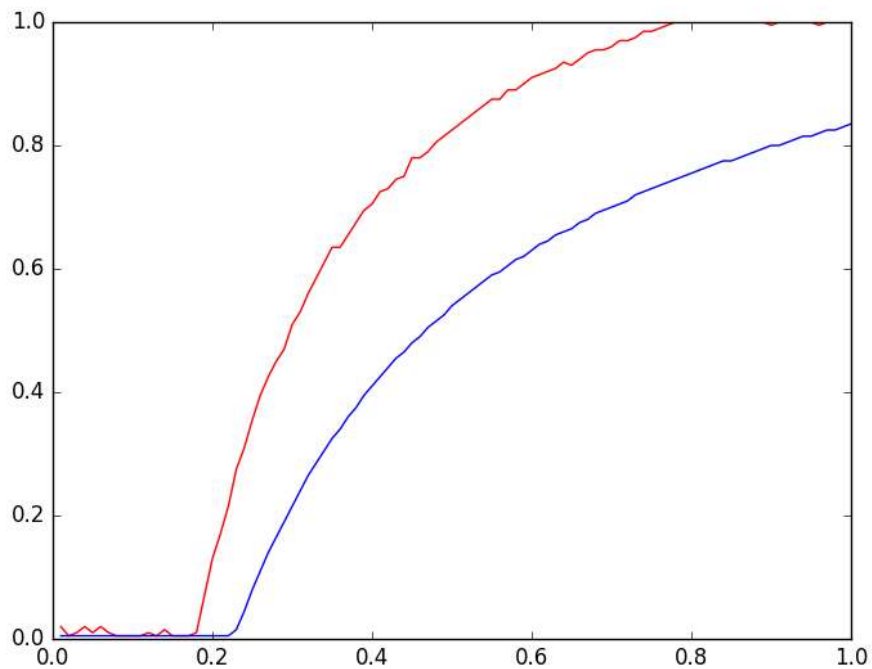
$r - \text{alt\_run2}/p_1:1.0, p_2:0.1 = 0.666675$ ;  $b - \text{alt\_run2}/p_1:1.0, p_2:1.0 = 0.54025$



