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Predicting Number of People Living with Chronic HCV Using Gray-Weighted Markov Chain Model (GW-MCM)

Mohammad Mahmood Fage Hussein ¹

¹ University of Sulaimani, College of Administration and Economics, Sulaimani, Iraq

Mohammad.fage@univsul.edu.iq¹

Abstract: Hepatitis C virus (HCV) infection is an important global health problem, with millions of people affected by chronic HCV worldwide. Accurate prediction of the number of individuals living with chronic HCV in Iraq is essential for public health planning, resource allocation, and the development of effective intervention strategies. This paper proposes a different approach to predicting chronic HCV prevalence using a weighted-gray Markov chain model. The GW-MCM model integrates Markov chain modelling principles with gray system theory, providing a powerful framework for capturing the dynamics of chronic HCV spread. The model takes into account multiple factors, including HCV transmission rate, treatment rates, and demographic changes. Data from multiple sources, including epidemiological studies, health care records, and population distribution, are integrated into the model to ensure accuracy. This research uses historical data to calibrate and validate the gray-weighted Markov chain model, ensuring its reliability in predicting the spread of chronic HCV over time. Data for this study were obtained from the website: <https://www.globalhep.org/country-progress/iraq>. The data shows the number of people infected with the disease in Iraq for the years 1990–2019. The results show that the prediction accuracy of the GW-MCM model is much higher than the GM model (1,1), and the number of people living with chronic HCV for the years 2020, 2021, and 2022 is not constant, meaning that it increases and decreases until 2025, then begins to increase. After 2025, it begins to decline until it reaches a stable level.

Keywords: Gray System Theory, Weighted Markov Chain, Probability Transition Matrix, Stochastic Modelling, HCV.

التنبؤ بعدد الأشخاص المصابين بفيروس التهاب الكبد الوبائي المزمن باستخدام نموذج سلسلة ماركوف الموزون- الرمادي

أ.م.د. محمد محمود فقي حسين¹

¹ جامعة السليمانية – كلية الإدارة والاقتصاد، السليمانية، العراق

المستخلص: تعد عدوى فيروس التهاب الكبد الوبائي (سي) مشكلة صحية عالمية مهمة، حيث يعاني ملايين الأشخاص من التهاب الكبد الوبائي المزمن في جميع أنحاء العالم. يعد التنبؤ الدقيق بعدد الأفراد المصابين بفيروس

التهاب الكبد الوبائي المزمن في العراق أمراً ضرورياً لتخطيط الصحة العامة وتخصيص الموارد وتطوير استراتيجيات التدخل الفعالة. تقترح هذه الورقة طريقة مختلفة للتنبؤ بانتشار فيروس التهاب الكبد الوبائي المزمن باستخدام نموذج سلسلة ماركوف الموزون- الرمادي. يدمج نموذج GW-MCM مبادئ نمذجة سلسلة ماركوف مع نظرية النظام الرمادي، مما يوفر إطاراً قوياً لالتقاط ديناميكيات انتشار فيروس التهاب الكبد الوبائي المزمن. يأخذ النموذج في الاعتبار عوامل متعددة، بما في ذلك معدل انتقال فيروس التهاب الكبد الوبائي، ومعدلات العلاج، والتغيرات الديموغرافية. ويتم دمج البيانات من مصادر متعددة، بما في ذلك الدراسات الوبائية، وسجلات الرعاية الصحية، وتوزيع السكان، في النموذج لضمان الدقة. يستخدم هذا البحث البيانات التاريخية لمعايرة نموذج سلسلة ماركوف الموزون- الرمادي والتحقق من صحته، مما يضمن موثوقيته في التنبؤ بانتشار فيروس التهاب الكبد الوبائي المزمن بمرور الوقت. تم الحصول على بيانات هذه الدراسة من الموقع: <https://www.globalhep.org/country-progress/iraq>. وتظهر البيانات عدد المصابين بالمرض في العراق للأعوام ١٩٩٠-٢٠١٩. أظهرت النتائج أن دقة التنبؤ لنموذج GW-MCM أعلى بكثير من نموذج GM (١،١)، وأن عدد الأشخاص المصابين بفيروس التهاب الكبد الوبائي المزمن للأعوام ٢٠٢٠ و ٢٠٢١ و ٢٠٢٢ ليس ثابتاً، مما يعني أن فيزداد ويتناقص حتى عام ٢٠٢٥، ثم يبدأ في الزيادة. وبعد عام ٢٠٢٥، يبدأ في الانخفاض حتى يصل إلى مستوى مستقر.

