Problem Chosen	2020 MCM/ICM	Team Control Number
A		0000012

Summary Sheet

Group Testing against Covid-19

Abstract

In response to question 1, we are required to make decisions about the total number of tests, false positive rate and false negative rate, establish a mathematical model, and perform calculations on the premise of determining the number of variable stages and the number of groups. First consider the total number of tests, false positive rate, and false negative rate. Secondly, consider the number of two variable stages and the group size.The diagnosis rate in Hong Kong is used to simulate the number of patients in the sample. The number of patients randomly distributed among different numbers of groups determines the total number of tests, so we use expectations to represent the average number of tests. Finally, we conduct a comprehensive gray correlation evaluation on the three decision goals. The optimal group detection program is finally obtained.the total number is 20,000, the prevalence rate is 0.001, the best grouping is: 20,000, the number of detections is: 1251, and the comprehensive score is: 0.027861071.

In response to question 2, the question asked us to test asymptomatic infected people and find a reasonable way to reduce the number of asymptomatic infected people in the population. The first step is to determine how to reduce the impact of asymptomatic infections on the population. Secondly, this article establishes the SIR model based on the infectious disease model. The model relies on the transformation relationship between asymptomatic people, positive people, and negative people. The length of time when the number of asymptomatic people is in a small state is used as the standard of the quality of the program. In the end, the parameter change ratios of the two programs were 30% and 60%. Observing the result images, we found that the time needed to implement the program is less than the original plan when there is no asymptomatic population before and after the implementation.

In response to question 3, we created a concentrated optimization group testing model. At the expense of the number of detection stages, we increased the groups of concentrated samples and reduced the total sample size to increase the infection rate of the total samples. Taking the case where the total number of samples is 30,000 people and the infection rate is 0.002 as an example, the expectation of the total number of detections of the concentrated optimization model is 1375.4, and the expectation of the total number of detections of the model in question one is 2624.3. It was found that the concentrated optimization method significantly improved the efficiency.

Keyword: **Principles of Probability and Statistics** **Grey relational model** **SIR infectious disease model** **Concentration model**

Contents

1. introduction

1.1 Background

The new crown epidemic has swept the world and has had a serious impact on the global economy and the normal lives of people around the world. In order to get the world back on track and **ease the global epidemic of the new crown epidemic**, testing is the most important part of it. Therefore, the problem of testing is It has become a difficulty and challenge that we have to face directly.

The biggest difficulty facing the detection problem is the limited amount of detection. Because this part is affected by the medical level, and the medical level is difficult to significantly improve in the short term, it is necessary to improve the model in the short term to **allow limited detection achieve the largest amount of coverage for the most people**.

Therefore, the question we face is, in the face of a large number of inspectors, how do we group them to improve the coverage and efficiency of the inspection volume? How should our detection methods be implemented to deal with various situations of the epidemic? Can the asymptomatic infection be effectively restricted? In response to these problems, we launched research and investigation.

1.2 Restatement

Part I: We are required to build a model to determine the number of stages and group size to calculate the total number of measurements and the false positive rate.
Part II: Make a reasonable detection model to make the coverage of the detection model wide and detect asymptomatic infections.
Part III: Provide and describe a new group detection scheme, and use specific values to explain why the detection efficiency will increase.
Part IV: Write a letter to the Department of Health of the Government of Hong Kong SAR and provide them with effective group testing strategy suggestions.

2. Assumption and Justification

- The error of the instrument and reagent is stable.
- If the samples are fused together, their properties will not change.
- Once someone is diagnosed as positive, they will be taken in by the hospital without transmission.
- People diagnosed as negative will not be restricted from activities.

3. Notations

symbol	Definition
N	group size
a	the number of each group

γ	infection rate
b	the number of infections
X	the total number of tests
c	there are infected persons in group
δ	the false positive rate
ε	the false negative rate
ρ	the probability of error of the experimental instrument
$y_i(k)$	the correlation coefficient
Z	the point of comprehensive method
r(t)	the negative population to the total population
P_J	the probability of each asymptomatic population
A	the number of samples that can be tested per day
M	the overall number of people. In other words
P_{S-I}	the probability of being tested positive
S	the asymptomatic population
k	the number of people in each group
x	the number of tests for each person
p	the probability of a positive test result
q	the probability of a negative test result
X_2	the remaining number of people
EX	the total number of detections
EX_2	the total number of detections of the remaining people

4. Group Testing Model

4.1 Problem Analysis

In order to improve the use efficiency under the same amount of resources, we consider using the group detection method. Question 1 requires us to make decisions about **the total number of tests, false-positive rates and false-negative rates,** establish mathematical models, and perform preliminary calculations and tests based on the number of stages and the number of groups in each stage[1].

First consider the **decision-making goals**. In order to perform the detection of the coronavirus more quickly, we must consider the three factors of the total number of tests, the false positive rate, and the false negative rate. Regarding the total number of detections, the smaller the total number of detections, the less resources can be saved, and more people can be tested under the premise of limited resources. Regarding the false-positive rate, that is, the percentage of negatives judged to be positives. As the grouped samples are positive, all members of the reorganization are determined to be positive, and further testing is performed until a positive individual is determined. The lower the false positive rate, the lower it can be Isolate the number of people to achieve efficient use of resources. Regarding the false-negative rate, that is, the percentage of positive being judged as negative, that is, regarding the error of the experimental instrument, reducing the number of tests can control

the error of the experiment.

Second, consider two variables-**the number of stages and the group size of each stage**. The number of stages should be considered in light of actual conditions. We first look up relevant information to get the upper limit of the daily test phase as the value range of the number of phase variables. For the group size of each stage, the overall sample should be tested in groups. Since each sample is united, it is inseparable. For the convenience of calculation, we consider the factor of the test sample as the number of groups.

Third, we use statistical probability samples to detect relevant knowledge, and **use the characteristics of the overall sample to estimate part of the sample**. We use the diagnosis rate in Hong Kong to estimate the number of patients in the sample. Since the number of patients will be randomly distributed in each group sample, the number of patients will be randomly distributed among different numbers of groups to determine the total number of tests, so we use expectations to represent the average number of tests. Using the principle of random sampling, through multiple experiments, the total number of tests stabilized.

Finally, we conduct a comprehensive evaluation of the three decision-making goals. Because there are connections between the three decision-making goals, we use **gray correlation** to obtain comprehensive indicators. By adjusting the number of stages, the number of groups and the number of samples in the group to reduce the comprehensive evaluation indicators, the optimal group detection program is finally obtained[3].

4.2 Model Design

4.2.1variables

The number of steps(steps)

Official information shows that the duration of a nucleic acid test to detect a sample is 6 hours, and the normal working time of a hospital clinic is 10 hours. Assuming that the hospital has a shift system during the epidemic, it is reasonable to consider that we believe that the detection cycle that can be performed in a day is two times, that is, the value range of the number of stages is 1-2. Since the number of stages equals to 1 means that all samples will be tested once, so we mainly consider the case where the number of stages is 2.

