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# Parameter Estimation of COVID-19 Second Wave B-H-R-P Transmission Model by Using Principle Component Analysis

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**Abstract**

This paper deals a principle component analysis (PCA) of B-H-R-P transmission model of COVID-19.Multivariate principle component analysis estimates the parameter values of this network model and investigated 25 parameter values.We calculated previous and current parameter values from COVID-19 data. The new parameters used in Mathematical modeling of COVID-19. We have to apply the values and get the new results of future prediction from the existing model.

**Keywords:** COVID-19, Parameter estimation, PCA, B-H-R-P transmission model, Multivariate principle component analysis.

## 1. INTRODUCTION

The endeavor against this virus is challenging and it continues to be an endless struggle. Though there has been statistically proved advancement in medical field in all the developed nations, they find itvery difficult and challenging task to control this deadly virus. As a result, approximately 25% of people died as they got infected[1, 2]. This virus belongs to the family of coronaviridae and directly causes respirator and neurological disease[3].The name of the novel corona virus disease 2019 [COVID-19] was given by the WHO on February 2020. It spreads very quickly and at first identified in Wuhan province in China in December 2019[4]. International Virus Classification Commission has declared, it is a severe acute respiratory syndrome corona virus 2 [SARS-CoV-2]. For the past two decades, COVID-19 has been spreading almost in all over the world which was announced as a pandemic by WHO [5].There are six human corona viruses (HCoVs), SARS and MERS found out till today. They are HCoV-229E, HCoV-HKU1, HCoV-OC43, HCoVNL63. There have been three epidemic diseases caused by corona virus such as COVID-19, SARS and MERS [6]. They can directly affect human being not showing any symptoms at the initial stage. COVID-19 shows the symptoms of dry cough, fever, fatigue, breathing difficulties and bilateral lung infiltration. All these symptoms match with SARS-CoV and MERS-CoV[7]. Moreover, some patients have the symptoms of vomiting anddiarrhea [8,9]. Due to the outbreak of corona, the number of virus infected people is getting increased as a result, the death rate also increased. The public opinion polls data shows that there has been a psychological depression caused by COVID-19. To prevent or control this disease, there is no vaccine or antiviral treatment invented till today. Timing solution suggested to control this virus is using surgical mask

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and gloves. However, it is strongly recommended to maintain physical distance and keeping the infected people Quarantined andso this virus can be controlled. WHO and Centers for Disease Control and Prevention (CDC) advised the public that surgical mask and gloves which are not helpful and not required to those who have immunity power [10].

The World Health Organization recommended that mathematical modeling can be the best method for providing the right health based decision. Moreover, it has been devised as a timely requirement. Indeed, modeling has given effective understanding to those who are doing the study on COVID-19 such as how this disease gets transmitted and how effectively the number of cases increased during the infectious period. During the course of infection, it's effect is so severe having the extreme power. International mathematical experts have accepted to design mathematical model for the dynamics of transmission and current outbreak of corona virus. Many of the models have been done with different estimated values till today [11]. Dighe.A. et alstudied a mathematical model of MERS-CoV which was transferred from dromedary camels to human being. They also conclude the reproduction number range is 3 to 6[12]. By using daily based real time data, Biao Tang. et al explored the dynamics transmission modelfor COVID-19 and re-estimateda reproduction number, by which transmission risk can be assumed [13]. Sanglier Contreras G . et al developed a modeland estimated the epidemiological evolution for the analysis of COVID-19 [14].JomarF.Rabajante has analyzed early mathematical models of COVID-19 dynamicswhich shows the exposure time that is an important factor for spreading the disease [15]. We extend the work of Tian-Mu Chen. Et al. they developed a four compartmental network model such as Bats-Hosts-Reservoir-People respectively for simulating the infection source to human infection.They simplified by excluding bats and hosts into RP model to find $R_0$ [16]. The aim of our study is to investigate the parameter values of BHRP model so that we take 21 parameters of this study of Tian-Mu Chen. Et al.The initial values taken for this study is shown in Table 1 and using PCA we validated the very strong, strong and weak parameters also we found the local stability analysis of this model [17]. There are many researchers studied the different approaches of principle component analysis inin whichthey used data analysis using statistical methods for collected data. But our approach is different from others because we analyze the parameters of mathematical modeling of an existing work [18]. It is the new approach for studying mathematical modeling of COVID 19 and also very useful for further studies especially to those who do a study on COVID 19 [19].

