An Evolutionary Systems Simulation of Bieber Fever: The Most Infectious Disease of Our Time?

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ABSTRACT. Bieber Fever has recently reached new heights, becoming possibly the most widespread pandemic of our age. With infection not only happening from peer to peer but also spontaneously occurring through exposure to media, full eradication is not an easily accomplished task. Using a mathematical model based upon the SIR model for epidemics, we have created an evolutionary system to simulate propagation of Bieber Fever throughout a population under various circumstances. In this model, individuals can either be susceptible, Bieber-infected or bored of Bieber. By varying factors such as positive and negative media attention, effectiveness of media and boredom rates we can deduce the worrying conclusion that, mainly thanks to the constant possibility of re-infection by media, the disease will forever remain able to resurface. Under realistic circumstances, best hopes are for an equilibrium in which infection level is kept low through a permanent stream of negative media.

1. Introduction

Bieber Fever n.
an individual's exorbitant obsession with Justin Bieber

With first occurrences dating back to 2007 after a video of Justin Bieber, aged 12, participating in a local singing contest, Bieber Fever has managed to develop into a full-fledged pandemic over the course of the past 8 years. While thriving mainly among teenagers in first world countries, recent evolution of the Fever seems to have lead to infections in a broader spectrum of ages and populations, making it impossible to ignore the severity of this pandemic for much longer.

Whilst showing similar traits to other infectious diseases, such as rapid transmission rate in large populations, eventual recovery and sometimes debilitating scarring (in the form of inappropriate tattoos of Biebers name or appearance [1], the disease distinguishes itself by transmission through not only peer to peer infection but also by outside media influences. This has made it impossible for researchers to correctly predict its progress by means of traditional epidemic models. Even similar trends spotted in recent decennia, such as during the reign of boy bands like the Backstreet Boys, have remained far from the level of infection which Bieber Fever has accomplished.

In 2012, mathematicians Valerie Tweedle and Robert J. Smith published a mathematical model for predicting the progress of Bieber Fever, based on the SIR epidemic model [1]. This model divides a population into one of three states, being either susceptible, Bieber-infected or bored of Bieber. Individuals can transfer between these states either through contact with direct neighbours or by outside influence of positive and negative media. Based upon this model, we have created an evolutionary systems simulation for populations, evaluating the progress of the disease for each individual of a population over the course of a given period. This model, implemented using the agent-based programming language Netlogo, allows us to find answers to what conditions cause Bieber Fever to thrive or die out.

2. The model

In order to simulate Bieber Fever as an evolutionary system a few adaptations had to be made to the mathematical model by Tweedle and Smith [1]. This model represents the entire population as a whole and evaluates the number of people to be in each state at a certain moment. The rewritten model applies to individual agents and for each agent individually evaluates their state. First an initial evaluation of the mathematical model and its parameters will be explained. Following this is an explanation of the altered evolutionary systems model.

2.1 The initial model

Figure 1 shows a schematic of the model by mathematicians Tweedle and Smith [1], with the population being divided over three states: S being susceptible for the disease, B being infected, - thus being a Belieber, - and finally R for Recovered. Transitions between states are indicated by the arrows. Since the model only concerns individuals aged 5-17, every month new people enter the population depicted by the recruitment rate π, all being susceptible to catch Bieber Fever. Once you belong to the population the only way to exit the population is by maturing [1] (p. 162).

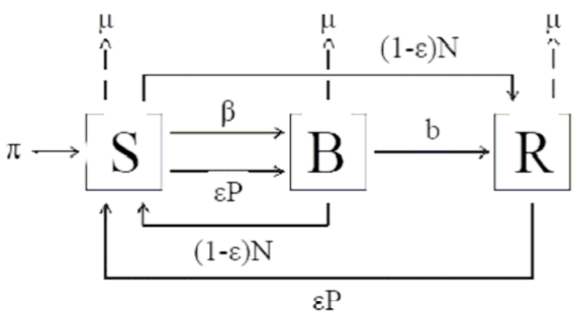

Figure 1. The mathematical model for a population [1] (p. 161)