Group size (N)

The group size of each stage (denoted by N) refers to the total number of samples that need to be tested at that stage. We want to group the overall sample for testing. Considering that each sample is a whole and cannot be divided, for the convenience of calculation, we only consider the case where the number of groups is the factor of the total number of samples. Where a represents the number of groups in the second stage, n represents the number of groups in the second stage, and the relationship is as follows:

$$N = na \tag{1}$$

4.2.2 Three decision goals

Detection times

The calculation steps of the number of detections are as follows:

1. the determination the number of infections in the total sample

As the number of infected persons in the sample is different, the probability that the infected persons will be randomly assigned to different groups will be different, resulting in different total number of tests. We set the infection rate as γ, and the number of infections is:

$$b = \gamma N \tag{2}$$

2. the consideration the total number of tests whose number of stages is 2

Consider the case where the number of stages is 2. For the first stage, first divide the total number of samples in the first stage into groups a, where a is a factor of N. Therefore, the number of detections in the first stage is a. Since the number of infected people is randomly allocated to different groups, for each group, as long as there is one infected sample in the group, it means that the group is infected. The random distribution example diagram is as follows:

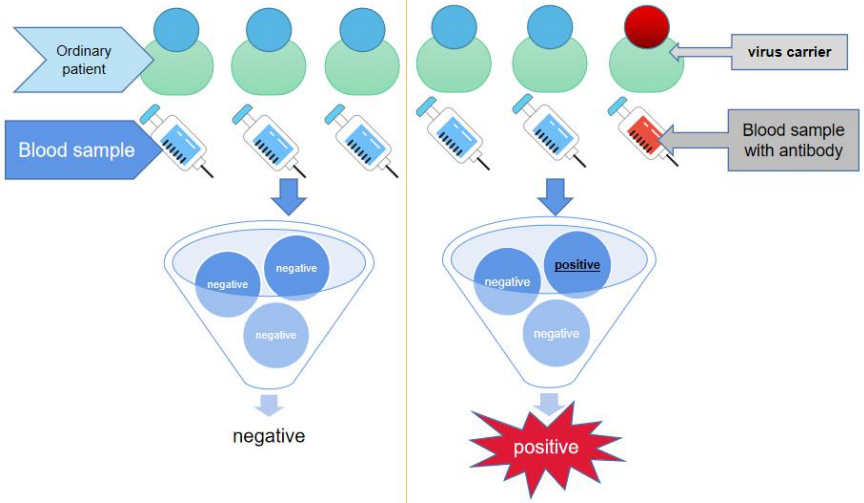


Figure 1: the random distribution example diagram

Then we discussed the number of groups with infected samples in the group after grouping. If the number of infected persons b is greater than the number of groups a, at most a group will be positive; if the number of infected persons b is less than the number of group a, then at most b groups will be positive[2].

Assuming that there are infected persons in group a and group c, the calculation formula for the total number of tests is as follows:

$$X = a + cn \tag{3}$$

Because of the difference in c, the number of detections is different, and the number of infected people will be randomly assigned to different numbers of groups. From the meaning of the question, the number of infected persons in a group indicates that all members of the group are infected. The next step is to check until whether a single sample is infected. Therefore, we only need to consider the number of infected groups, so we refer to the probability of fakes. The principle of counterfeit probability is that **there are some fake coins in a pile of coins**. **The quality of the fake coins is lower than that of the real coins**. The pile of coins is randomly grouped. Among them, there are groups with fake coins whose quality is less than that of all real coins. There is a probability $P(Y = c)$ of the number of fake coin groups. Using the probability to find the expected number of detections indicates the average number of detections in different groups. The expected formula is as follows[4]:

$$EX_1 = \begin{cases} \sum_{i=1}^{a} XP(Y = i), (b \geq a) \\ \sum_{i=1}^{b} XP(Y = i), (b < a) \end{cases} \tag{4}$$

Therefore, we have to find the grouping method with the smallest expectation as the

optimal group detection scheme with stage 2.

False-positive rate

Regarding the false positive rate[1], that is, the percentage of negative being judged to be positive, because the grouped samples are positive, all members of the reorganization are determined to be positive, and further testing is performed until a positive individual is determined. The lower the false positive rate, the lower it can be reduced Number of people in quarantine. Suppose the false positive rate is δ, the calculation formula is:

$$\delta = \frac{cn - \lambda N}{N} \tag{5}$$

False-negative rate

Regarding the false negative rate[3], that is, the percentage of positives that are judged as negative, that is, the error of the experimental instrument. Let the probability of error of the experimental instrument be ρ, and the calculation formula of the false negative rate is:

$$\varepsilon = \rho * EX \tag{6}$$

3. comprehensive evaluation model

From the perspective of decision-making goals, we chose the total number of tests, false positive rate, and false negative rate as indicators to evaluate the pros and cons of group detection methods. Since the various indicators are related to each other but have properties that reflect different aspects, a scientific and reasonable comprehensive evaluation model must be established. We choose the gray correlation model. The specific model is as follows:

Determine the overall sample size. Different groups will get different total number of tests, false positive rates, and false negative rates, as shown in the following table:

The number of groups	The times of tests	False-positive rate	False-negative rate
a_1	x_{11}	x_{12}	x_{13}
...	...	...	...
a_n	x_{n1}	δ_{n2}	x_{n3}

Figure 2: the determined value

Select the parent index

In process 2, we find the formula about the total number of tests, false positive rate, and false negative rate. We can find that the false negative rate and false positive rate are related to the total number of tests, and the total number of tests most intuitively reflects the pros and cons of group detection , So choose the parent index of the total number of detections.

Calculate the correlation coefficient

Define the correlation coefficient $y_i(k)$ between the parent index ZB_0 and ZB_i at the kth point as:

$$y_i(k) = \frac{a + b\rho}{\Delta_i(k) + b\rho} \tag{7}$$

In which $\Delta_i(k)$can be calculated as follow:

$$\Delta_i(k) = |x_{ki} - x_{k0}|, i = 1,2, \ldots, m, k = 1,2, \ldots, n \tag{8}$$

And the formula of a and b are:

$$a = \min_{1 \ll k \ll n} \min_{1 \ll i \ll m} \Delta_i(k) \tag{9}$$

$$b = \max_{1\ll k\ll n}\ \max_{1\ll i\ll m} \Delta_i(k) \tag{10}$$

In which the range of ρ is $(0,1)$,and we take $\rho = 0.5$.

Calculate the degree of relevance

$$r_i = \frac{1}{n}\sum_{k=1}^{n} y_i(k)\,, i = 1,2,\ldots,m \tag{11}$$

Build a comprehensive evaluation model

From the relevance obtained in the previous step, calculate the weight of each indicator:

$$r_j^{'} = \frac{r_j}{r_1+r_2+r_3} \tag{12}$$

As the weight of each indicator, a comprehensive indicator Z is obtained.

$$Z = r_1^{'}x_{k1} + r_2^{'}x_{k2} + r_3^{'}x_{k3} \tag{13}$$

Finally, the grouping number corresponding to the smallest comprehensive index is the grouping method with the best overall sample number N.