## 2. MATHEMATICAL MODELING OF BHRP COVID-19

In the BHRP transmission network model, it is believed that initially, the virus got transferred from the bats; then it was transferred to strange hosts which are assumed as wild animals. Hunting the assumed wild animals, the hunters brought them to the market which has been considered the virus reservoir [20].Whoever goes to themarketplaceexposed to the possibility of infection? This model was defined on the basis of facts given below [21]. The first and second compartments are SEIR model which represents suspected, exposed, infected and removed virus respectively [22]. Here, $X$ is denoted as bats and $Y$ is denoted as host and $P$ is denoted as the people. The number of newborn of bats was taken by $\varphi_X = b_X \times N_X$ here $N_X$ be the total population of $X$. In the first compartment, the transmission happens if $S_X$ getscontacted with $I_X$ and its rate is denoted as $\beta_X$.The number of new hosts was taken as $\varphi_Y = b_Y \times N_Y$ here $N_Y$ is the total population of $Y$. In the second compartment, the transmission happens if $S_Y$ gets contacted with $I_X$ and $I_Y$ its rates are denoted as $\beta_{XY}$ and $\beta_Y$, respectively. The third compartment is the market which is represented as $C$. The frequency of virus in the purchases has been defined as $I_Y / N_Y$. So, the rate of carried virus from host to $C$ is $eCI_Y / N_Y$ ,here e is the purchasing rate of virus. Then, it leaves from the third compartment $(C)$ in the rate $\delta_C$, here $1/\delta$ is

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defined as the virus lifetime [23]. The fourth compartment is defined as the SEIFR model where the infected people are classified as symptomatic and asymptomatic, which are denoted as $I_P$ and $F_P$ respectively. Here, both the recovered and death people existing in $R_P$ .The newborn population has been defined as $\varphi_P = n_P \times N_P$, where $N_P$ is the total population. In this compartment, the transmission happens if $S_P$ gets contacted with $C$ and $I_P$ its rates are denoted as $\beta_C$ and $\beta_P$, respectively. Also $F_P = rI_P$ be the transmissibility of $F_P$, where the range of $r$ is between 0 and 1.Table1 shows the parameter values of BHRP model [24]. The model becomes,

$$\frac{dS_X}{dt} = \varphi_X - d_X S_X - \beta_X S_X I_X$$
$$\frac{dE_X}{dt} = \beta_X S_X I_X - \mu_X E_X - d_X E_X$$
$$\frac{dI_X}{dt} = \mu_X E_X - (\alpha_X + d_X) I_X$$
$$\frac{dR_X}{dt} = \alpha_X I_X - d_X R_X$$

$$\frac{dS_Y}{dt} = \varphi_Y - d_Y S_Y - \beta_{XY} S_Y I_X - \beta_Y S_Y I_Y$$
$$\frac{dE_Y}{dt} = \beta_{XY} S_Y I_X + \beta_Y S_Y I_Y - \mu_Y E_Y - d_Y E_Y$$
$$\frac{dI_Y}{dt} = \mu_Y E_Y - (\alpha_Y + d_Y) I_Y$$
$$\frac{dR_Y}{dt} = \alpha_Y I_Y - d_Y R_Y$$

$$\frac{dS_P}{dt} = \varphi_P - d_P S_P - \beta_P S_P (I_P + rF_P) - \beta_C S_P C$$
$$\frac{dE_P}{dt} = \beta_P S_P (I_P + rF_P) + \beta_C S_P C - (1-\gamma_P)\mu_P E_P - \delta_P \mu'_P E_P - d_P E_P$$
$$\frac{dI_P}{dt} = (1-\gamma_P)\mu_P E_P - (\alpha_P + d_P) I_P$$
$$\frac{dF_P}{dt} = \gamma_P \mu'_P E_P - (\alpha'_P + d_P) F_P$$

$$\frac{dR_P}{dt} = \alpha_P I_P + \alpha'_P F_P - d_P R_P$$
$$\frac{dC}{dt} = eC\frac{I_Y}{N_Y} + \rho_P I_P + \rho'_P F_P - \delta C$$