الكلمات المفتاحية: نظرية النظام الرمادي، سلسلة ماركوف الموزون، مصفوفة الاحتمال الانتقالي، النماذج العشوائية، HCV.

Corresponding Author: E-mail: Mohammad.faqe@univsul.edu.iq

1 Methodology

A. Introduction

The Grey Model, also known as Grey System Theory (GST), is a mathematical approach used for prediction and analysis when data is limited, uncertain, or incomplete. Created by Professor Deng Julong in the 1980s, it tackles forecasting issues in cases where traditional statistical methods struggle due to inadequate historical data or significant uncertainties.

The Grey Model works by identifying data patterns and trends in a process called "whitening," and then projecting these patterns into the future for predictions in a process known as "blackening." The core concept is to capture essential data characteristics while minimizing the effects of noise and uncertainty.[2][8]

One commonly used type is GM (1,1), which employs 1-order differential equations to estimate future data values based on known past values. It assumes a linear or exponential growth model to describe the relationship between data and its underlying trends.

The Grey Model is applied in various fields like economics, engineering, and environmental science, especially when dealing with scarce historical data or when conventional forecasting methods fall short.

However, it's worth noting that the Grey Model has limitations. It might struggle with intricate data patterns and depends heavily on assumptions about data dynamics. Its effectiveness is influenced by data quality as well.

In conclusion, the Grey Model offers a valuable tool for forecasting and decision-making in challenging data situations. Yet, its use should be considered alongside other models and domain-specific knowledge.[5]

B. Benefits and Drawbacks of Gray Models:

(1) Benefits of Gray Models:[5][6]

- (A) Simplicity and Perception: Gray models are straightforward and easy to comprehend, making them accessible to various users, including those without strong statistical backgrounds.
- (B) Minimal Data Requirements: Gray models can operate effectively with limited data, which is advantageous in scenarios where only a small data set is available.
- (C) Adaptability: Gray models can be applied to different types of systems, accommodating linear, nonlinear, and time-varying systems, showcasing their versatility across various domains.

- (D) Prediction and Projection: Primarily used for short-term prediction and forecasting, grey models can still provide reasonable predictions even when confronted with insufficient data.
- (E) Transparency: Gray models offer a certain level of transparency in their prediction process, which can be valuable when understanding the rationale behind predictions is important.

(2) Disadvantages of Gray Models:

1. Limited Precision: Gray models generally exhibit lower accuracy in comparison to more intricate and advanced forecasting methods, as they might struggle to capture complex data patterns.
2. Linearity: Certain grey models assume a linear connection between variables.
3. Weakness to Initial Conditions: Gray models are sensitive to the initial parameter values, potentially leading to significantly divergent outcomes with slight changes in these conditions.
4. Inadequate Validation Techniques: Gray models might lack established validation techniques, posing challenges in evaluating the dependability of their predictions.
5. Limited Applicability: Gray models are most suitable for short-term predictions and might not perform well when applied to extended forecasting or complex systems with multiple interacting variables.
6. Absence of Widely Accepted Standards: Gray models lack standardized methodologies and guidelines compared to more established forecasting methods, which could yield inconsistent outcomes if not carefully employed.[2][7]