4.3 Model Solution

Regarding the value of the infection rate, we use the characteristics of the overall sample to estimate part of the sample, that is to say, use the confirmed rate in Hong Kong to estimate the number of patients in the sample. According to data from the National Bureau of Statistics, there are currently 70,000 infected people in Hong Kong, of which the total population of Hong Kong is 7,345,670. The infection rate is one in a thousand, so we take A=0.001.

When calculating the number of tests, since the probability of a group being positive after grouping is easy to calculate, as long as there are positive individuals in the group, it means that the group is positive. It is too complicated to calculate the probability of how many groups are positive samples, but they must exist, so we choose a large Random simulation gets the probability and expectation. Below we show the image of random times and expectation:

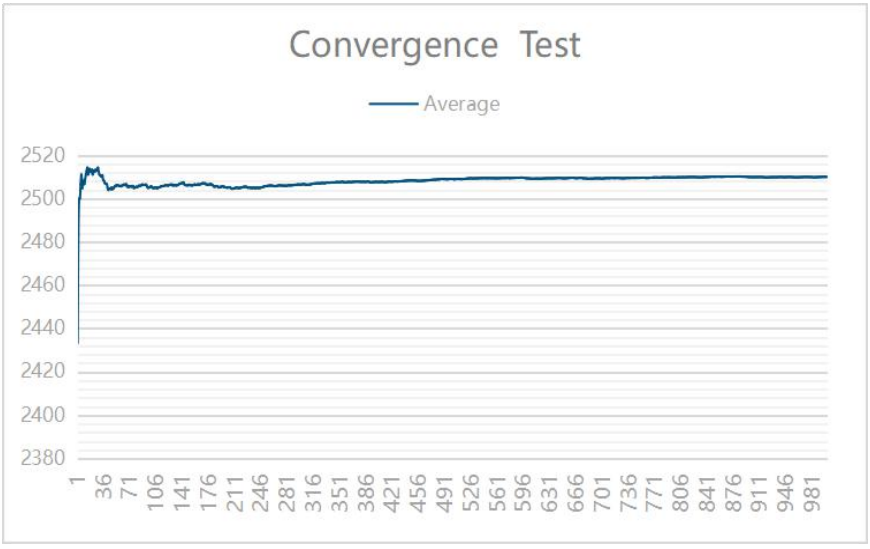


Figure 3:the image of random times and expectation

From the image, when the random number reaches 350 times, the expectation of the detection times basically tends to be the same, fluctuates in a very small range. In order to

reduce the calculation error, we take the random number of 10000 when calculating the expected number of detections.

Calculate the values under different groups by using the formula of false positive rate and false negative rate in the model. Here is an example where the total number of samples is 20,000, and the data values in different grouping situations are shown in the following table:

The number of infected people	The times of tests	False-positive rate	False-negative rate
20	1251.763979	0.031328	0.000285
40	1764.176201	0.042819	0.000396
100	2772.505343	0.065685	0.000624
200	3891.00172	0.08849	0.00087

Figure 4: the data values in different grouping situations

According to the gray correlation model, the correlation between the three indicators and the parent indicator is shown in the following table:

The number of infected people	The times of tests	False-positive rate	False-negative rate
correlation	0.999999999	0.910954924	0.910954837

Figure 5:the three indicators and the parent indicator

The weight of each indicator is shown in the following table:

The number of infected people	The times of tests	False-positive rate	False-negative rate
Weight	0.745446	0.139456	0.115098

Figure 6: the weight of each indicator

The comprehensive evaluation indicators are:

$$Z = r_1' x_{k1} + r_2' x_{k2} + r_3' x_{k3} \quad (14)$$

The smaller the comprehensive evaluation index value, the more efficient the grouping scheme.

The comprehensive indicators calculated for each group are shown in the following table:

The number of groups	The comprehensive indicator	Rank
1020	0.972138929	1
1024	0.97210998	2
1071	0.972096827	3

Figure 7: the comprehensive indicators calculated for each group

The optimal group with a population of 20,000 is obtained as 200 groups.

Repeat the above steps to get the optimal grouping scheme in the case of different sample numbers. The results are shown in the following table:

Total detection	Prevalence	Number of patients	Number of groups	Time of tests	False-positive rate	False-negative rate	score
4000	20	0.005	271.2	553.954888	0.065689	0.000624	0.054968158
4000	40	0.01	379.8	777.215	0.089354	0.000877	0.070881357

				848			
10000	20	0.002	439.8	881.818882	0.042202	0.00039	0.037706762
10000	100	0.01	935.6	1944.595555	0.0909	0.000891	0.071062632
20000	20	0.001	605.2	1251.763979	0.031328	0.000285	0.027861071
20000	40	0.002	867.8	1764.176201	0.042819	0.000396	0.03767999
40000	40	0.001	1212.5	2503.446565	0.031328	0.000285	0.02438544

Figure 8: the result of different samples

4.4 Sensitivity Analysis

In the above model, we use the diagnosis rate in Hong Kong as the prevalence rate in the test sample, but the prevalence rate will change for different regions. In areas with high epidemics, the prevalence rate will increase; in safe areas, the prevalence rate is relatively small. In order to cope with the detection of different areas, we adjusted the infection rate to obtain the optimal grouping strategy corresponding to different infection rates. Below we have done a sensitivity analysis for the overall sample of 4000, 10000 and 20000

The following table shows the grouping strategies corresponding to the total number of people tested for 4000 and different infection rates:

Total detection	Prevalence	Number of patients	Number of groups	Time of tests	False-positive rate	False-negative rate	score
4000	4	0.001	122.6	250.35529	0.030939	0.000282	0.01545349
4000	10	0.0025	198	393.948366	0.046487	0.000433	0.031818349
4000	20	0.005	271.2	553.954888	0.065689	0.000624	0.054968158
4000	40	0.01	379.8	777.215848	0.089354	0.000877	0.070881357

Figure 9: the total number of people and different infection rates

When the total number of people tested is 10,000, the results are as follows:

Total detection	Prevalence	Number of patients	Number of groups	Time of tests	False-positive rate	False-negative rate	score
10000	20	0.002	439.8	881.818882	0.042202	0.00039	0.037706762
10000	50	0.005	683.2	1385.71	0.065251	0.00062	0.054973315

				4887			
10000	100	0.01	935.6	1944.595555	0.0909	0.000891	0.071062632

Figure 10: the total number of people and different infection rates

5. Identical Model

5.1 Problem Analysis

Question two requires us to detect asymptomatic infections and establish a mathematical model to find a reasonable way to **reduce the number of asymptomatic infections in the population**.

First of all, we must determine the method to reduce the impact of asymptomatic infections on the population. By consulting the literature, there are two ways to reduce the impact of asymptomatic infections on the population. The first is to **carry out large-scale nucleic acid testing** to find asymptomatic populations. Individuals carrying the new coronavirus in China; the other is **a policy of restricting travel for residents who have not been checked**.