**Table 1Parameter values from previous COVID-19 data**

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| No | Parameter | Description | Ranges | Mean | Variance |
|---|---|---|---|---|---|
| 1 | $b_X$ | The birth rate of bats | 0.92 | 0.9112 | 0.00005716 |
| 2 | $b_Y$ | The birth rate of hosts | 2.43-19.51 | 11.798 | 31.0169 |
| 3 | $b_P$ | The birth rate of people | 0.0018 | 0.00179953 | 0.0000003 |
| 4 | $d_X$ | Death rate of bats | 75%-80% | 78.092 | 2.793756 |
| 5 | $d_Y$ | Death rate of hosts | 1.99–2.15 | 2.1033 | 0.0051005 |
| 6 | $d_P$ | Death rate of people | 0.0018 | 0.0017888 | 0.000000001 |
| 7 | $1/\mu_X$ | Incubation period of bats | 20-90 days | 58 | 501 |
| 8 | $1/\mu_Y$ | Incubation period of hosts | 6.5-37.4 | 23.423 | 142.05748 |
| 9 | $1/\mu_P$ | Incubation period of people | 5.2 | 5.18841 | 0.0008784 |
| 10 | $1/\mu'_P$ | Latent period of people | 5.2 | 5.19796 | 0.0000084 |
| 11 | $1/\alpha_X$ | Infectious period of bats | <180 days | 175.5 | 8.875 |
| 12 | $1/\alpha_Y$ | Infectious period of hosts | 18-130 | 69.8 | 1380.36 |
| 13 | $1/\alpha_P$ | Infectious period of symptomatic infection people | 5.8 | 5.79948 | 0.0000254 |
| 14 | $1/\alpha'_P$ | Infectious period of asymptomatic infection of people | 2.5 | 2.49897 | 0.000023 |
| 15 | $\beta_X$ | Transmission rate from $I_X$ to $S_X$ | 95-108 days | 101.4 | 21.24 |
| 16 | $\beta_{XY}$ | Transmission rate from $I_X$ to $S_Y$ | 3-12.5 | 9.64 | 8.9544 |
| 17 | $\beta_Y$ | Transmission rate from $I_Y$ to $S_Y$ | 10-14 days | 12.155 | 1.71623 |
| 18 | $\beta_P$ | Transmission rate from $I_P$ to $S_P$ | 3-14 days | 9.2 | 11.16 |
| 19 | $\beta_C$ | Transmission rate from C to $S_P$ | 1.4-2.5 | 1.99 | 0.1209 |
| 20 | e | The retail purchases rate of the hosts in the market | 0.1 | 1.2 | 1.9 |

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| | | | | | |
|---|---|---|---|---|---|
| 21 | $\rho_P$ | Shedding coefficients from $I_P$ to C | 0.2 | 0.5 | 0.00079 |
| 22 | $\rho'_P$ | Shedding coefficients from $F_P$ to C | 0.5 | 0.49845 | 0.000004 |
| 23 | $1/\delta$ | The lifetime of the virus in C | 10 | 9.82 | 0.0249 |
| 24 | $\gamma_P$ | The proportion of asymptomatic infection rate of people | 0.5 | 0.4845 | 0.0003053 |
| 25 | r | The multiple of the transmissibility of $F_P$ to that of $I_P$ | 0.5 | 0.49842 | 0.000023 |

**3 Parameter estimation using PCA**

Principal component analysis (PCA) is a technique helpingto comprehendthe data analysis. It reduces the dimensionality of datasets and increases interpretability minimizing information loss. It is mainly used for feature extractioncombining our input variables dropping the least significant and retaining the most significant variables [25]-[29]. Two or three principal components are generally required to plot however, the number of important components must be properly determined for modeling. It is combined linearlywith the n-variables $V_1, V_2, \ldots, V_n$ which selects anew system with $V_1, V_2, \ldots, V_n$ are the co-ordinate axes [24].

As principle components only based on the covariance matrix $\sum$ of $V_1, V_2, \ldots, V_n$, their progress does not need a multivariate normal assumption. Let the random vector $V' = [V_1, V_2, \ldots, V_n]$ having $\sum$ with eigenvalues $\lambda_1 \geq \lambda_2 \geq \ldots \geq \lambda_p \geq o.$

We assume the linear combinations below,

$$\begin{aligned} U_1 &= x_1' V = x_{11}V_1 + x_{12}V_2 + \ldots + x_{1n}V_n, \\ U_2 &= x_2' V = x_{21}V_1 + x_{22}V_2 + \ldots + x_{2n}V_n, \\ &\vdots \\ U_n &= x_n' V = x_{n1}V_1 + x_{n2}V_2 + \ldots + x_{nn}V_n. \end{aligned} \tag{3.1}$$

We get,

$$Var(U_1) = x_i' \sum x_i, \qquad i = 1, 2, \ldots, n. \tag{3.2}$$

$$Cov(U_1, U_k) = x_i' \sum x_k, \qquad i, k = 1, 2, \ldots, n. \tag{3.3}$$

Principle components are not correlated with $U_1, U_2, \ldots, U_n$ and increases the variances.

