|  |  |  |
| --- | --- | --- |
| **Problem Chosen A** | **2020 MCM/ICM**  **Summary Sheet** | **Team Control Number 0000012** |

# 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**

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### 1. introduction

#### 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 |
|  | infection rate |
| b | the number of infections |
| X | the total number of tests |
| c | there are infected persons in group |
|  | the false positive rate |
|  | the false negative rate |
|  | the probability of error of the experimental instrument |
|  | the correlation coefficient |
| Z | the point of comprehensive method |
| r(t) | the negative population to the total population |
|  | 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 |
|  | the probability of being tested positive |
| S | the asymptomatic population |
|  | the number of people in each group |
|  | the number of tests for each person |
|  | the probability of a positive test result |
|  | the probability of a negative test result |
|  | the remaining number of people |
|  | the total number of detections |
|  | the total number of detections of the remaining people |

### 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:

(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 sampl**e

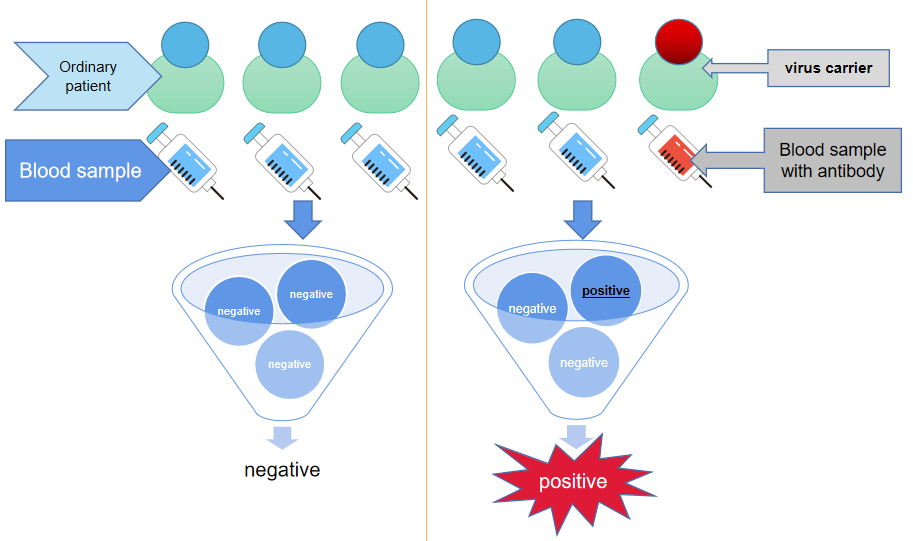
As the number of infected persons in the sample is different, the probability that the infected persons will be randomly assigned to different groups will be different, resulting in different total number of tests. We set the infection rate as , and the number of infections is:

(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:

(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 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]:

(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 , the calculation formula is:

(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 , and the calculation formula of the false negative rate is:

(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 |
|  |  |  |  |
| ... | ... | ... | ... |
|  |  |  |  |

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 coefficien**t

Define the correlation coefficient between the parent index and at the th point as:

(7)

In which can be calculated as follow:

(8)

And the formula of a and b are:

(9)

(10)

In which the range of is ,and we take .

**Calculate the degree of relevance**

(11)

**Build a comprehensive evaluation model**

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

(12)

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

(13)

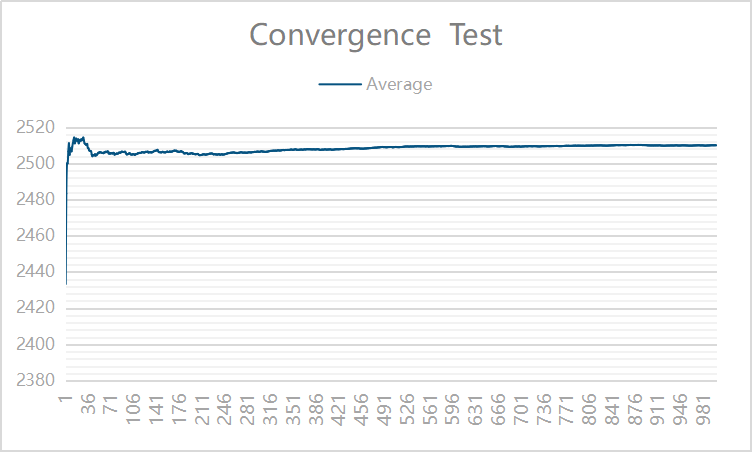
Finally, the grouping number corresponding to the smallest comprehensive index is the grouping method with the best overall sample number N.