All the flows containing media, either positive P or negative N, allow transition between states independent of other individuals. Furthermore, they allow transfer from recovered back to susceptible; a variation to the standard SIR (Susceptible-Infected-Recovered) model [2]. This, paired with permanent inflow of new susceptible agents, means that true extinction of Bieber fever is impossible. The factor ε reflects the effectiveness of positive media compared to negative media. The remaining two flows are derived from the standard SIR-model, the transition rate (β) from susceptible (S) to infected (B) and boredom rate (b) from infected (B) to recovered (R).

Before rewriting the model, a behaviour analysis of the model was performed with the help of Excel, the results of which can be found in appendix 1. For the given boredom rates 2 weeks and 2 years, the model was found to always result in one of two equilibria: either total extinction of Bieber Fever or an epidemic equilibrium, with an epidemical threshold R0 determining which of the equilibria the population approaches.

2.2 Our model

As described in the paper [1] (p. 163) the population size will equilibrate to a specific number regardless of the starting size, or the division between the three states. Ensuring that the chosen population size remains constant during the simulation, using a recruitment rate π of 10 per month [1], the maturation rate has to be adapted accordingly, yielding $\mu = \frac{1}{(\text{population size/recruitment rate})}$.

The model was altered to evaluate on a weekly basis instead of a monthly basis like the original model, for more precise results on short intervals. The values for the parameter β and b are transformed so that it can be applied to a single individual rather than a population. The transition rate β, in the paper [1] (p. 163, table 1) initiated to $8{,}3 * 10^{-4}$ people^{-1}month^{-1} , is adapted to a probability that a single person in the population will become infected per time interval, converted from month to week; ensuring that the overall transition of the population will behave identical to the initial model. The same conversion applies to the boredom rate, and multiple values were added for tests ranging from 2 weeks up until 10 years. During each evaluation, each agent in the population determines at random which transition to possibly take, and will have a chance proportionate to that current transition parameter value to actually follow the transition to another state. This allows the population to behave different upon each run of the simulation, while still resulting in the same general outcome for the entire population.

The original age limitation of 5 to 17 years dating from the paper in 2011 is no longer representative of the ever growing fan base of Bieber. However, since the model does not incorporate the age of its agents, and only states that for a given age x and y, agents either enter or exit the population, any arbitrary age can be chosen to enter or exit the population without needing alteration of the model.

The simulation itself was written using the agent-based programming language Netlogo, a commented version of the code can be found in appendix 2. All parameters used in the evolutionary systems model, together with their units and specific values if applicable, are shown in the table of figure 2.

Variable	Symbol	Sample/initial value	Units
Population size	T	100 - 1500	People
Susceptible	S	0.99 T	People
Bieber-infected	B	0.01 T	People
Recovered	R	0	People
Recruitment rate	π	T / 650	People week^{-1}
Transmission rate	β	$1.915 * 10^{-4}$	People^{-1} week^{-1}
Maturation rate	μ	π / T	week^{-1}
Boredom rate	b	$4.62 * 10^{-1}$ (2 weeks) $1.15 * 10^{-1}$ (2 months) $3.85 * 10^{-2}$ (6 months) $9.62 * 10^{-3}$ (2 years) $1.92 * 10^{-3}$ (10 years)	week^{-1}
Positive media rate	P	Varies	week^{-1}
Negative media rate	N	Varies	week^{-1}
Positive media proportion	ε	0.01, 0.25, 0.5, 0.75 or 0.99	-

Figure 2. Parameters and values used in evolutionary systems model

2.3 Media and effectiveness

To determine the influence of media on this evolutionary system, multiple scenarios are available in the model and ratio between the effectiveness of positive and negative media can be chosen from a set of predefined values.