r - alt\_run3/p1:1.0,p2:0.1= 0.59895; b - alt\_run3/p1:1.0,p2:1.0= 0.5303

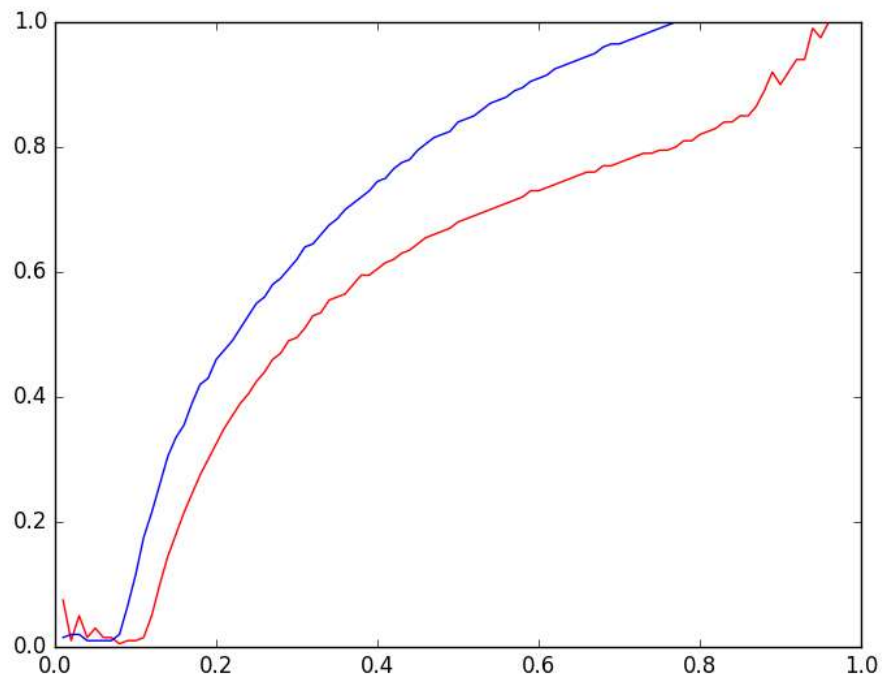


r - alt\_run4/p1:1.0,p2:0.1= 0.6545; b - alt\_run4/p1:1.0,p2:1.0= 0.447

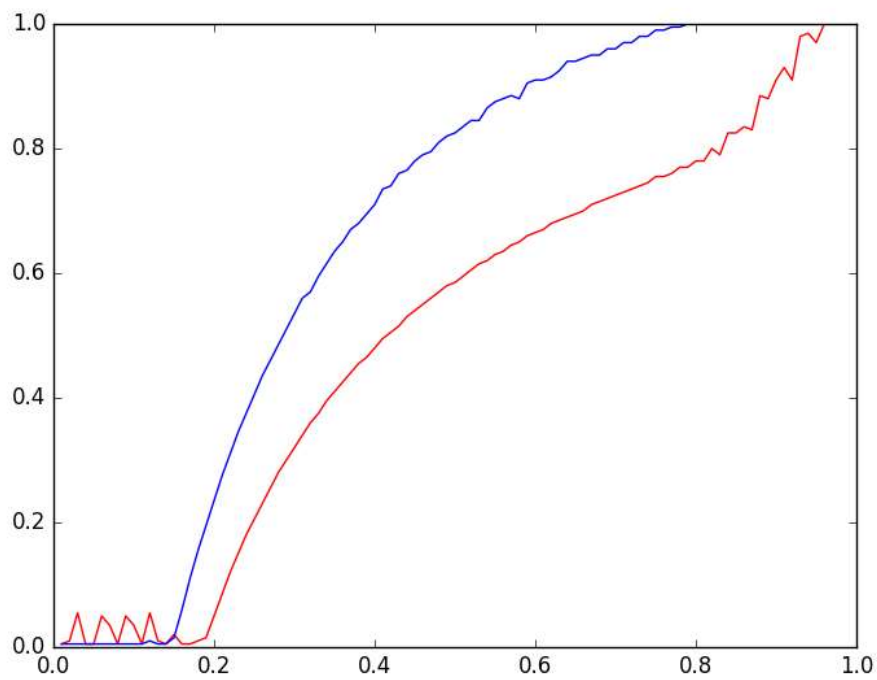


- for a bad bacterial environment ( $p_2 = 0.1$ ), bettering the phage environment ( $p_1 = 0.1$  to  $p_1 = 1.0$ ) leads to a larger curve

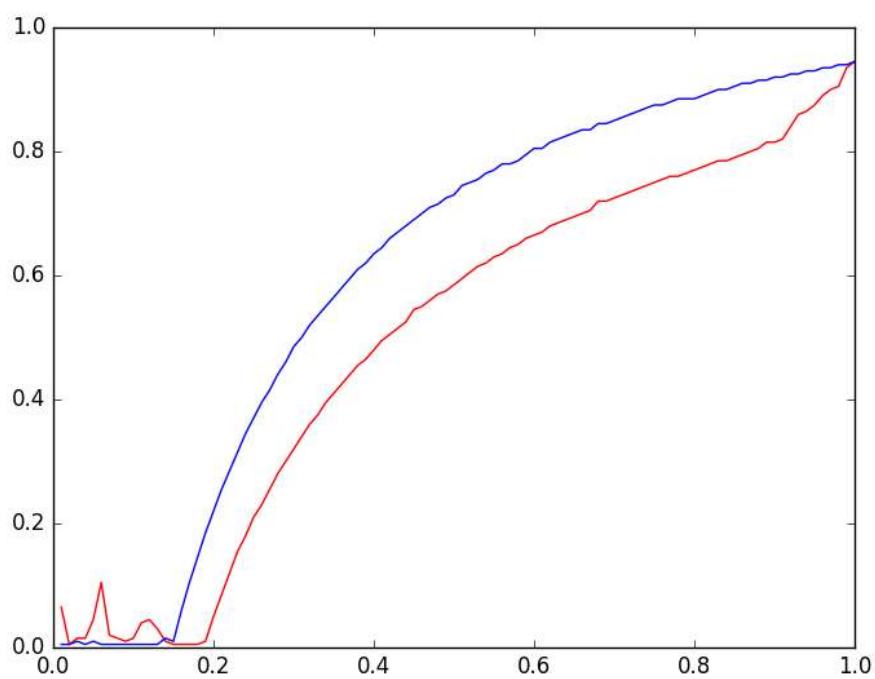
r - alt\_run/p1:0.1,p2:0.1= 0.589375; b - alt\_run/p1:1.0,p2:0.1= 0.716275