Secondly, in order to integrate the above two solutions, this article considers dividing the entire population into asymptomatic people, confirming that the virus-carrying people and confirming that the healthy people who do not carry the virus, based on the SIR model in the infectious disease model, establishes a model for dealing with asymptomatic infections , The model relies on the **transformational relationship** between the three populations. The parameters in the transformation relationship were changed to simulate the control and treatment of asymptomatic people in the two programs, and the length of time when the number of asymptomatic people was in a small state was used as the standard of the quality of the program.

Finally, the parameter change ratios of the two programs are 30% and 60%. The larger the parameter change ratio, the wider the impact of the program. Therefore, compare the effects of different program strengths before and after the implementation, and explain how we should deal with this effect. Asymptomatic infections continue to spread the epidemic.

5.2 Problem Model

By consulting the literature, there are two ways to reduce the impact of asymptomatic infection on the population[5]:

1. Conduct a large-scale nucleic acid test to find individuals who carry the new coronavirus among asymptomatic people.

2. Implement a travel restriction policy for residents who have not been inspected.

5.2.1 SIR-based asymptomatic transmission model

Before establishing the model, we first determine the type of population and the probability of asymptomatic population receiving nucleic acid testing. The specific discussion is as follows[8]:

Crowd type

In the spread of the epidemic, different types of people have different types of effects on the spread of the epidemic. After consulting the information, we found that the model can be compared to the SIR model, in which the population is divided into susceptible, infected, and cured. Similarly, we divide the population into three parts: S, I, and R, the specific meanings are as follows:

symbol	meaning	Abbreviation
S	Asymptomatic people (infected and healthy)	Asymptomatic
I	People diagnosed as positive	positive
R	People diagnosed as negative	negative

Figure 11: the specific meanings

The proportion of the negative population to the total population is r(t), and the initial value is recorded as $s(0) = s_0$, $i(0) = i_0$, $r(0) = r_0$. Since the total population remains unchanged, the ratio of the three populations obviously has the following formula:

$$s(t) + i(t) + r(t) = 1 \tag{15}$$

The probability of asymptomatic people receiving nucleic acid testing

When the government conducts large-scale nucleic acid testing, the probability of each asymptomatic population being tested is[6]:

$$P_J = \frac{A}{M - i_0 i(t) - r_0 r(t)} \tag{16}$$

Where A represents the number of samples that can be tested per day, and M represents the overall number of people. In other words, the probability of the above formula is the proportion of the number of detectable samples in the total asymptomatic population. If the amount of testing is expanded, it means that A increases, and the probability of each asymptomatic sample being tested is higher.

5.2.2 Establishment of asymptomatic transmission model

First consider the relationship between asymptomatic population S, positive population I, and negative population R. Through analysis, the transformation relationship between the three is obtained. The schematic diagram of the transformation relationship is as follows:

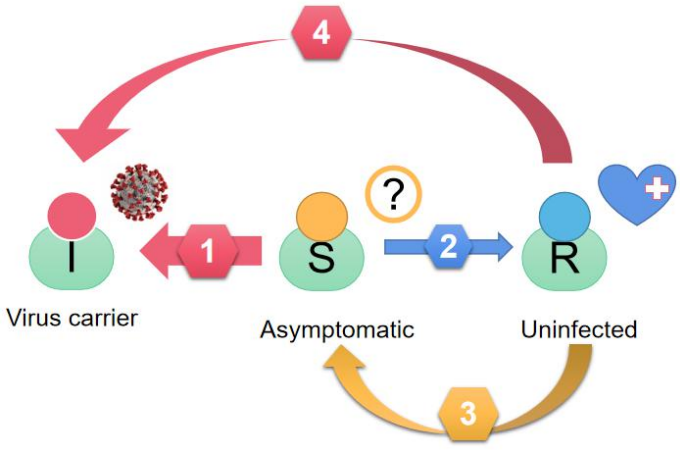


Figure 12:The schematic diagram of the transformation relationship

1.Asymptomatic people who were diagnosed as positive after S test changed to positive people I.

2.The asymptomatic population was diagnosed as negative after S test and changed to negative population R.

3.The negative population I is easily infected by the virus-carrying people in the non-infected population S, but it does not show that the symptoms become asymptomatic population S.

4.The negative population I is easily infected by the virus-carrying people in the non-infected population S, and it turns into the positive population S by seeking medical attention after showing symptoms.

Secondly, **analyze the four transformation relations and get the differential equation**. The specific steps are as follows:

Considering the situation 1,4,The increase in the positive population comes from the asymptomatic population S is tested according to the probability $P_J$and the result is positive and the negative population I is infected and turns into a positive population. Suppose the probability of being tested positive is P_{S-I}, the probability of being infected with symptoms is P_{R-I} the above information $i(t)$, and the rate of change obtained is:

$$\frac{di}{dt} = P_J P_{S-I} s(t) + P_{R-I} r(t)$$

(17)

Considering the situation 1,2, for asymptomatic people, asymptomatic people will reduce the inflow of positive and negative people respectively. Suppose the probability of the test being negative is P_{S-R}, then the rate of change $s(t)$ obtained is:

$$\frac{ds}{dt} = -(P_J P_{S-I} + P_J P_{S-R}) s(t) \quad (18)$$

From $P_{S-I} + P_{S-R} = 1$, the simplified rate of change $s(t)$ is:

$$\frac{ds}{dt} = -P_J s(t) \quad (19)$$

Considering the situation 2,3,4, for the negative population, the increase in the number comes from the number of asymptomatic people who are negative after testing. The reduction in the number of people is in two aspects. One is the people who have been infected and turned to be positive when they have symptoms. In the same way, the rate of change $r(t)$ is

$$\frac{dr}{dt} = P_J P_{S-R} s(t) - P_{R-S} r(t) - P_{R-I} r(t) \quad (20)$$

Based on the above discussion, the asymptomatic transmission model based on SIR is obtained

$$\begin{cases} \frac{di}{dt} = P_J P_{S-I} s(t) + P_{R-I} r(t) \\ \frac{ds}{dt} = - P_J s(t) \\ \frac{dr}{dt} = P_J P_{S-R} s(t) - P_{R-S} r(t) - P_{R-I} r(t) \\ P_J = \frac{A}{M - i_0 i(t) - r_0 r(t)} \\ 0 \le P_{S-I}, P_{S-R}, P_{R-S}, P_{R-I} \le 1 \\ s(0) = s_0 \\ i(0) = i_0 \\ r(0) = r_0 \\ P_{S-I} + P_{S-R} = 1 \end{cases} \tag{21}$$

5.3 The Asymptomatic Propagation Model Solution

Using Matlab to solve the model, we assign values to the parameters in the model through literature data, and the assignment results are as follows:

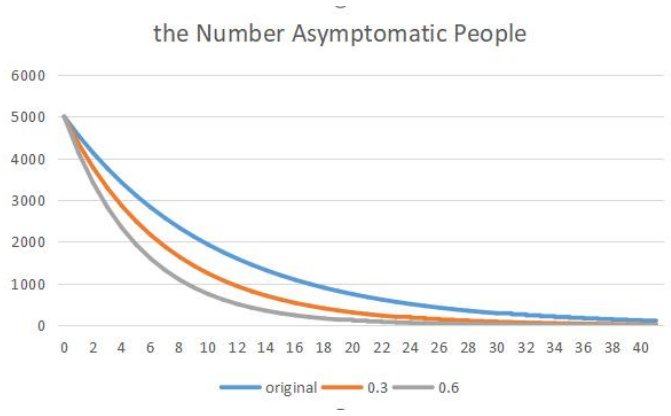
parameter	value	parameter	value	parameter	value
s_0	0.6	M	7000000	P_{S-R}	0.99
i_0	0.1	A	10000	P_{R-S}	0.63
r_0	0.3	P_{S-I}	0.01	P_{R-I}	0.03

Figure 13: the assignment results

The above two intervention methods are to adjust parameter A and parameters. Regarding the analysis of parameter A, due to the large area of nucleic acid testing in the program, the number of people tested daily has to increase. Regarding the analysis of the parameters, the program requires isolation of people who have not undergone testing, in order to reduce the transmission of virus to negative people among asymptomatic people who carry the virus. Adjust the two parameters, the adjustment ratio is as follows:

parameter	changes	changes
A	Increase 30%	Increase 60%
P_{R-I}	Cut back 30%	Cut back 60%

Figure 14: the adjustment ratio



plot

The resulting plot is as follows:

We found that it takes less time for the asymptomatic people to reduce to zero with the changed graph than the unchanged graph. At the same time, the larger the change ratio, the less time it takes.

In summary, we found that a large area of nucleic acid testing and the control of untested people's outing can **cope with the spread of virus-carrying individuals in the uninfected population to the entire population**.

6. Concentration Model

6.1 Problem Analysis

Question 3 requires us to propose a new group detection scheme, which does not need to be constrained by grouping, and needs to use specific numerical cases to illustrate the efficiency of detection under this method. What we consider is to determine the necessity of grouping first, and then to **establish a more efficient detection program** by narrowing the positive infected persons to a smaller sample range.

First consider our goal. According to the requirements of the topic, we need to develop a more efficient model. Therefore, our model uses the number of detections as a criterion to achieve high efficiency by reducing the number of detections under the condition that the sample and the infection rate remain unchanged. .

Secondly, we consider the process. Our idea is to use the idea of concentration to condense the limited positive samples of infected persons into a smaller sample range than the total sample range, **increase the infection rate within the sample range**, and then condense the latter model is substituted into the group detection model to calculate a total number of detections.

Finally, we analyzed the results and established a model that condensed a limited number of positive samples into a smaller range of samples, and brought in multiple sets of data values, calculated the total number of detections under multiple sets of data, and compared it with the number of detections in the first model. effectiveness.

6.2 Model Construction

6.2.1 Factor

The number of groups (a):

From the reference[4], we know that if the samples are not grouped for testing, the number of inspections for each person is 1. If you want to group for testing, then the average number

of inspections per person after grouping is less than 1, then the effect of grouping testing is considered to be better than that of no testing. Group detection, otherwise the detection effect without grouping is better. Therefore, we use calculations to verify whether grouping can effectively improve efficiency[9].

In the case of grouping, suppose there is k for the number of people in each group, variable x represents the number of tests for each person, p represents the probability of a positive test result, and q represents the probability of a negative test result. Where $p=1-q$.

If the test result of a group of mixed samples is negative, the probability of the group being tested negative can be calculated as q^k. Because there is no need to perform separate tests, the average number of tests for each person in the group is $\frac{1}{k}$.

If the test result of a group of mixed samples is positive, because there are only two possible test results for a group of negative and positive, the probability of a negative test result is q^k, so the probability of a positive test for this group is $1-q^k$. Everyone in the group needs to do Individual testing, so the average number of tests for each person is $1+\frac{1}{k}$.

List the distribution law of the number of tests x through mathematical knowledge

Number of test	$\frac{1}{k}$	$1+\frac{1}{k}$
probability	q^k	$1-q^k$

Figure 16: the distribution law of the number of tests x

Find the number of inspections per capita Ex

$$Ex=\frac{1}{k}\bullet q^k+\left(1+\frac{1}{k}\right)\bullet\left(1-q^k\right)=1-q^k+\frac{1}{k} \tag{22}$$

We transformed the problem of determining the group[4] by the number of inspections per capita into the problem of determining the necessity of grouping through the relationship between $1-q^k+\frac{1}{k}$ and 1. After a series of mathematical calculations such as derivation, it is found that when p is less than 0.31, the grouping will become efficient, and our prevalence rate in Hong Kong derived from Hong Kong's infection rate p is about 0.001, which is much smaller than the calculated value of 0.31.

Therefore, through calculation, we can know that grouping is beneficial to the detection method in the context of our model conditions, so we can conclude that grouping is needed.

6.2.2 the process of construction

Through the rigorous calculation process in step 1, we can know that grouping is necessary, so we established a concentrated and optimized group detection model. The core idea of the condensed model is to use group detection to screen out those with positive test results, eliminate grouped people with negative results, reduce the total number of samples with a limited number of positive samples, increase the infection rate in the remaining samples, and reuse problem one In the group detection model. **We consider the maximum number of detections of the model**, because when the detection efficiency of the specific value under the possibility of the maximum number of detections is higher than the efficiency of the group detection model of question 1, then it can be known that the efficiency of the model will be higher than the group of question 1. Check the model. Specific steps are as follows[7]

Since the number of infected persons in the sample is different, the probability of the infected persons being randomly assigned to different groups will be different. We consider the case of the largest number of tests, that is, each infected person is in a group, that is, there is only one in each group. The number of infected persons is:

$$b = \gamma \bullet N \tag{23}$$

Among them, b is the number of infected persons, that is, the lower limit of the number of groups, γ is the infection rate, and N is the total number of samples. We will traverse the number of groups that meet the conditions. From all the groups, select the one that requires the least total number of detections to group.

6.2.3 calculated process

Use the traversal method in step 1 to find the number of groups a under the highest number of detections. The number of groups containing infected persons is a. Then the mixed samples of each group are tested and analyzed, and the number of patients with negative mixed samples is calculated as

$$N - \frac{N \bullet b}{a} \tag{24}$$

Among them, b is the number of groups where there are infected persons under the highest number of tests, that is, the number of infected persons, N is the total number of samples, and a is the number of groups.

Therefore, we can easily know that the remaining number of people to be tested X_2 is,

$$X_2 = \frac{N \bullet b}{a} \tag{25}$$

Then we use the group detection model of question 1 to calculate the total number of detections in the remaining part, and add the calculated result to the number of detections in the enrichment, which is the number of groups, to calculate the total number of the enrichment optimization model Number of inspections[6]:

$$EX = EX_2 + a \tag{26}$$

Among them, EX is the total number of detections, EX_2 is the total number of detections of the remaining people calculated after substituting into the model 1.