#### 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:

(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 | 777.215848 | 0.089354 | 0.000877 | 0.070881357 |
| 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 | 1385.714887 | 0.065251 | 0.00062 | 0.054973315 |
| 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 ，,. Since the total population remains unchanged, the ratio of the three populations obviously has the following formula:

(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]:

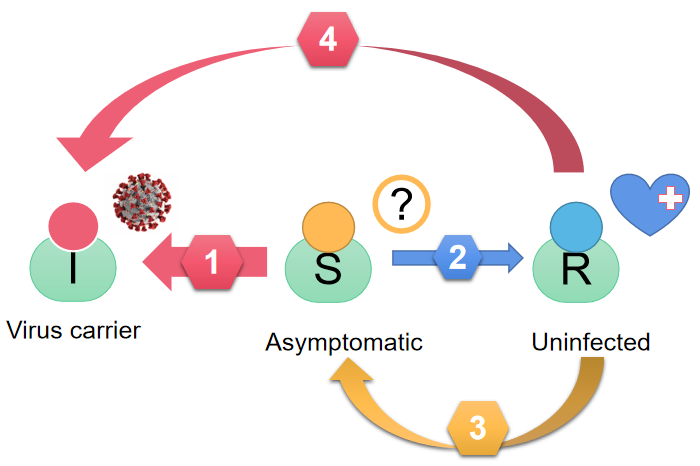
(16)

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 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 , the probability of being infected with symptoms is the above information , and the rate of change obtained is:

(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, then the rate of change obtained is:

(18)

From , the simplified rate of change is:

(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 is

(20)

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

(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 |
|  | 0.6 | M | 7000000 |  | 0.99 |
|  | 0.1 | A | 10000 |  | 0.63 |
|  | 0.3 |  | 0.01 |  | 0.03 |

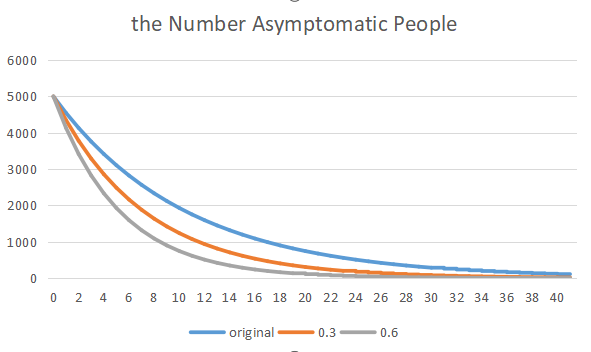
Figure 13: the assignment results

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% |
|  | Cut back 30% | Cut back 60% |

Figure 14: the adjustment ratio

Figure 15: The resulting 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 ():

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  for the number of people in each group, variable  represents the number of tests for each person,  represents the probability of a positive test result, and  represents the probability of a negative test result. Where .

If the test result of a group of mixed samples is negative, the probability of the group being tested negative can be calculated as . Because there is no need to perform separate tests, the average number of tests for each person in the group is .

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 , so the probability of a positive test for this group is . Everyone in the group needs to do Individual testing, so the average number of tests for each person is .

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

|  |  |  |
| --- | --- | --- |
| Number of test |  |  |
| probability |  |  |

Figure 16: the distribution law of the number of tests 

Find the number of inspections per capita 

 (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  and 1. After a series of mathematical calculations such as derivation, it is found that when  is less than 0.31, the grouping will become efficient, and our prevalence rate in Hong Kong derived from Hong Kong's infection rate  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:

 (23)

Among them,  is the number of infected persons, that is, the lower limit of the number of groups,  is the infection rate, and  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  under the highest number of detections. The number of groups containing infected persons is . Then the mixed samples of each group are tested and analyzed, and the number of patients with negative mixed samples is calculated as

 (24)

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

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

 (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]:

 (26)

Among them,  is the total number of detections,  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  calculated by the enumeration traversal method are as follows:

|  |  |  |  |
| --- | --- | --- | --- |
| Numerical Number |  |  |  |
| 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 | Group detection model |
| 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  is **much smaller than** the  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.

### 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,



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### 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 |