Where the initial model works with a set amount of media for the entire simulation, our model can vary media per week, using data generated from the normal distribution. In the first case, normal conditions[1](p. 163), the total number of influential publications in the media equals 3 per month, two of which are positive and one being of a negative nature. These publications can for example be a newly released album or a big news story. Using these numbers as a mean (ν) for the distribution, -converted to weeks,- and standard deviation equal to $\nu/4$, a sample can be derived as shown in figure 3. Applying the 2-sigma rule [3] this ensures some variation in the data with a 95% confidence interval $[\nu - \frac{\nu}{2}, \nu - \frac{\nu}{2}]$.

The model also allows total absence of media and, lastly, the so-called "Lindsay Lohan effect": a positive peak of media followed by permanent and everlasting reign of negative media [1] (p. 174), the seemingly only solution to a disease such as Bieber Fever. In this case, for a period of 3 months, on average 2 positive publications will be made per week, leaving the negative media equal to normal condition. The remaining period negative media publications will increase to an average of one per week while positive publications only occur approximately once every three months. The standard deviation for both distributions is set to 0.1, allowing only little variation, in order to clearly observe the effects.

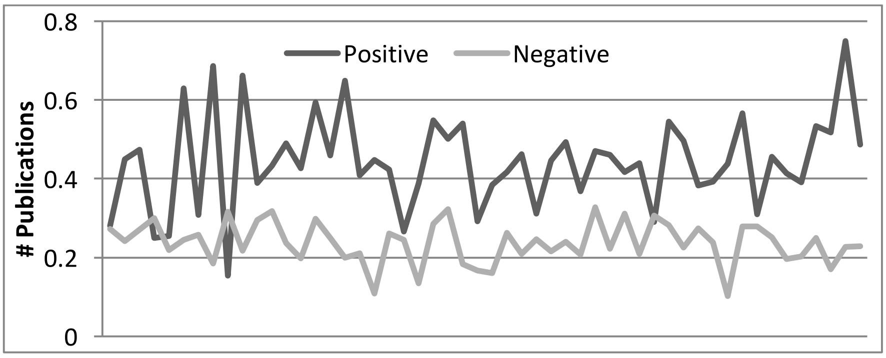

Figure 3. Number of publications per week for a period of a year.

3. Results

For modelling the different circumstances, a population of 500 was chosen. Each case is simulated for a boredom rate of both two years and two years. Two years represents a real fan, outlasting more than one album. Since Bieber Fever traditionally mostly occurred during teenage years, a longer period such as 10 years would not be appropriate. Two months represents individuals being infected by one or two songs recently released, but losing interest soon after these have left the charts.

3.1 Absence of Media

The base case to simulate is the propagation of Bieber Fever in a media-free environment, as shown in figure 4. In this case, an arbitrary value for ε can be chosen. When boredom rate b is set to two years, infection reaches its peak after about 22 weeks with ~82% of the population infected. This is followed by a steep descent until after 6.5 years the equilibrium is reached with an infection level of ~7%.

When boredom rate is set to two months, Bieber Fever does not manage to achieve widespread infection, reaching its peak after 10 weeks with ~38% infected. After exactly a year, an almost disease-free equilibrium is reached with infection remaining below 2%.