1st Principle Component = linear combination $x_1' V$ increases $Var(x_1' V)$

subject to $x_1' x_1 = 1.$

2nd Principle Component = linearcombination $x_2' V$ increases $Var(x_2' V)$

subject to $x_2' x_2 = 1$ and $Cov(x_1' V, x_2' V) = 0.$

$\vdots$

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i[th] Principle Component = linear combination $x_i'V$ increases $Var\left(x_i'V\right)$ subject to $x_i'x_i = 1$ and

$$Cov\left(x_i'V, x_k'V\right) = 0 \text{ for k<i.}$$

Principle components may also be found from standardized variables.

$$A_1 = \frac{\left(V_1 - m_1\right)}{\sqrt{q_{11}}}$$

$$A_2 = \frac{\left(V_2 - m_2\right)}{\sqrt{q_{22}}}$$

$$\vdots$$

$$A_n = \frac{\left(V_n - m_n\right)}{\sqrt{q_{nn}}}$$

In matrix notation,

$$A = \left(Q^{1/2}\right)^{-1}\left(V - M\right).$$

Here the diagonal standard deviation matrix $Q^{1/2}$ and M is population mean.

E(A)=0 and $C\text{ov}\left(A\right) = \left(Q^{1/2}\right)^{-1}\sum\left(Q^{1/2}\right)^{-1} = \text{P.}$

Here P is the correlation matrix of A. The principle component of A can be gotten from the eigenvectors of P. The i[th] principle component of the standard variables $A' = \left[A_1, A_2, ..., A_n\right]$ with $C\text{ov}\left(A\right) = \text{P}$, is given by

$$V_i = a_i'A = a_i'\left(Q^{1/2}\right)^{-1}\left(V - M\right), \qquad i = 1, 2, ..., n.$$

Moreover, $\sum_{i=1}^{n} Var\left(V_i\right) = \sum_{i=1}^{n} Var\left(A_i\right) = P.$ (3.4)

And $PV_{i,A_k} = a_{ik}\sqrt{\lambda_i}$, $i, k = 1, 2, ..., n.$

In this case, $\left(\lambda_1, a_1\right), \left(\lambda_2, a_2\right), ..., \left(\lambda_n, a_n\right)$ represents the eigenvalue-eigenvector pairs for P, with

$\lambda_1 \geq \lambda_2 \geq ... \geq \lambda_p \geq o.$

*Proof:* Let us consider $q_{11} + q_{22} + ... + q_{nn} = tr\left(P\right)$ with B=$\sum$.

We take $\sum = R\Lambda R'$, here $\Lambda$ be the diagonal matrix of eigenvalues, $R = \left[a_1, a_2, ..., a_n\right]$ so that $RR' = R'R = I.$

We have

$tr\left(P\right) = tr\left(R\Lambda R'\right) = tr\left(\Lambda R'R\right)$

$= tr\left(\Lambda\right) = \lambda_1 + \lambda_2 + ... + \lambda_n.$

Thus, $\sum_{i=1}^{n} Var\left(V_i\right) = tr\left(P\right) = tr\left(\Lambda\right)$

$$= \sum_{i=1}^{n} Var\left(U_i\right).$$

Total population variance $= q_{11} + q_{22} + ... + q_{nn}$

$$= \lambda_1 + \lambda_2 + ... + \lambda_n.$$ (3.5)

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Due to k[th] principle component $= \frac{\lambda_k}{\lambda_1 + \lambda_2 + ... + \lambda_n},\ k = 1, 2, ..., n.$ (3.6)

$$= \frac{\lambda_k}{n},\ k = 1, 2, ..., n. \quad (3.7)$$

Where the $\lambda_k$ 's are the eigenvalue of P.

Each component of the coefficient vector $a_i^{'} = \left[ a_{i1}, a_{i2,}, ..., a_{ik}, ..., a_{in} \right]$ also checks values. Thus, $a_{ik}$ represents the position of the k[th] variable to the i[th] principle component, not considering the other variables.