C. Steps for applying Gray Models GM (1,1) equation:[2][8]

The gray prediction relies on the GM(n,m) method, where “n” represents the order of the grey model, and “m” denotes the number of variables. Within spectrum of grey forecast models, GM (1, 1) stands out by striking a balance between simplicity and result accuracy. Set the authentic data sequence

$$z^{(0)} = \{z^{(0)}(1), z^{(0)}(2), \dots, z^{(0)}(n)\} \quad (1)$$

The original data sequence is accumulated once to generate a new series $z^{(1)}$ is created by accumulating generation operator (AGO):

$$z^{(1)} = \{z^{(1)}(1), z^{(1)}(2), \dots, z^{(1)}(n)\} \quad (2)$$

Within ,

$$z^{(1)}(k) = \sum_{j=1}^k z^{(0)}(j), \quad k = 1, 2, 3, \dots, n \quad (3)$$

The Gray Model (1,1) model can be built by creating a 1-order differential equation for $z^{(1)}(k)$ as:

$$\frac{dz^{(1)}(k)}{dk} + \varphi z^{(1)}(k) = \emptyset \quad (4)$$

Where parameters φ and $\emptyset$ are called the developing coefficient and grey input, respectively.

In practice, parameters φ and $\emptyset$ are not calculated directly from Eq. (4). Therefore, the solution, also identified as time response function, of above equation is given by

$$\hat{z}^{(1)}(k+1) = \left[z^{(1)}(1) - \frac{\emptyset}{\varphi} \right] e^{-\varphi k} + \frac{\emptyset}{\varphi} \quad (5)$$

Where, $\hat{z}^{(1)}(k+1)$ denotes the prediction y at time point k+1 and the coefficients $[\varphi, \emptyset]'$ can be obtained by the Ordinary Least Squares (OLS) method:

$$\hat{\varphi} = [\varphi, \emptyset]' = (\beta' \beta)^{-1} \beta' Z \quad (6)$$

In that:

$$y_n = [z^{(0)}(2), z^{(0)}(3), \dots, z^{(0)}(n)]' \quad (7)$$

$$\beta = \begin{bmatrix} -\frac{(z^{(1)}(1)+z^{(1)}(2))}{2} & 1 \\ -\frac{(z^{(1)}(2)+z^{(1)}(3))}{2} & 1 \\ \vdots & \vdots \\ -\frac{(z^{(1)}(n-1)+z^{(1)}(n))}{2} & 1 \end{bmatrix} \quad (8)$$

Accumulated decrease is used to find forecast values of $\hat{z}^{(0)}(k+1)$ as follow:

$$\hat{z}^{(0)}(k+1) = \hat{z}^{(1)}(k+1) - \hat{z}^{(1)}(k) = [z^{(0)}(1) - \frac{\phi}{\phi}](1 - e^{\phi})e^{-\phi k} \quad (9)$$

The gray fitted precision index is given as follows is given as:

$$y^{(k)} = \frac{z^{(0)}(k)}{\hat{z}^{(0)}(k)} \quad (10)$$

D. Gray-Weight Markov Chain Model

Step 1: We determined the benchmark for the grade of relative error by configuring the Markov chain's status bar based on the GM (1,1) solution.[3][4]

Step 2: The grade of the relative error sequence is verified against this established standard.

Step 3: We compute the ρ_k using the following method:

$$\rho_k = \frac{\sum_{i=1}^{n-k} (z_i - \bar{z})(z_{i+k} - \bar{z})}{\sum_{i=1}^n (z_i - \bar{z})^2} \quad (11)$$

$\bar{z}$: is the mean of relative error, n is the length.