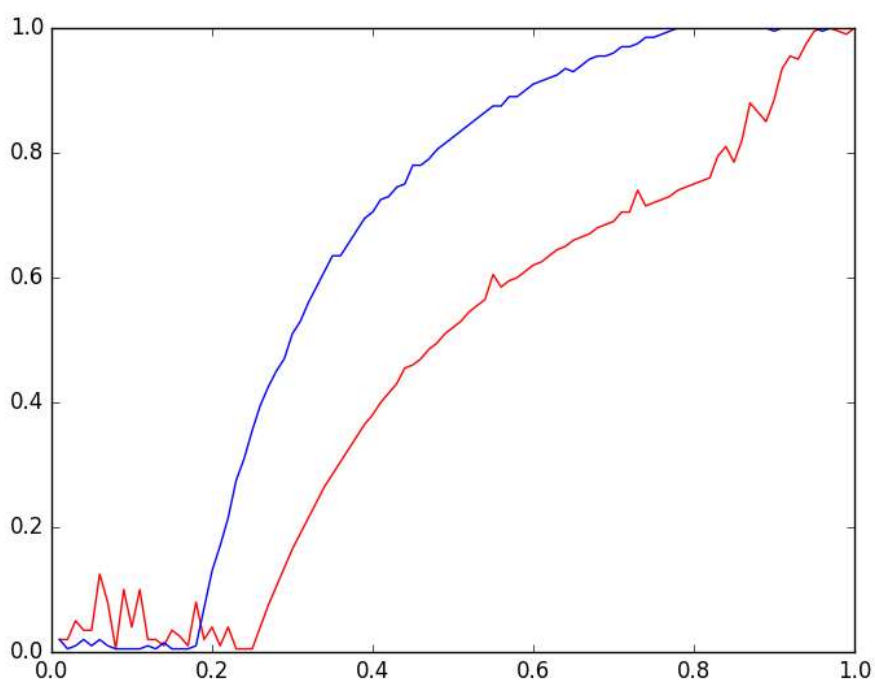
r - alt\_run2/p1:0.1,p2:0.1= 0.506175; b - alt\_run2/p1:1.0,p2:0.1= 0.666675