Suppose the data $v_1, v_2, ..., v_p$ represents p-independent. Let us consider the sample mean vector is $\bar{m}$ , T is the sample covariance matrix and C is the sample correlation matrix. The sample mean and variance of linear combination $x_1^{'}v = x_{11}v_{j1} + x_{12}v_{j2} + ... + x_{1n}v_{jn},\ j = 1, 2, ..., p$ are $x_1^{'}\bar{v}$ and $x_1^{'}Tx_1$ respectively. Also $\left( x_1^{'}v_j, x_2^{'}v_j \right)$ be two linear combinations have sample variance $x_1^{'}Tx_2$ . Each coefficient vectors should satisfy $x_i^{'}x_i = 1$ .

**4. Results and Discussion**

It shows the first 8 parameters which have been considered asvery strongparameters but the remaining 13 parameters which are considered as strong parameters.As our PC1 solution accounted for 89% of the cumulative variance is better and stronger but the solution below 40% which is not considered very strong [20].Our PC2 solution accounted for 10.2% of the cumulativevariance is not very strong. PC1 has 5 negative parameters on the other hand PC2 has only 3 negative parameters.Jantien.A.Backer et al.stated in their study that the mean incubation period is 6.4 days and the range is between 2.1 to 11.1 days [7]. Stephen.A.Lauer et al.mentioned in their study the median is5.1 days for the same. 95 percentof people carry the symptom within 4.5 to 5.8 daysbut for 97.5 percent of people, it is11.5 days [11]. But, in this studythe mean incubation period was 5.2 daysand the latent period also same.Therefore, the value of $\mu_P$ and $\mu'_P$should be taken as 0.1923. Symptoms have been identified the mean of 5-days later after infection. As the period of infection is 5.8 days, the value of $\alpha_P$ is 0.1724. The starting value of 0.5 was taken as the rate of asymptomatic infection ($\gamma_P$) because of the non-availability of data. The transmission of asymptomatic infection ($F_P$) is high when compared with symptomatic infection ($I_P$). Therefore, the ratio of $F_P$ was the assumed the multiplicity value (r) 0.5 times of $I_P$. As per the data mentioned in the previous study, the value of $b_P$and $d_P$ is 0.0018. The transmission rates $\beta_P$ and $\beta_C$ have been assessed based on how the collected data fits with the model. The range of transmission rate from infected people to suspected people $\beta_P$ is 3 – 14 days and the mean value is 9.2 days. The range of transmission rate from reservoir to suspected people is 1.4 – 2.5 days and the mean value is 1.99 days. Initially, it was assumed that the occurrence of the virus in the reservoir was 0.00001.The virus remains to be active and infectious on inanimate objects from 2 hrs to 9 days [22]. But, this modeltaken the lifetime of the virus is $\delta = 0.1$. According to Tian-Mu Chen [16] this model hasof too many parameters and several limitations existing. But, when the principle component analysis was done, we identified the verystrong and strong parameters. Based on the study done, the weak parameters have been eliminated,as they are having the least eigenvalues which is shown. It shows that scree plot for parameter estimation. For reducing the complexity of the modeling, we decreased the number of parameters based on the Scree plot. So, we conclude it bysaying that this model is highly effective and satisfied with only the strong parameters [25]. In Figure 1 shows the Calculate the mean, variance and ranges. In Figure 1 shows the

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calculated values and ranges. Figure 3 shows the percentage calculation of PC1 and PC2. In table 2, we calculated the parameter values from current COVID-19 data.