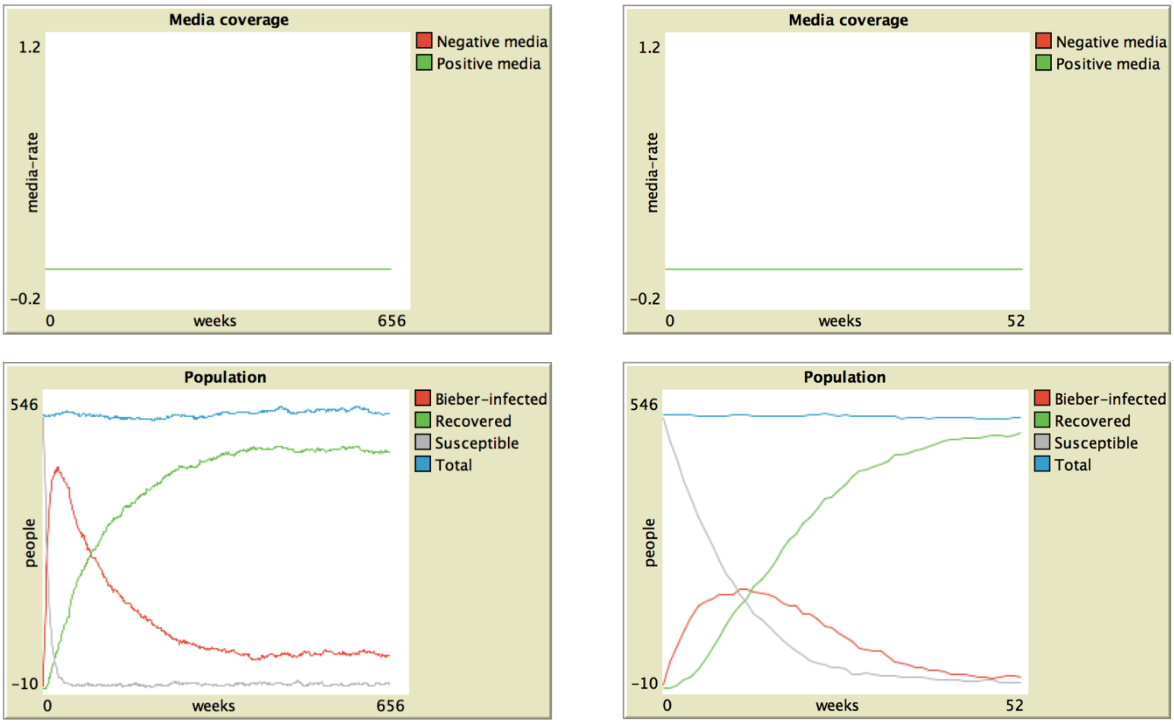

Figure* 4. Absence of media, simulated *for boredom rates of 2 years (left) and 2 months (right)

3.2 Normal Media

In the case where normal [1] amounts of media are present, positive media is thought to be spread more effective thanks to Bieber's management. Thus, ε is set to 0.75 meaning positive stories are spread three times more efficient than negative ones. Figure 5 shows the simulations for this scenario. With boredom rate set to two years, a peak of ~83% infection occurs after about 27 weeks followed by a gradual descent. Equilibrium of ~65% infection arises after about 88 weeks.

For a boredom rate of two months, Bieber Fever peaks at ~36% after 8 weeks. A gradual descent of infection halts at an equilibrium of ~11% about 50 weeks from the start of the infection.