6.3 Result Comparison

We substitute the specific values into the group detection model in problem one and the condensed optimization model in problem three. A comparison of the efficiency of a variety of different situations proved that the efficiency of the enrichment optimization model is higher than that of the group detection model. The specific values of the substituting values and the number of groups a_1 calculated by the enumeration traversal method are as follows:

Numerical Number	a_1	γ	N
1	400	0.001	40000
2	200	0.001	20000
3	100	0.001	10000
4	500	0.002	30000
5	625	0.002	40000

Figure 17: the specific values

Using the above values, we respectively substitute the optimized concentration model and the basic group detection model in question 1 to perform reasonable calculations, and obtain the following expectations of the respective models. A. The larger the value, the more detection times will be required , The corresponding model efficiency is also lower. We compare the efficiency of the two and visually reflect the relationship between the two through graphs:

Numerical Number	Concentrate optimization results EX	Group detection model EX
1	1160.252	2504.995
2	586.6901	1252.5

3	290.0631	626.25
4	1375.4	2624.283
5	1831.566	3499.044

Figure 18: the efficiency of two model

We can find from the chart that the concentrated optimization model in question 3 takes the maximum number of detections and the calculated EX is **much smaller than** the EX of the basic group detection model in question 1, so we can know that the efficiency of the concentrated optimization model is much higher than that of the group check the efficiency of the model.

7. Model Analysis

7.1 Advantages

① The group detection model of question 1 uses a large amount of data and a reasonable staged model to calculate the effective number of detections. Based on the relationship between the number of detections and the false positive rate and false negative rate, the grey correlation comprehensive evaluation method is reasonably used. , Get effective conclusions;

② Question 3 adopts a concentrated and optimized algorithm model, which will use group thinking to narrow the large sample interval where the positive samples are located, so as to increase the infection rate in the sample interval, increase the probability of detecting positive samples, and reduce the number of tests. Improve efficiency;

③ The condensed model in question 3, in the case of the largest number of detections, after multiple sets of data, the number of detections of the model is still less than that of the group detection in question 1, and the efficiency is higher.

7.2 Disadvantages

① In the group detection model in question 1, only the group detection method with the number of stages in one day is considered, and there is no further study of the number of stages and then increase the model to reduce the number of detections;

② The concentration optimization model in question three does not consider the staged factors. Multi-step concentration can be carried out to reduce the total sample interval size, thereby increasing the infection rate in the sample interval, and a few stages can be introduced through reasonable mathematical calculations Under the situation where the optimal number of sample tests can be achieved;

③ In the process of sample testing, the influence of time factor is ignored. A more reasonable model should consider the time factor more carefully, including the doctor's rotation time and the different methods of testing samples, which lead to different results;

④ In the sample detection model, the efficiency is simply linked to the total number of detections, while ignoring the actual considerations of time cost and labor cost.

9. A recommendation to the Department of Health of the Government of Hong Kong SAR

The darkness before dawn: before the vaccine comes

After implementing a strict epidemic prevention strategy, as early as July this year, mainland China announced the full resumption of work. Due to various reasons, the Hong Kong area was not able to withstand the third wave of the epidemic well, and the people of Hong Kong suffered the peak of the second diagnosis. This is really sad. Fortunately, medical resources are now sufficient to fight the epidemic, and domestic doctors are also experienced. The highly anticipated COVID-19 vaccine will also be fully available in early 2020. During the period before the vaccine came out, how to control the epidemic and restore the economy was the top issue for Hong Kong. Here, we hope to use our mathematical model to provide some suggestions for epidemic prevention and control and testing in Hong Kong.

Testing 10,000 people does not require 10,000 tests. Based on the randomization process and probability theory, we creatively designed a group inspection strategy optimized by the enrichment method. Divide the test subjects into several groups, extract a part of each person's saliva sample, mix them and test them uniformly. The Lancet claims that this method is feasible and can greatly improve efficiency. At the end of the article we have attached a specific grouping procedure. You only need to provide the total number of people to be tested and the approximate disease ratio, and we will provide you with the most optimized grouping method. Based on the current number of confirmed confirmed cases in Hong Kong, it is conservatively estimated that our method can increase the efficiency by at least 10 times.

The third wave of epidemics is characterized by strong transmission capacity but weaker pathogenicity. This also means that asymptomatic infections will become a difficult problem for epidemic prevention. To this end, we have established an SIR (infectious disease) model. Be careful! An undetected asymptomatic infection can usually infect 6 to 20 people. To completely eliminate these threats, on the one hand, we must strengthen the control of external sources of infection, on the other hand, we must accelerate the pace of comprehensive nucleic acid testing and antibody testing. In addition, the model also shows that isolating potentially ill groups and protecting healthy groups through home isolation and wearing masks are very effective methods of epidemic prevention. If one less person is infected today, there may be dozens of fewer troubles in the future, which can save a lot of social resources. The Hong Kong Department of Health is also requested to strengthen anti-epidemic propaganda and let the people of Hong Kong know the benefits.

Fighting the epidemic is a war. In the face of the powerful enemy of the virus, the people

of the world should unite. Finally, I wish Hong Kong's epidemic prevention work an early success！

Sincere,

Reference

- [1] Venkatesh Saanika, Bahsoun MohamadAli, Arezza Giordano, Digregorio Justin, Schweizer Tom A., Churchill Nathan W, Munoz David G., Fischer Corinne E., Khademi April, “White matter texture abnormalities are associated with delusional severity in a cognitively mixed sample of older adults”, The Alzheimer's Association, 2020
- [2] N/A, “Sensitivity evaluation of 2019 novel coronavirus (SARS-CoV-2) RT-PCR detection kits and strategy to reduce false negative.” Public Library of Science , 2020
- [3] Xingfa Meng, Qunying Xu, Yueqiang Fang, “Research and Application of Calculation Model of Optimal Content of Mixed Samples”, Chinese Journal of Preventive Medicine, 1993
- [4] Qing Ma, Ling Chen, Qingtang Hou, Yuling Yang, “Preliminary Study on the Calculation Method and Application of the Component Content of Mixed Biological Sample”, Chinese Journal of Forensic Medicine, 2013
- [5] Kaili Cui, Junke Kou, “Convergence Rates of Wavelet Density Estimators for Strongly Mixing Samples”, Bulletin of the Iranian Mathematical Society, 2020
- [6] Gerstgrasser Marcel, Cloots Michael, Stirnimann Josef, Wegener Konrad, “Focus shift analysis, to manufacture dense and crack-free SLM-processed CM247LC samples”, Journal of Materials Processing Technology, 2020
- [7] Nan Guo, “Focus shift analysis, to manufacture dense and crack-free SLM-processed CM247LC samples”, China Practical Medicine, 2020
- [8] Xiaofei Li, Yingrong Du, Songqin Lv, Wanlan Li, Liping Xu, Juan Zhang, Yongrui Yang, “Preliminary study on the clinical application of novel coronavirus antibody detection”, Chinese Journal of Virology, 2020
- [9] Tingting Yu, Xiaofei Yu, Hongying Wang, Runwu Zhang, Caimei Ding, Lihua Li, Jing Bai, Dongling Li, Dong Pu, “Application of Viral Load Test in Diagnosis of 102 Cases of Uncertain HIV Antibody Samples”, Journal of Kunming Medical University, 2020