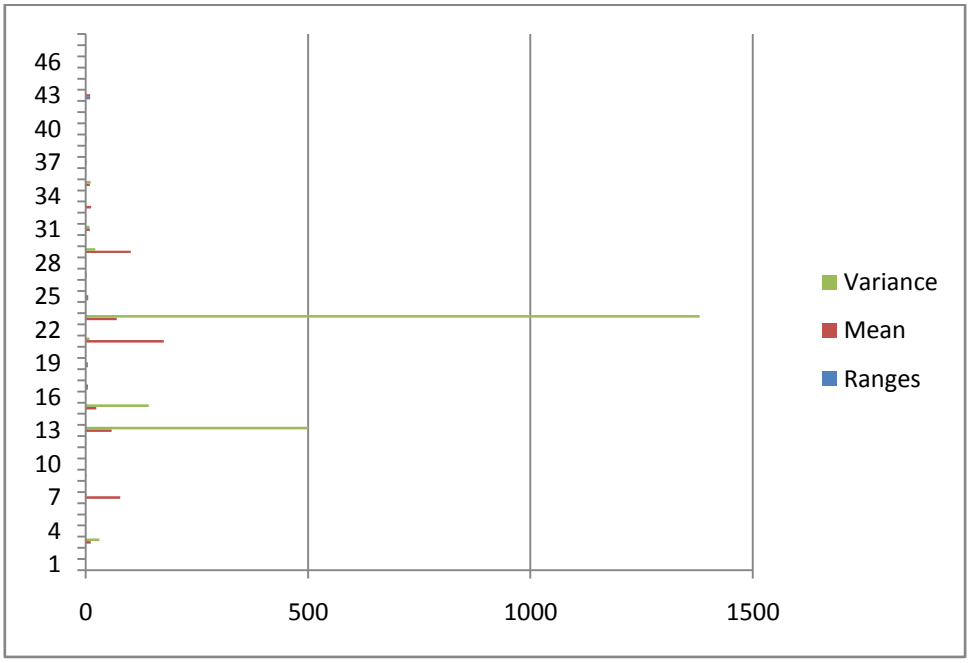


**Figure 1 Calculate the mean, variance and ranges**

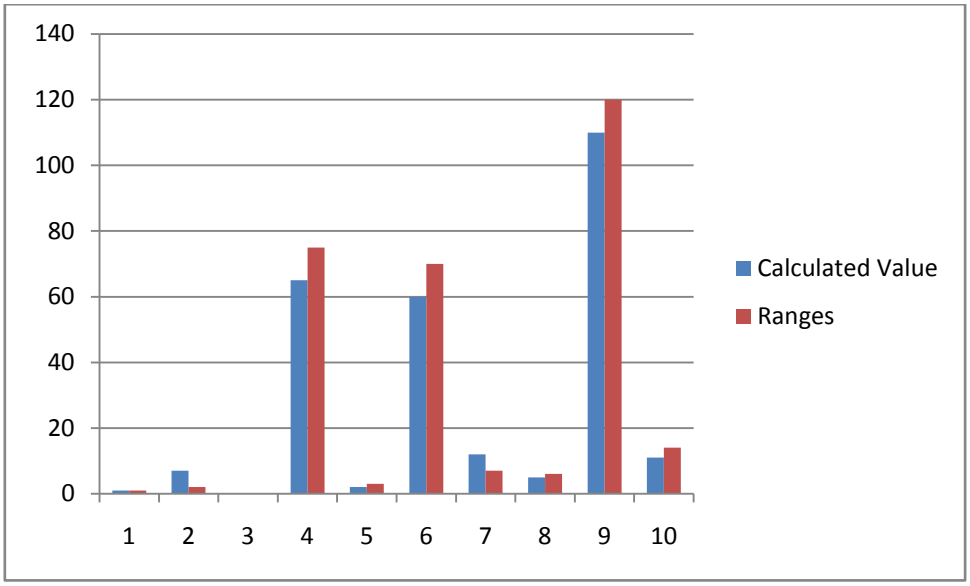


**Figure 2 Evaluate the calculated values and ranges**

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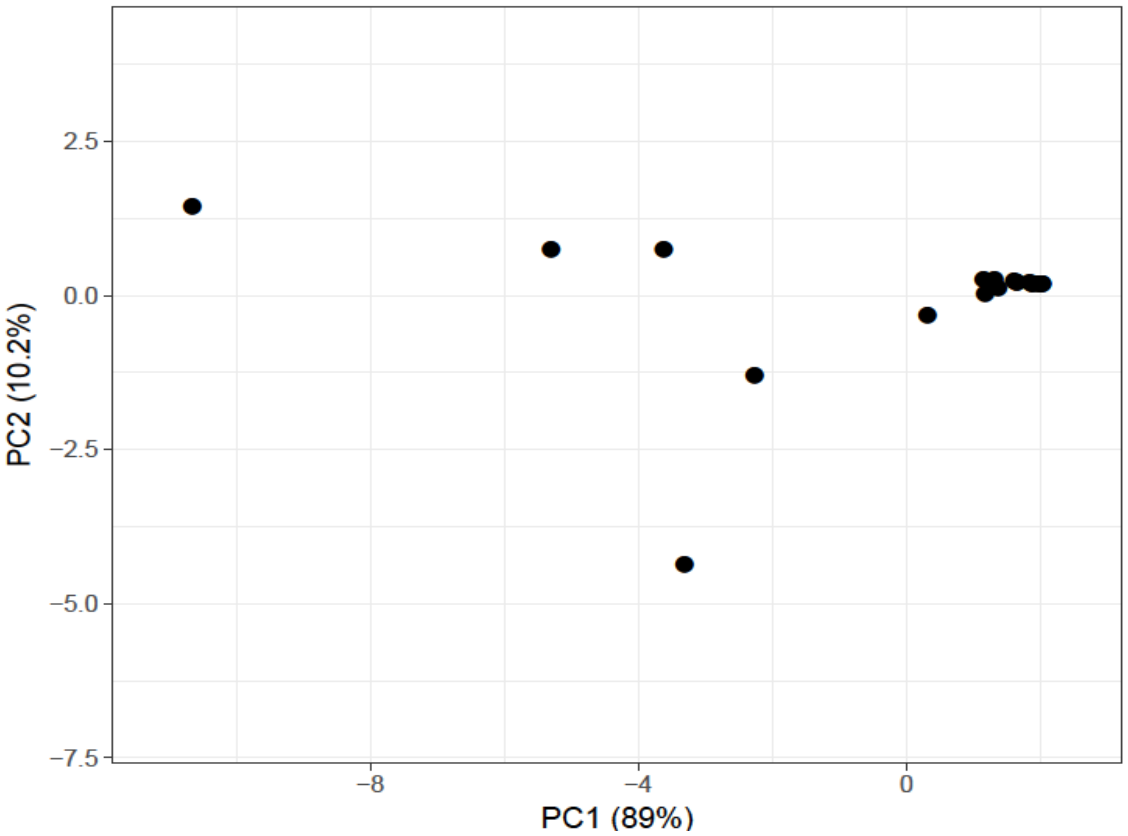


**Figure 3 PCA of correlation loadings for parameter estimations**

**Table 2Parameter values from current COVID-19 data**

| No | Parameter | Calculated Value | Ranges |
|---|---|---|---|
| 1 | $b_X$ | 0.93 | 0.92-0.95 |
| 2 | $b_Y$ | 7.49 | 2.43-19.51 |
| 3 | $b_P$ | 0.0019 | 0.0018-0.0023 |
| 4 | $d_X$ | 75% | 75%-80% |
| 5 | $d_Y$ | 2.00 | 1.99–2.15 |
| 6 | $d_P$ | 0.0020 | 0.0018-0.0023 |
| 7 | $1/\mu_X$ | 60 days | 20-90 days |
| 8 | $1/\mu_Y$ | 11.77 | 6.5-37.4 |
| 9 | $1/\mu_P$ | 5.3 | 5.2-5.5 |

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| | | | |
|---|---|---|---|
| 10 | $1/\mu'_P$ | 5.4 | 5.2-5.5 |
| 11 | $1/\alpha_X$ | 150 days | <180 days |
| 12 | $1/\alpha_Y$ | 110 | 18-130 |
| 13 | $1/\alpha_P$ | 5.9 | 5.8-6.2 |
| 14 | $1/\alpha'_P$ | 3.5 | 2.5-5.0 |
| 15 | $\beta_X$ | 100 days | 95-108 days |
| 16 | $\beta_{XY}$ | 11.00 | 3-12.5 |
| 17 | $\beta_Y$ | 12 days | 10-14 days |
| 18 | $\beta_P$ | 12 days | 3-14 days |
| 19 | $\beta_C$ | 2.00 | 1.4-2.5 |
| 20 | e | 0.3 | 0.1-0.4 |
| 21 | $\rho_P$ | 0.4 | 0.2-0.6 |
| 22 | $\rho'_P$ | 0.6 | 0.5-1.0 |
| 23 | $1/\delta$ | 9 | 10-14 |
| 24 | $\gamma_P$ | 0.6 | 0.5-1.0 |
| 25 | r | 0.4 | 0.5-1.0 |

## 5. Conclusion

We discussed the parameter estimation for PCA analysis of COVID-19 equation. We found current parameter values from COVID-19 data. From this study, we study the very strong and strong parameters keeping mathematics as base and the complication of the previous study is well reduced.Therefore, this research idea could be a fundamental structure for budding researchers as well as the scientists for further study and develop modeling. It is useful for future prediction of COVID-19 equation from real life data.

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