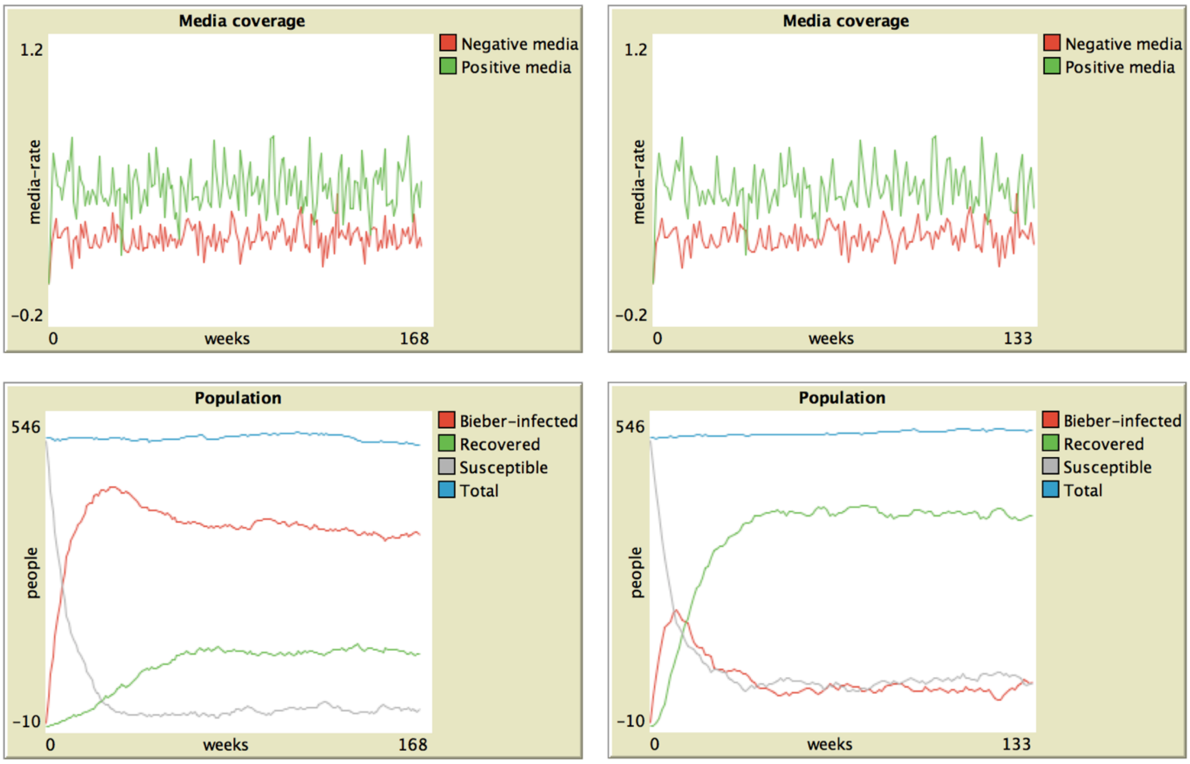

Figure 5. Normal media simulated for boredom rates of 2 years (left) and 2 months (right)

3.3 Prevailing negative media

This case, also known as the "Lindsay Lohan Effect", is simulated by first providing a peak of mostly positive media, to let infection level rise. The first case modelled uses boredom rate of 2 years. After 14 weeks, positive media drops and takes place for prevailing negative media. It takes a while for the increasing infection to respond, with peak of the infection at 28 weeks, 14 weeks after the turnover of media. At peak level, ~84% of individuals is infected, although this is dependent on duration of the initial positive peak, so should only be kept for evaluation of the speed with which infection rate drops. From this peak, it takes 6.8 years for the infection to settle at an equilibrium of ~53%.

With boredom rate set to 2 months, negative media is much more effective in eradicating Bieber Fever. After about 1.4 year, infection settles at ~3%, with its peak occurring at an infection level of ~38% after 12 weeks.