Appendix

```
N40000
r=[0.0001   0.0002  0.0003  0.0004  0.0005  0.0006  0.0007
0.0008  0.0009  0.0010  0.0015  0.0020  0.0025  0.0030
0.0035  0.0040  0.0045  0.0050  0.0055  0.0060  0.0065
0.0070  0.0075
];
E=[998.95   1197.91    1394.17    1588.79    1774.07
1943.84    2096.91    2241.50    2375.87    2503.43
3061.86    3529.82    3942.70    4312.27    4652.55
4971.15    5265.39    5546.13    5811.91    6065.44
6309.18    6542.47    6765.70
];
a=[800.20   800.80  801.80  817.60  874.20  971.80  1037.80
1095.00    1192.40    1250.80    1511.00    1713.40
1924.40    2135.00    2284.00    2420.00    2558.40
2713.80    2854.80    2968.00    3066.00    3215.00
3325.20
];
plot(r,a,'k-');

N4000
r=[0.001    0.002   0.003   0.004   0.005   0.006   0.007
0.008   0.009   0.01    0.015   0.02    0.025   0.03    0.035
0.04    0.045   0.05    0.055   0.06    0.065   0.07    0.075
0.08    0.085   0.09    0.095   0.1
];
E=[250.3553 352.67072   430.5417    496.42652   553.48684
605.1929    653.3514    697.07838   738.76368   777.26912
946.1744    1087.40578  1209.7616   1319.88988  1420.50166
1513.45622  1599.61382  1680.94978  1756.3382   1828.7859
1898.50662  1964.98666  2027.12618  2088.84272  2146.60632
2204.91974  2258.81296  2311.48544
];
a=[122.6    177.8   214 245.6   266.6   292.4   325 335 360
371.2   450.4   521.6   565.8   609.2   666.8   719.8   755.2
788.2   823 859 871.2   908.6   913.4   956.4   967.2   988.4
1032    1039.8
];

plot(r,a,'k-');

r1e3
```

```
N=[1000.0   2000.0  4000.0  7000.0  10000.0    12000.0
14000.0    16000.0    18000.0    20000.0    22000.0
24000.0    26000.0    28000.0    30000.0    32000.0
34000.0    36000.0    38000.0    40000.0    43000.0
46000.0    50000.0
];
E=[999.0    1197.9  1394.2  1588.8  1774.1  1943.8  2096.9
2241.5  2375.9  2503.4  3061.9  3529.8  3942.7  4312.3
4652.6  4971.2  5265.4  5546.1  5811.9  6065.4  6309.2
6542.5  6765.7
];
a=[30.8    63.6    125.0   220.0   310.8   367.4   438.2
485.0   563.8   600.6   666.6   751.4   807.8   865.0   932.6
989.8   1066.0  1110.8  1178.6  1245.8  1351.0  1434.2
1541.8
];
r_b=0.03577;
A=E./r_b;
plot(N,E,'ko');


R5e4
N=[2000.0000    4000.0000   6000.0000   8000.0000
10000.0000  12000.0000  14000.0000  16000.0000  18000.0000
20000.0000  22000.0000  24000.0000  26000.0000  28000.0000
30000.0000
];
a=[43.4000  89.0000    129.0000    181.6000    225.6000
264.0000    305.8000    348.2000    395.8000    436.2000
493.2000    524.4000    559.2000    618.0000    669.8000
];
E=[88.5992  177.3872    266.3366    354.4862    443.1809
531.3124    621.0274    709.2072    798.2149    886.3788
975.9661    1064.5808   1153.2044   1241.2974   1330.7903
];
r_b=0.03577;
A=E./r_b;
plot(N,a,'k-');


Calculate data
#include<bits/stdc++.h>
using namespace std;
typedef long long ll;
```

```
double E[200050];
int cnt[200050];
double N,n,r;
const int repN=100;
double testN,testr;
double fakene_rate=0.00883;
void init(){
   memset(E,0,sizeof(E));
}
double qsm(double x,ll ex){
   double ans=1;
   double tmp=x;
   while(ex){
      if(ex&1)ans*=tmp;
      tmp*=tmp;
      ex>>=1;
   }
   return ans;
}
double comb(int A,int B){
   double ans=1;
   for(int i=1;i<=A;i++){
      ans=ans*(B-i+1)/i;
   }
   return ans;
}
const int TOTturn=5;
int main(){
   freopen("需要测试的N和r.txt","r",stdin);

   freopen("不同N和r的测试结果.txt","w",stdout);
   default_random_engine DRE;
   init();
   int num;
   scanf("%d",&num);
for(int i=0;i<num;i++){
   scanf("%lf%lf",&testN,&testr);

   N=testN;
   r=testr;
   n=N*r;
   double resA=0,resE=0,po=0,ne=0;
   printf("N=%.0lf\nr=%.5lf\n",N,r);
```

```
   for(int i=1;i<=TOTturn;i++){
      int mina;
      double minE=1e6;
      init();

      for(int a=N/50;a<=N/3;a++){          //改这里可以加速

         double p=N/a;
         uniform_int_distribution<unsigned>choose(0,a);
         for(int i=0;i<repN;i++){
            double e=0;

            for(int i=1;i<=a;i++)cnt[i]=0;

            int tot=0;
            while(tot<n){
               int tmp=choose(DRE);
               if(cnt[tmp]<p){
                  cnt[tmp]++;
                  tot++;
               }
            }
            tot=0;
            for(int i=1;i<=a;i++)if(cnt[i])tot++;
            E[a]+=(double)(a+p*tot)/repN;
         }
      // printf("a= %d   E= %.4lf\n",a,E[a]);
         if(E[a]<minE){
            minE=E[a];
            mina=a;
         }
      }
      printf("%d\t\t%.4lf\n",mina,minE);
      resA+=mina;
      resE+=minE;
   }
   resA/=TOTturn;
   resE/=TOTturn;
   double resNE=(resE-resA)*fakene_rate/N;
   double resPO=(resE-resA-n)/N;
   printf("final:\n");
   printf("a=%.4lf\nE=%.6lf\npo=%.6lf\nne=%.6lf\n\n",resA,
resE,resPO,resNE);
}
   return 0;
```

```
}
```

Format conversion

```
#include<bits/stdc++.h>
using namespace std;
typedef long long ll;
int main(){
   int n=28;
   double x[99];
   double E[99];
   double a[99];
   memset(x,0,sizeof(x));
   memset(a,0,sizeof(a));
   memset(E,0,sizeof(E));

   freopen("N=40000,r 的比较结果（没测试完）.txt","r",stdin);
   freopen("output1.txt","w",stdout);
   for(int i=1;i<=28;i++){
      string s;
      cin>>s;
      scanf("\nr=%lf\n",&x[i]);
      for(int j=0;j<5;j++){
         double e,tmp;
         scanf("%lf%lf",&tmp,&e);
         E[i]+=e;
         a[i]+=tmp;
      }
      a[i]/=5;
      E[i]/=5;
   }
   for(int i=1;i<=28;i++)printf("%.5lf\n",x[i]);
   printf("\n");
   for(int i=1;i<=28;i++)printf("%.5lf\n",a[i]);
   printf("\n");
   for(int i=1;i<=28;i++)printf("%.5lf\n",E[i]);
   printf("\n");
   return 0;
}
```