Step 4: Standardizing the Autocorrelation Coefficient. We define the weight of the Markov chain with a step size of k as:

$$w_k = \frac{ABS(\rho_k)}{\sum_{k=1}^m \rho_k} \quad m \text{ is the maximum order which the forecast model need} \quad (12)$$

Step 5: Forecast the probability of the gray fitting accuracy index for the upcoming year.

$$p_i^{(k)}, i \in E_i(z_{1i}, z_{2i}) \text{ where } k \text{ is the step size, } k = 1, 2, \dots, m.$$

The prediction probability for the gray fitting accuracy index being in a particular state is determined by the weighted sum of individual prediction probabilities within that same state.

$$P_i = \sum_{k=1}^m w_k p_i^{(k)}, i \in E \quad (13)$$

The "i" that corresponds to the maximum value among $\{P_i, i \in E\}$ represents the predicted state of the gray fitting accuracy index for the given year.[1]

Step 6: Prediction of the Gray Fitting Accuracy Index Value: Once we establish the state of the gray fitting accuracy index, we employ the state probability linear interpolation technique to compute the precise value of the gray fitting precision index.[6][7]

$$\hat{M}(i) = z_{1i} \frac{P_{i-1}}{P_{i-1} + P_{i+1}} + z_{2i} \frac{P_{i+1}}{P_{i-1} + P_{i+1}} \quad (14)$$

E. Model Evaluation and accuracy Indicators

The GM (1,1) model evaluation involves three components: assessing residuals, examining correlation levels, and conducting posterior difference testing.[3][4]

(1) Mean Absolute Percentage Error (MAPE)

We can gauge the overall precision of this forecasting model by calculating its Mean Absolute Percentage Error (MAPE). MAPE is defined as follows:[4]

$$MAPE = \frac{1}{n} \sum_{k=2}^n ABS\left(\frac{x^{(0)}(k) - \hat{x}^{(0)}(k)}{x^{(0)}(k)}\right), k = 1, 2, \dots, n \quad (15)$$

Where $x(k)$ is real value and $\hat{x}^{(0)}(k)$ is predicted values, and n is the sample size.

(2) Accuracy Rate (P)

Accuracy Rate, which procedures the level of the closeness of the statement of prediction quantity and the real value, P is defined as follows: [4]

$$P = 1 - \text{MAPE} \quad (16)$$

(3) Posterior Difference Test

Posterior difference inspection is i.e. on residual distribution statistical properties of the inspection.

(A) Compute the mean of the original sequence:[4]

$$\bar{x}^{(0)} = \frac{x^{(0)}(1) + x^{(0)}(2) + \dots + x^{(0)}(n)}{n}$$

(B) Computing the Std1 :

$$\text{Std1} = \text{SQRT} \left(\frac{\sum_{i=1}^n [x^{(0)}(i) - \bar{x}^{(0)}]^2}{n-1} \right) \quad (17)$$

(C) Computing means of residual:

$$\bar{\Delta}^{(0)} = \frac{\Delta^{(0)}(1) + \Delta^{(0)}(2) + \dots + \Delta^{(0)}(n)}{n}$$

$$\text{Std2} = \text{SQRT} \left(\frac{\sum_{i=1}^n [\Delta^{(0)}(k) - \bar{\Delta}^{(0)}]^2}{n-1} \right) \quad (18)$$

(D) Computing variance ratio C:

$$z = \frac{\text{Std2}}{\text{Std1}} \quad (19)$$

Table (1): Show the posterior difference test discriminant reference table

P	> 0.95	> 0.80	> 0.70	< 0.70
C	< 0.35	< 0.5	> 0.55	> 0.65
Model accuracy	Excellent	Good	Fair	Poor

2 Data Description and Analysis data

Hepatitis C Virus (HCV) is a viral infection transmitted through contact with infected blood, posing a significant risk to liver health. It is a major contributor to chronic liver conditions, ranging from mild to severe, including cirrhosis and liver cancer. HCV is a substantial global health concern, affecting a large number of individuals worldwide. The research data was obtained through the website: <https://www.globalhep.org/country-progress/iraq>. The data shows the number of people infected with the disease in Iraq for the years 1990–2019