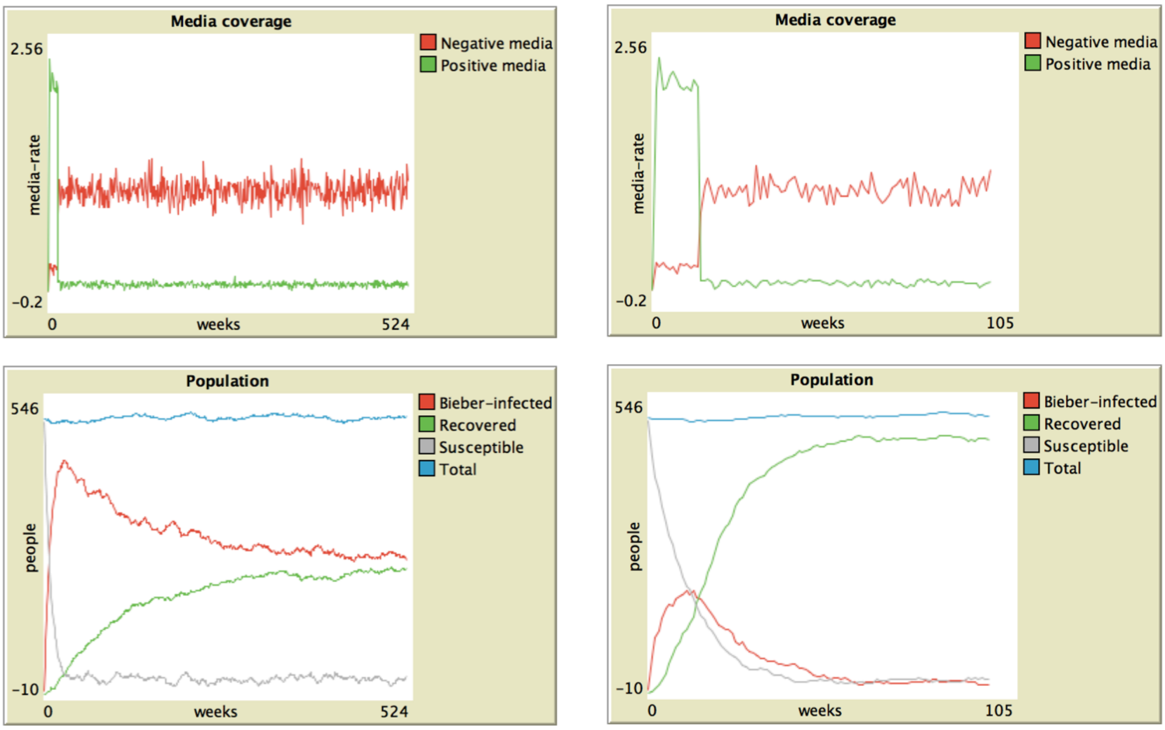

Figure 6. Prevailing negative media, simulated for boredom rates of 2 years (left) and 2 months (right)

4. Conclusion

Looking at the results, the conclusion can be drawn that boredom rate outweighs media influence in determining spread or demise of Bieber Fever. A fast boredom rate of two months does not allow the disease to infect more than 40% of individuals at any time, and allows for faster reach of equilibrium, even up to 34 times as fast in the case of total absence of media.

For this model, equilibrium below 4% is considered as dying out, due to the fact that a constant new influx of susceptible individuals will never allow total extinction. Using this classification, two cases can be labelled as successful eradication of Bieber Fever. These are in total absence of media (<2 % infection) and in the case of reigning negative media (3%), both with fast boredom rate of 2. Thus, even with negative media vastly outnumbering positive media, this will positively influence spread of the disease when compared to total absence.

The reason for this can be deduced from the used mathematical model. The only transition allowing individuals to return from recovered state back to susceptible state is provided by positive media. The reason for this model preventing extinction such as in the classic SIR model is based on both this transition and the permanent inflow of susceptible individuals, with the first reason greatly outweighing the second one. When all media is removed from the simulation, recovered individuals will remain recovered until they exit the population, with the only option for new infections provided by the influx of new susceptible individuals into the population. Since this influx is determined by the recruitment rate, which is a small amount compared to the entire population, this case is the only case where Bieber Fever can with certainty be determined to never resurface again.

In all other cases involving media, due to the transition rates being compared to a randomly generated chance for determining state transition, there is always the possibility, however small, for a full-fledged outbreak of Bieber Fever to return at any time. Normal media, as can be seen in the real world, produce an ideal environment for Bieber Fever to flourish, with recovered individuals being constantly returned to susceptible by positive media occurrences. As Justin Bieber's fan base has a substantial amount of (to put it mildly) dedicated followers, a boredom rate of 2 months is an inaccurate representation of reality. A boredom rate of 2 years would model the current situation more accurately. Furthermore, total absence of media, be it positive or negative, is not feasible in real life. This situation could be approached as Justin Bieber will eventually die, resulting in diminishing media reports and a halt to new songs being published. Bieber Fever will then likely approach the outcome of the absence of media simulation, allowing for a glimmer of hope that Bieber Fever will eventually, in a distant future, die out.

While Justin Bieber is still among the living, however, all hope lies with a lasting reign of negative media, to counteract the inevitable positive media occurrences. Although one can never know what the future holds, chances are that fainting teens, Bieber tattoos, and bedroom walls filled with life-size posters of the Canadian singer will not soon be a thing of the past. But of course, never say never.