r - alt\_run3/p1:0.1,p2:0.1= 0.49315; b - alt\_run3/p1:1.0,p2:0.1= 0.59895

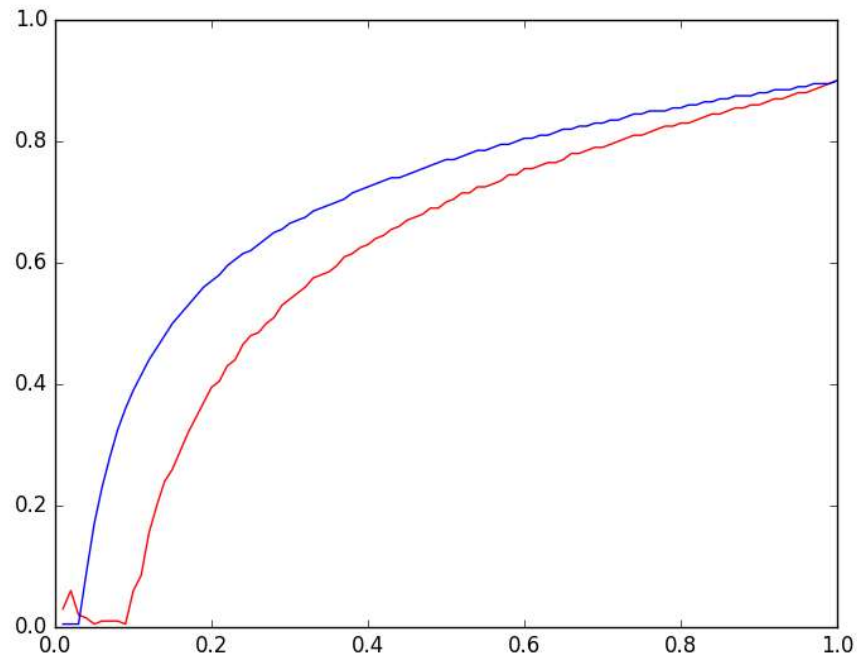


r - alt\_run4/p1:0.1,p2:0.1= 0.4619; b - alt\_run4/p1:1.0,p2:0.1= 0.6545

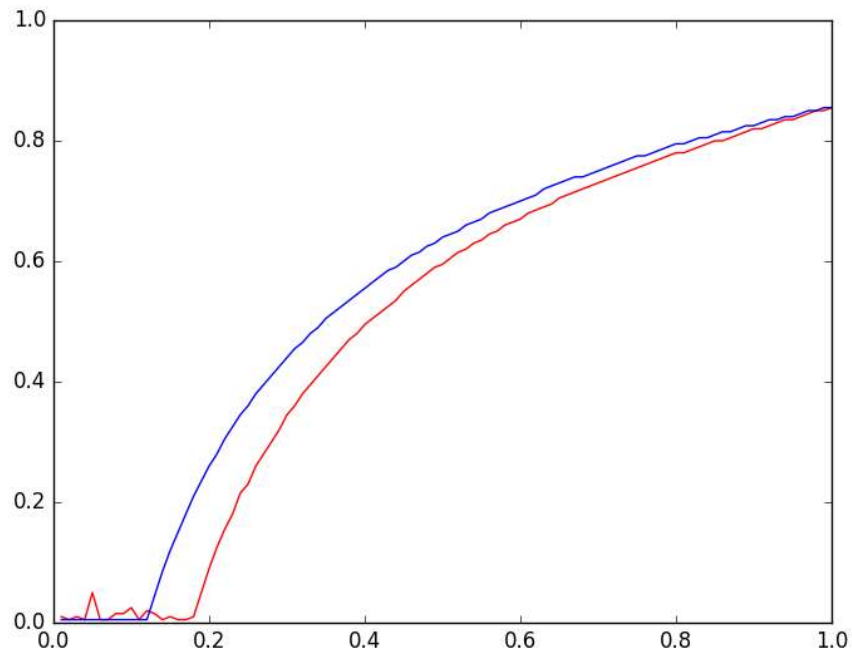


- for a good bacteria environment ( $p_1 = 1.0$ ), bettering the bacterial environment ( $p_2 = 0.1$  to  $p_2 = 1.0$ ) makes the curve slightly larger, with the increase decreasing with increase in  $\lambda_p$