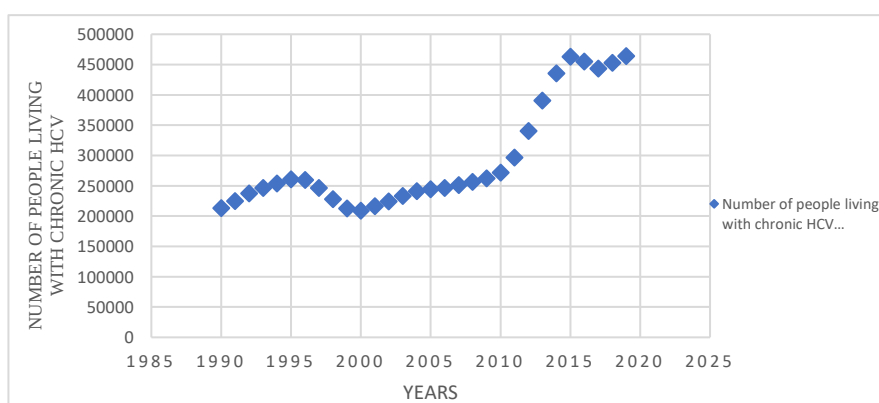


Figure (1): The Number of people living with chronic HCV (RNA+/cAg) in Iraq from (1990-2019)

A. Model Specifications

The numbers of people living with chronic HCV (RNA+/cAg) from 1990 to 2019 forms and original discrete data sequences:

$x^{(0)} = [212964, 224246, 237436, 246368, 253541, 260273, 259125, 246089, 227808, 212261, 208816, 215809, 223841, 232861, 240790, 244058, 246075, 250862, 256310, 262072, 271245, 296178, 339927, 390303, 435435, 462882, 454509, 443125, 452699, 463503]$

The following data series can be calculated through the Accumulating Generation Operator (AGO)
 $x^{(1)} = [212964, 437210, 674646, 921014, 1174555, 1434828, 1693953, 1940042, 2167850, 2380111, 2588927, 2804736, 3028577, 3261438, 3502228, 3746286, 3992361, 4243223, 4499533, 4761605, 5032850, 5329028, 5668955, 6059258, 6494693, 6957575, 7412084, 7855209, 8307908, 8771411]$

Further, data Matrices β and x can be established as:

$$\beta = \begin{bmatrix} -325087 & 1 \\ -555928 & 1 \\ -797830 & 1 \\ \vdots & \vdots \\ -7633646.5 & 1 \\ -8081558.5 & 1 \\ -8539659.5 & 1 \end{bmatrix}$$

$Z^T = [246368, 253541, 260273, 259125, 246089, 272808, 212261, 208816, 215809, 223841, 232861, 240790, 244058, 246075, 250862, 256310, 262072, 271245, 296178, 339927, 390303, 435435, 462882, 454509, 443125, 452699, 463503]$

According to the formula (6), we have

$$\hat{\alpha} = [\alpha, \delta]^T = (\beta^T \beta)^{-1} \beta^T Z$$

Substituting relevant data into the above formula, we have

$$\hat{a} = \begin{bmatrix} \alpha \\ \delta \end{bmatrix} = \begin{bmatrix} -0.0327551 \\ 167642 \end{bmatrix}$$

Then get the predicted value

$$\hat{x}^{(0)}(k+1) = \left[x^{(0)}(1) - \frac{\delta}{\alpha} \right] (1 - e^{\alpha}) e^{-\alpha k}, k = 1, 2, \dots, n-1$$

$$= 171788.8 e^{0.0327551k}$$

B. Evaluate of GM (1,1) forecasting model:

Table below show the precision of GM (1,1) forecasting model:

Table (2): Accuracy of the model	
Test	GM (1,1) accuracy
Residual Test	0.01076
C	0.04138
MAPE	14.028
P=100-MAPE	85.97225

Form table (2) it is clear that the GM (1,1) depending the above tests has a good model with acceptable accuracy. The specific results are shown in Table 1.