5. Discussion

The current evolutionary system is based on a model initialized using data from up to 2011 [1]. Now, five years later, the disease has mutated in several ways, with an ever growing number of casualties. This fact, and the shortcomings of using a mathematical model to simulate a real world phenomenon, leaves several points for inclusion in further research.

The first aspect to consider is severity of the disease per individual, ranging from appreciating his work and turning the volume up when "Sorry" or "Never Say Never" comes on the radio, up to a full-blown case of the Bieber Fever, paired with severe symptoms as described earlier in this paper, These observations may force to re-evaluate the use of one boredom rate for the entire population; some may never cure, while for others it may just be that one summer hit during their holiday spent on the Costa del Sol. An improvement to the current model would be to allow combining of both dedicated and quickly bored agents in one simulation.

Next shortcoming is the lack of age-specific behaviour. The current model inserts individual agents as they enter and leave the required ages to be affected by Bieber Fever (in the original model 5 till 17 years). Besides the fact that any arbitrary combination of ages can be chosen for this without altering the model (other than the size of the population), every individual, be it young or old, is equally susceptible to the Fever. Experience has however shown that teenagers are far more susceptible than elder individuals. An implementation using arrays holding different parameter values for every age for an individual would imitate real life, having only a subset of the population being as easily influenced and the elders more likely to remain in the state in which they already were.

A third misrepresentation is caused by recent developments in media distribution, both in intensity and the increase in number of supporting platforms; including Facebook, Twitter, Instagram and many more. Looking at the increase in Bieber's followers on Twitter solely, there is an increase of over 500%, from 12 million on August 18, 2011 [4], up over 73 million on January 15, 2016[5]. This significant increase can be incorporated in the model, boosting the media influence in relation to peer to peer influence. In addition, real data from social media analysis can be used as input to find out whether the model follows growth and demise of Bieber's fan base after major media events of the past.

6. References

[1] Valerie Tweedle and Robert J. Smith, Understanding the Dynamics of Emerging and Re-Emerging Infectious Diseases Using Mathematical Models (p. 157-177: A mathematical model of Bieber Fever: The most infectious disease of our time?), Transworld Research Network, 2012. (http://mysite.science.uottawa.ca/rsmith43/bieberfever.pdf)

[2] SIR-Model. http://mathworld.wolfram.com/Kermack-McKendrickModel.html (Accessed January 12, 2016)

[3] Chapman & Hall , Basic Statistical Methods and Models for the Sciences, CRC, 2002. (Accessed January 12, 2016)
(https://books.google.nl/books?id=JzlmzkBAeH0C&redir_esc=y)

[4] "Justin Bieber Reaches 12 Million Twitter Followers", Justin Bieber Zone, 2011
(http://www.justinbieberzone.com/2011/08/justin-bieber-reaches-12-million-twitter-followers/)
(Accessed January 15, 2016)

[5] Justin Bieber, Twitter Account
(https://twitter.com/justinbieber) (Accessed January 15, 2016)

Appendix 1 - Data Analysis

A data analysis of the initial model:

In the absence of media, the model is [1] (p. 164, (4.2)):

$$S' = \pi - \beta SB - \mu S$$

$$B' = \beta SB - bB - \mu B \quad \textit{(Corrected version)}$$

$$R' = bB - \mu R$$

S, B, R being the number of people in respectively state Suscepitble, Bieber Infected and Recovered and S', B', R' being the change in each state per period.

$$\text{for } i > 0 \begin{cases} S_{i+1} = S_i + S', & S_0 = 0.99 * \text{initial populations size} \\ B_{i+1} = B_i + B', & B_0 = 0 \\ R_{i+1} = R_i + R', & R_0 = 0.01 * \text{initial populations size} \end{cases}$$