r - alt\_run/p1:0.1,p2:1.0= 0.6029; b - alt\_run/p1:1.0,p2:1.0= 0.692725

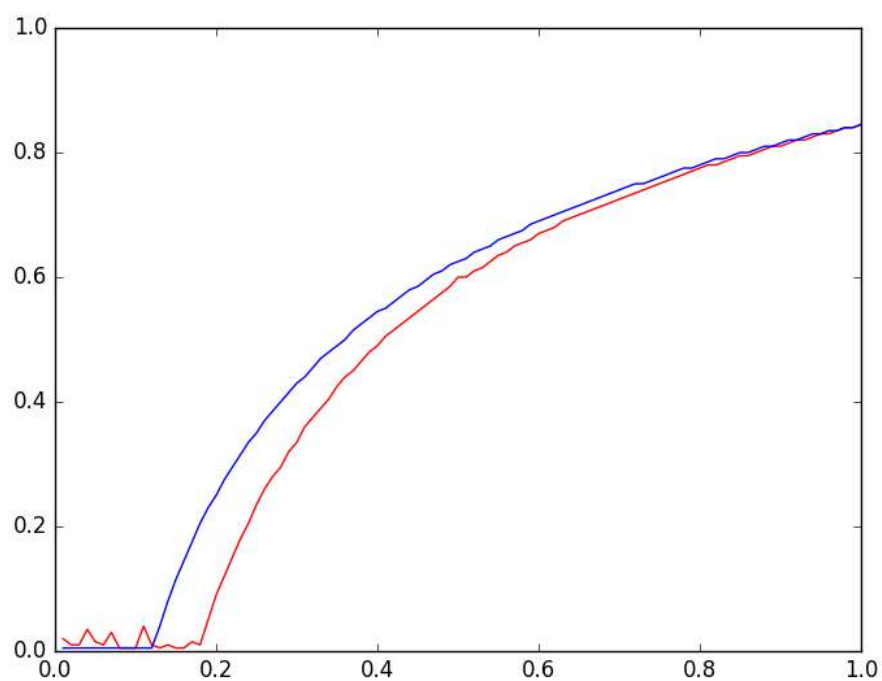


r - alt\_run2/p1:0.1,p2:1.0= 0.495825; b - alt\_run2/p1:1.0,p2:1.0= 0.54025

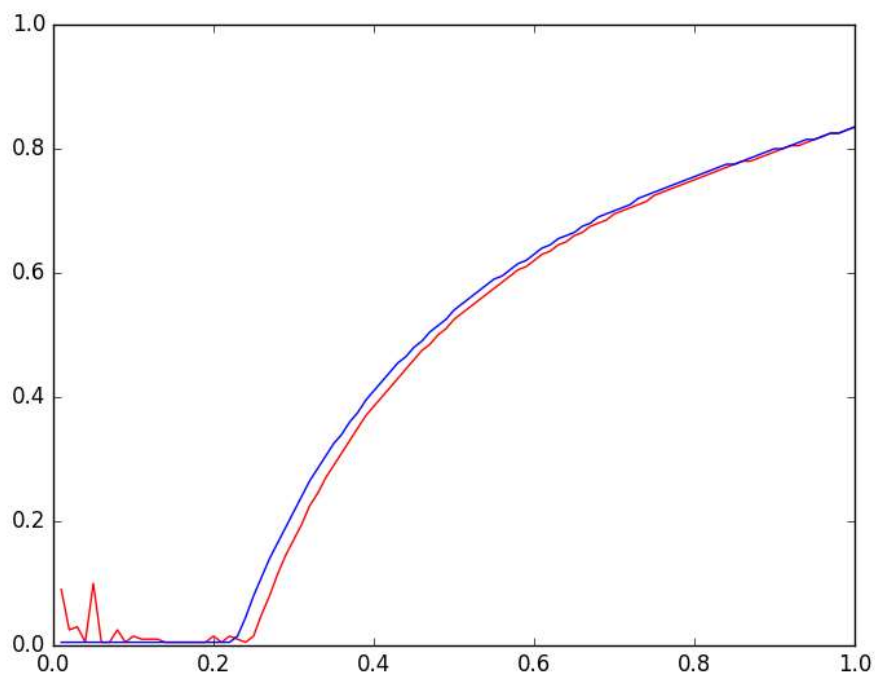




r - alt\_run3/p1:0.1,p2:1.0= 0.492675; b - alt\_run3/p1:1.0,p2:1.0= 0.5303

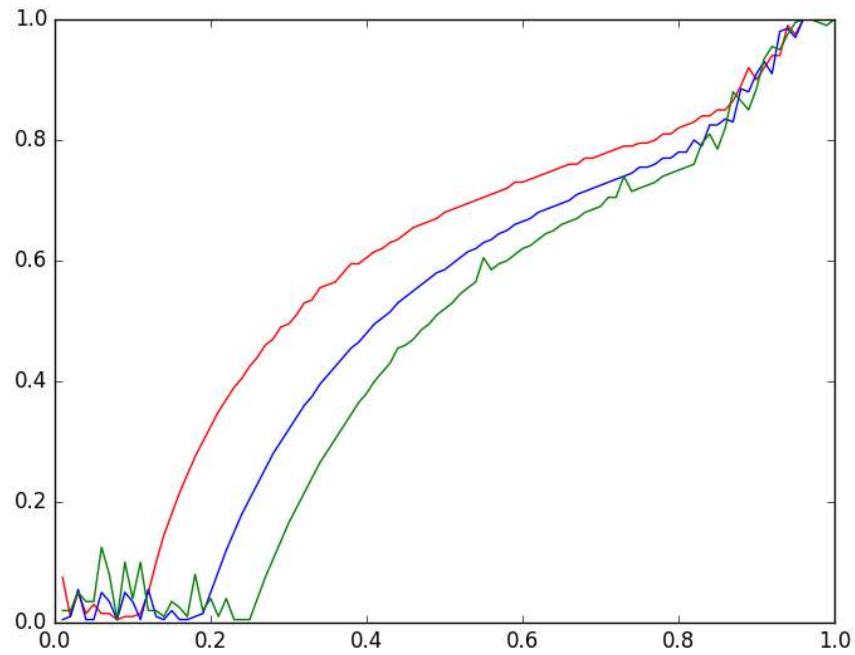


r - alt\_run4/p1:0.1,p2:1.0= 0.437325; b - alt\_run4/p1:1.0,p2:1.0= 0.447