Table (3): Number of people living with chronic HCV (RNA+/cAg) in Iraq during 1990 to 2019

Years	# of people living with chronic HCV (RNA+/cAg) ($x^{(0)}$)	$\hat{x}^{(0)}(k+1)$	$X^k = x^{(0)}/\hat{x}^{(0)}(k+1)$	States
1990	212964	212964	1	2
1991	224246	177508.9	1.263	3
1992	237436	183419.5	1.294	3
1993	246368	189526.9	1.300	3
1994	253541	195837.7	1.295	3
1995	260273	202358.6	1.286	3
1996	259125	209096.6	1.239	3
1997	246089	216059	1.139	2
1998	227808	223253.2	1.020	2
1999	212261	230687	0.920	1
2000	208816	238368.3	0.876	1
2001	215809	246305.3	0.876	1
2002	223841	254506.7	0.880	1
2003	232861	262981.1	0.885	1
2004	240790	271737.7	0.886	1
2005	244058	280785.9	0.869	1
2006	246075	290135.3	0.848	1
2007	250862	299796.1	0.837	1
2008	256310	309778.6	0.827	1
2009	262072	320093.4	0.819	1
2010	271245	330751.7	0.820	1
2011	296178	341764.9	0.867	1
2012	339927	353144.8	0.963	2
2013	390303	364903.6	1.070	2
2014	435435	377054	1.155	3
2015	462882	389608.9	1.188	3
2016	454509	402581.9	1.129	2
2017	443125	415986.8	1.065	2
2018	452699	429838.1	1.053	2
2019	463503	444150.7	1.044	2

The states are divided by hierarchical clustering. The results are shown in table (3). The state interval is shown in table (5)

Table (4): Explain the state division

States	Interval
S_1	0.819-0.979
S_2	0.979-1.140
S_3	1.140-1.300

C. Calculating Autocorrelation Coefficient and Markov Chain weighted of different step

Step 1: Construct the transition Probability Matrix

$$P^{(1)} = \begin{bmatrix} 0.923 & 0.077 & 0.000 \\ 0.125 & 0.625 & 0.250 \\ 0.000 & 0.250 & 0.750 \end{bmatrix}, P^{(2)} = \begin{bmatrix} 0.862 & 0.119 & 0.019 \\ 0.194 & 0.463 & 0.344 \\ 0.031 & 0.344 & 0.625 \end{bmatrix}$$

$$P^{(3)} = \begin{bmatrix} 0.810 & 0.146 & 0.044 \\ 0.236 & 0.390 & 0.373 \\ 0.072 & 0.373 & 0.555 \end{bmatrix},$$

Step 2: Calculating Autocorrelation (r_k) and Markov Chain weighted (w_k)

Table (5): Autocorrelation (r_k) and Markov Chain weighted (w_k)

Project	k		
	1	2	3
r_k	0.909	0.737	0.524
w_k	0.419	0.340	0.241

Step 3: Forecasting the status of the gray model accuracy

According to the gray fitting accuracy index and the corresponding state transition probability matrix of numbers of people living with chronic HCV (RNA+/cAg) in Iraq from 1990 to 2019, the state of gray fitting precision index of numbers of people living with chronic HCV (RNA+/cAg) in Iraq wa predicted.