Model 1:

N	r	EX
40000	0.001	2504.994858
20000	0.001	1252.5
10000	0.001	626.25
30000	0.002	2624.282631
40000	0.002	3499.043508

Model 2:

N	r	EX
40000	0.001	1160.252
20000	0.001	586.6901
10000	0.001	290.0631
30000	0.002	1375.4
40000	0.002	1831.566

Dividing group number:

a	N	r	EX	condense	
	40000	**0.001**	2505		
50	32000	0.00125	2231.63354	2281.63354	
64	25000	0.0016	1963.831388	2027.831388	
80	20000	0.002	1749.521754	1829.521754	
100	16000	0.0025	1558.599371	1658.599371	
125	12800	0.00313	1389.582739	1514.582739	
160	10000	0.004	1221.886773	1381.886773	
200	8000	0.005	1088.544314	1288.544314	
250	6400	0.00625	969.7532935	1219.753293	
320	5000	0.008	853.3802358	1173.380236	
400	4000	0.01	760.2522781	1160.252278	
500	3200	0.0125	677.2872187	1177.287219	
625	2560	0.01562	603.282896	1228.282896	
800	2000	0.02	530.9692212	1330.969221	
1000	1600	0.025	473.0254382	1473.025438	
1250	1280	0.03125	421.4049634	1671.404963	
1600	1000	0.04	370.8352108	1970.835211	
2000	800	0.05	330.3665845	2330.366585	
2500	640	0.0625	294.3142318	2794.314232	
4000	400	0.1	230.7319467	4230.731947	
5000	320	0.125	205.5525553	5205.552555	
8000	200	0.2	161.1459321	8161.145932	

10000	160	0.25	143.5603461	10143.56035
20000	80	0.5	100.2642509	20100.26425
			0	0
	20000	**0.001**	1252.5	1252.5
25	16000	0.00125	1115.81677	1140.81677
32	12500	0.0016	981.9156942	1013.915694
40	10000	0.002	874.7608769	914.7608769
50	8000	0.0025	779.2996856	829.2996856
80	5000	0.004	610.9433867	690.9433867
100	4000	0.005	544.2721568	644.2721568
125	3200	0.00625	484.8766467	609.8766467
160	2500	0.008	426.6901179	586.6901179
200	2000	0.01	380.1261391	580.1261391
250	1600	0.0125	338.6436093	588.6436093
400	1000	0.02	265.4846106	665.4846106
500	800	0.025	236.5127191	736.5127191
625	640	0.03125	210.7024817	835.7024817
800	500	0.04	185.4176054	985.4176054
1000	400	0.05	165.1832923	1165.183292
1250	320	0.0625	147.1571159	1397.157116
2000	200	0.1	115.3659733	2115.365973
2500	160	0.125	102.7762776	2602.776278
4000	100	0.2	80.57296607	4080.572966
5000	80	0.25	71.78017306	5071.780173
10000	40	0.5	50.13212545	10050.13213
			0	0
	10000	**0.001**	626.25	626.25
16	6250	0.0016	490.9578471	506.9578471
20	5000	0.002	437.3804385	457.3804385
25	4000	0.0025	389.6498428	414.6498428
40	2500	0.004	305.4716933	345.4716933
50	2000	0.005	272.1360784	322.1360784
80	1250	0.008	213.345059	293.345059
100	1000	0.01	190.0630695	290.0630695
125	800	0.0125	169.3218047	294.3218047
200	500	0.02	132.7423053	332.7423053
250	400	0.025	118.2563596	368.2563596
400	250	0.04	92.7088027	492.7088027
500	200	0.05	82.59164614	582.5916461
625	160	0.0625	73.57855794	698.5785579
1000	100	0.1	57.68298667	1057.682987
1250	80	0.125	51.38813882	1301.388139
2000	50	0.2	40.28648304	2040.286483

2500	40	0.25	35.89008653	2535.890087
5000	20	0.5	25.06606273	5025.066063
			0	0
	30000	**0.002**	2624.282631	2624.282631
75	24000	0.0025	2337.899057	2412.899057
80	22500	0.00267	2262.417032	2342.417032
100	18000	0.00333	2013.338188	2113.338188
120	15000	0.004	1832.83016	1952.83016
125	14400	0.00417	1795.183426	1920.183426
150	12000	0.005	1632.81647	1782.81647
200	9000	0.00667	1407.156882	1607.156882
240	7500	0.008	1280.070354	1520.070354
250	7200	0.00833	1253.052371	1503.052371
300	6000	0.01	1140.378417	1440.378417
375	4800	0.0125	1015.930828	1390.930828
400	4500	0.01333	982.4198054	1382.419805
500	3600	0.01667	875.3998928	1375.399893
600	3000	0.02	796.4538318	1396.453832
625	2880	0.02083	779.7336163	1404.733616
750	2400	0.025	709.5381573	1459.538157
1000	1800	0.03333	611.3012593	1611.301259
1200	1500	0.04	556.2528162	1756.252816
1250	1440	0.04167	544.6382413	1794.638241
1500	1200	0.05	495.5498768	1995.549877
1875	960	0.0625	441.4713477	2316.471348
2000	900	0.06667	426.9709397	2426.97094
2500	720	0.08333	380.3598098	2880.35981
3000	600	0.1	346.09792	3346.09792
3750	480	0.125	308.3288329	4058.328833
5000	360	0.16667	265.6554941	5265.655494
6000	300	0.2	241.7188982	6241.718898
7500	240	0.25	215.3405192	7715.340519
10000	180	0.33333	185.5342688	10185.53427
15000	120	0.5	150.3963764	15150.39638
			0	0
	40000	**0.002**	3499.043508	3499.043508
100	32000	0.0025	3117.198743	3217.198743
125	25600	0.00313	2779.165479	2904.165479
160	20000	0.004	2443.773547	2603.773547
200	16000	0.005	2177.088627	2377.088627
250	12800	0.00625	1939.506587	2189.506587
320	10000	0.008	1706.760472	2026.760472
400	8000	0.01	1520.504556	1920.504556

500	6400	0.0125	1354.574437	1854.574437
625	5120	0.01562	1206.565792	1831.565792
800	4000	0.02	1061.938442	1861.938442
1000	3200	0.025	946.0508764	1946.050876
1250	2560	0.03125	842.8099267	2092.809927
1600	2000	0.04	741.6704216	2341.670422
2000	1600	0.05	660.7331691	2660.733169
2500	1280	0.0625	588.6284635	3088.628464
4000	800	0.1	461.4638933	4461.463893
5000	640	0.125	411.1051105	5411.105111
8000	400	0.2	322.2918643	8322.291864
10000	320	0.25	287.1206922	10287.12069
20000	160	0.5	200.5285018	20200.5285