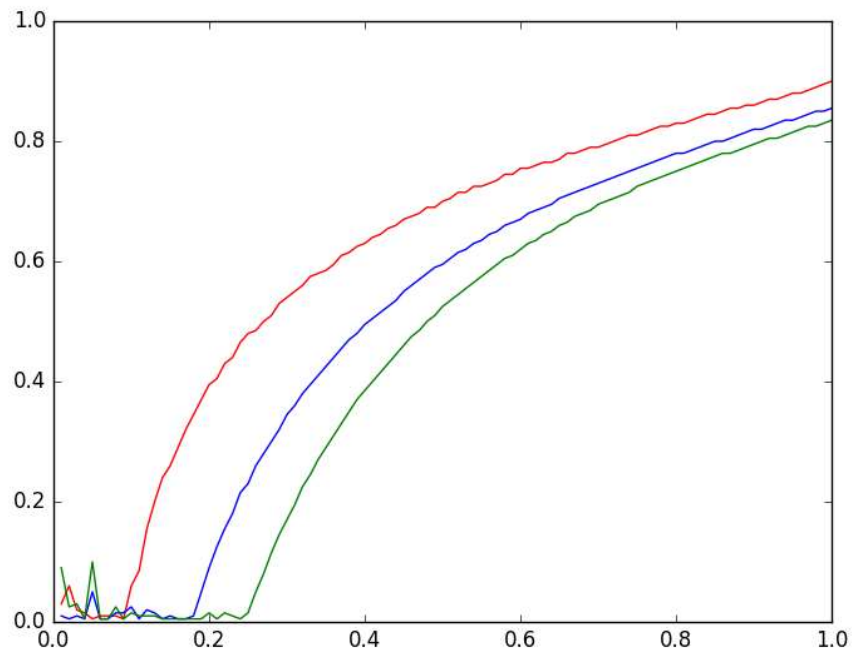


- Now, we consider the relation between environments with different  $\lambda_p$  but same values of  $p_1$  and  $p_2$ .  $\lambda_b$  is kept constant at 0.1,  $\lambda_p$  takes the values 1, 2 and 3. The curves decrease with increasing values of  $\lambda_p$  as seen below

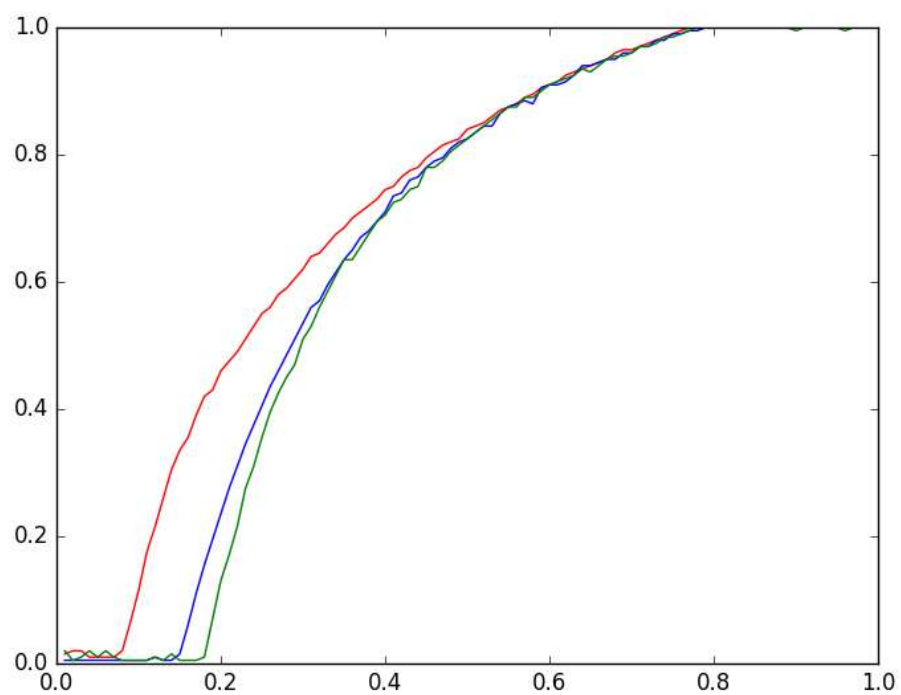
p10.1, p20.1: r - alt\_run= 0.589375; b - alt\_run2= 0.506175; g - alt\_run4= 0.506175