Table (6): Show Gray fitting accuracy index

Initial year	State	Time lag/year	w_k	State probability			Probability source
				State1	State2	State3	
2018	2	1	0.419	0.125	0.625	0.250	$p^{(1)}$
2017	2	2	0.340	0.194	0.463	0.344	$p^{(2)}$
2016	2	3	0.241	0.236	0.390	0.373	$p^{(3)}$
2019				0.175	0.513	0.312	

Depending on the table above, $\max\{P_i, i \in S\} = 0.510$ and at this point $i=1$. It can be seen that the possible state of gray fitting accuracy index in 2019 is 2

Step 4: Prediction value use gray fitting accuracy index

It can be known from the previous calculation output that possible state of grey fitting accuracy index in 2019 is S4 and its adjacent states are S1, S2 and S3 , the specific index value is calculated by interpolation in the interval [a,b], and

$$\hat{x}(2019) = (0.879) \frac{0.18}{0.18 + 0.31} + (1.140) \frac{0.31}{0.18 + 0.31}$$

Data restore, get $x_{2019}^{(0)} = \hat{Y}(2019) \times \hat{x}_{2019}^{(0)} = 1.044 \times 444150.7 = 463747.717$

It can be seen form table (6) that the prediction accuracy of gray weighted Markov model is much higher than that of GM (1,1) prediction model.

Step 5: Forecasting the # of people living with chronic HCV (RNA+/cAg) from 2019 to 2030

Table (7): Prediction Number of people living with chronic HCV (RNA+/cAg) in Iraq from 2020-2030

Years	Prediction Value
2020	464007.3
2021	462994.2
2022	463719.9
2023	463108.4
2024	463663.8
2025	462978.8
2026	465727
2027	463987.4
2028	463309.7
2029	463317.3
2030	463321.1

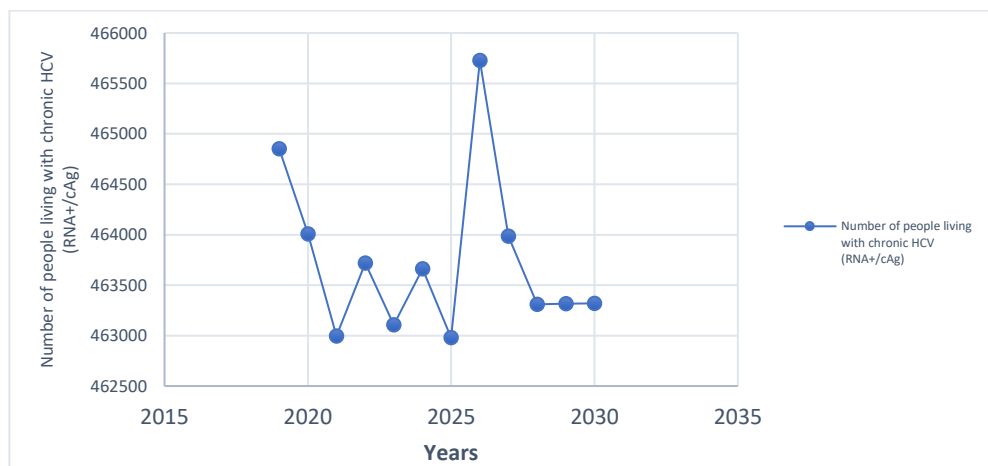


Figure (2): Predicting the number of people living with chronic HCV (RNA+/cAg) in Iraq from 2020 to 2030

3 Conclusion and Recommendations

A. Conclusions

Based on the analysis of the results, the conclusions are the following:

- (1) Predicting the number of people in Iraq infected with chronic HCV in the first three years 2020, 2021, and 2022 is unstable, meaning it increases and decreases until 2025, then begins to increase, and after 2025, it begins to decline, then it begins to reach a stable level.
- (2) The prediction accuracy of Gray Weighted Markov Chain Model (GW-MCM) is much higher than that of GM (1,1) prediction model
- (3) The results obtained through forecasting using the Gray-Weighted Markov Chain Model are close to reality through a comparison of the realistic data for the year 2019 with the data obtained through the analysis.

B. Recommendations

Based on the results of the conclusions, it is recommended the followings:

- (1) Use this type of model in application to other types of diseases.
- (2) We recommend that other researchers apply this study to a relatively long series in order to confirm the accuracy of the results.

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