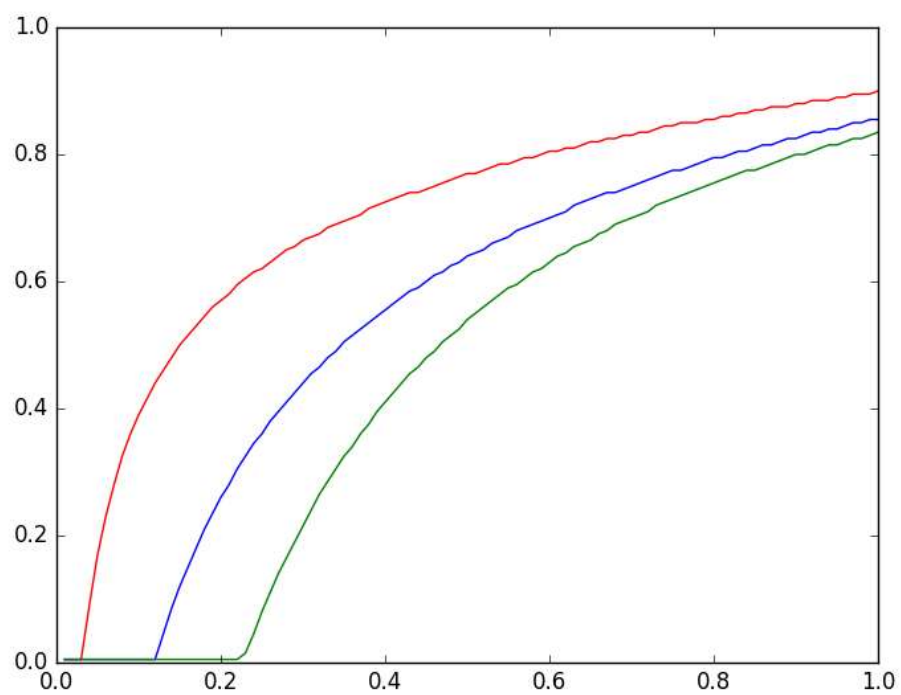
p10.1, p21.0: r - alt\_run= 0.6029; b - alt\_run2= 0.495825; g - alt\_run4= 0.495825



p11.0, p20.1: r - alt\_run= 0.716275; b - alt\_run2= 0.666675; g - alt\_run4= 0.666675

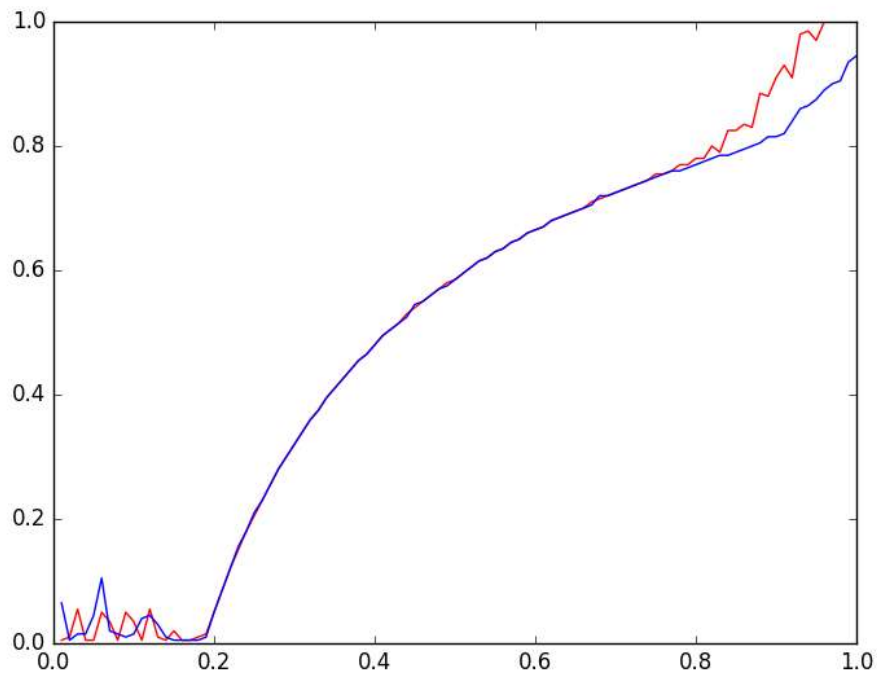


p11.0, p21.0: r - alt\_run= 0.692725; b - alt\_run2= 0.54025; g - alt\_run4= 0.54025

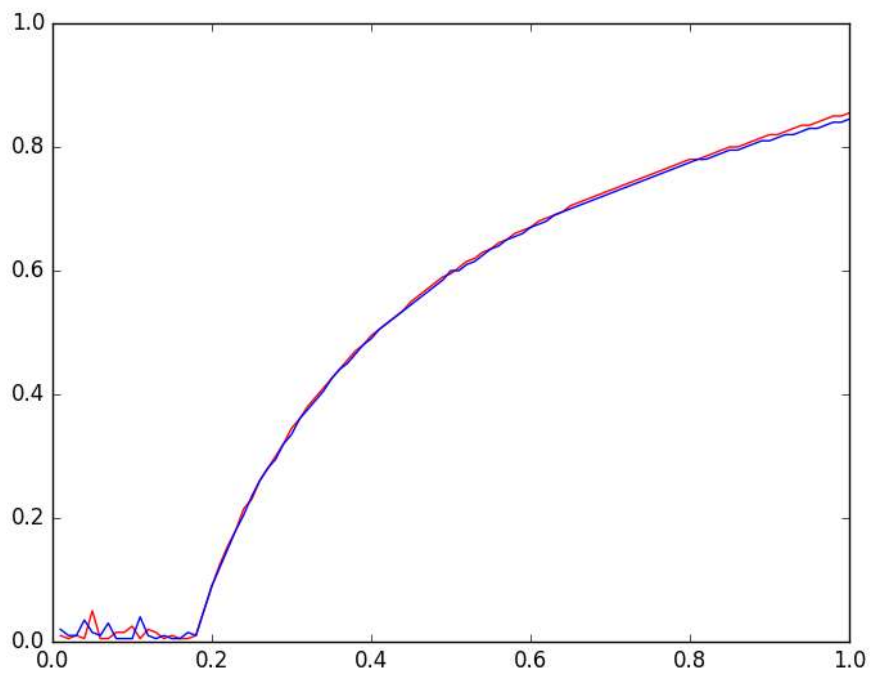


- In the next analysis, we compare the plots for different values of  $\lambda_b$  keeping  $\lambda_p$  constant. Surprisingly, changing the value of  $\lambda_b$  does not affect the graphs much

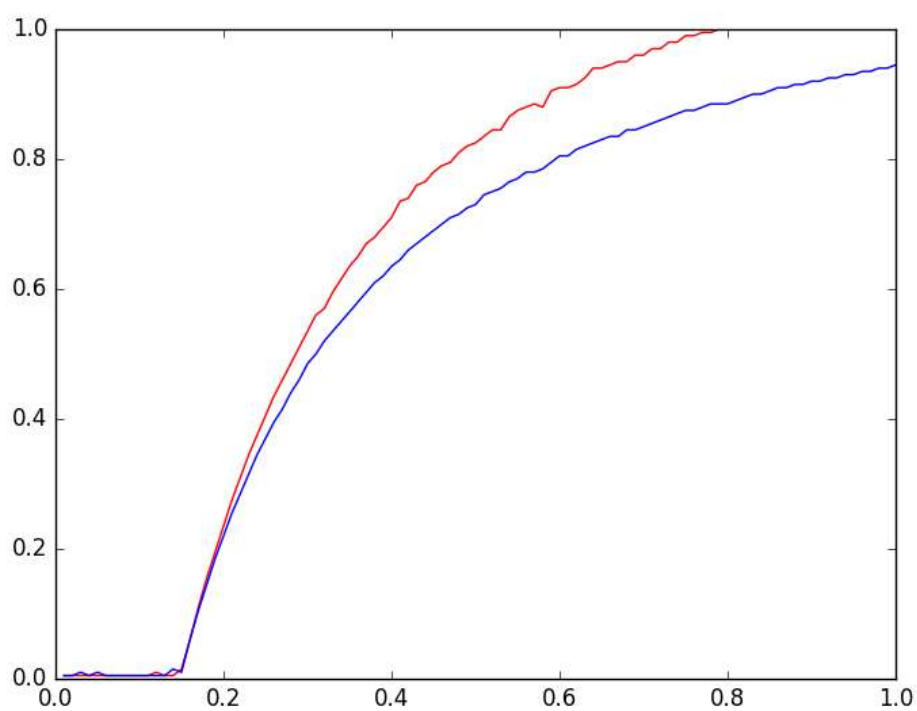
r - alt\_run2/p1:0.1,p2:0.1= 0.506175; b - alt\_run3/p1:0.1,p2:0.1= 0.49315



r - alt\_run2/p1:0.1,p2:1.0= 0.495825; b - alt\_run3/p1:0.1,p2:1.0= 0.492675



r - alt\_run2/p1:1.0,p2:0.1= 0.666675; b - alt\_run3/p1:1.0,p2:0.1= 0.59895



r - alt\_run2/p1:1.0,p2:1.0= 0.54025; b - alt\_run3/p1:1.0,p2:1.0= 0.5303