Equilibriums

Let $r = \pi - \frac{\mu(b+\mu)}{\beta}$:

$$(S,B,R) = \begin{cases} r > 0, & (\frac{\pi - r}{\mu}, \frac{br}{\mu(b+\mu)}, \frac{r}{b+\mu}) \\ \text{else}, & (\frac{\pi}{\mu}, 0,0) \end{cases} \quad \textit{(Corrected version)}$$

Parameter settings: (Absence of media)

Recruitment rate	π	10	person per month
Transmission rate	β	0.00083	per person per month
Maturation rate	μ	0.006944	per month

Boredom rate of 2 weeks:

Boredom rate	b	2	per month
	r	-6.7917	
Epidemiological threshold	R0	0.595532	

Population growth and change over time (rounded values)

Time-period	S	B	R	Total	S'	B'	R'	Population growth
0	500.00	5.00	0.00	505.00	4.45	-7.96	10.00	6.49
5	524.73	0.58	5.39	530.70	6.10	-0.92	1.13	6.31
10	555.91	-0.03	5.97	561.84	6.15	0.05	-0.11	6.10
15	586.19	0.00	5.72	591.91	5.93	0.00	-0.04	5.89
20	615.43	0.00	5.53	620.95	5.73	0.00	-0.04	5.69
50	770.99	0.00	4.48	775.47	4.65	0.00	-0.03	4.61
100	964.51	0.00	3.19	967.70	3.30	0.00	-0.02	3.28
200	1204.78	0.00	1.58	1206.36	1.63	0.00	-0.01	1.62
500	1410.92	0.00	0.19	1411.12	0.20	0.00	0.00	0.20

Boredom rate of 2 years:

Boredom rate	b	0.04167	per month
	r	9.593281	
Epidemiological threshold	R0	24.58697	

Population growth and change over time (rounded values)

Time-period	S	B	R	Total	S'	B'	R'	Population growth
0	500.00	5.00	0.00	505.00	4.45	1.83	0.21	6.49
5	511.62	17.68	1.41	530.70	-1.06	6.65	0.73	6.31
10	467.96	84.93	8.95	561.84	-26.24	28.86	3.48	6.10
15	257.58	293.35	40.99	591.91	-54.50	48.45	11.94	5.89
20	63.38	441.33	116.25	620.95	-13.65	1.76	17.58	5.69
50	43.13	254.34	478.00	775.47	0.60	-3.26	7.28	4.61
100	57.77	198.93	714.28	970.98	0.06	-0.13	3.33	3.26
200	58.57	197.35	950.45	1206.36	0.00	0.00	1.62	1.62
500	58.57	197.35	1155.00	1410.92	0.00	0.00	0.20	0.20

Appendix 2 – Netlogo Model Code

```
;;      Authors: Bushra Malik and Tim Nederveen
;;
;;      This program simulates outbreaks of Bieber Fever,
;;      using a mathematical model based on the model used
;;      in the paper "A mathematical model of Bieber Fever:
;;      The most infectious disease of our time?", published
;;      by mathematicians Valerie Tweedle and Robert J Smith.
;;      The program was written as part of the course
;;      Collective Intelligence, as taught on the VU University Amsterdam.
;;
;;
;;

;;Individual agent properties
turtles-own
 [ infected?                    ;; if true, the turtle is infected
   recovered? ]                 ;; if true, the turtle is recovered

globals
 [ %infected                    ;; What % of the population is infectious
   %recovered                   ;; What % of the population is recovered
   #infected                    ;; Number of infected people
   #recovered                   ;; Number of recovered people
   transmission-rate
   recruitement-rate
   maturation-rate
   boredom-rate-list            ;; Used to convert boredom-rate to a value
   boredom-rate-value
   media-type                   ;; Used for choosing correct media array
   positive-media
   positive-media-rate-list
   positive-media-rate
   negative-media
   negative-media-rate-list
   negative-media-rate ]


;;Setup a new simulation
to setup
 clear-all
 setup-constants
 setup-turtles
 update-global-variables
 update-display
 reset-ticks
end

;; This sets up basic constants of the model.
to setup-constants
 ;;Use values from model transformed from 'per month' to 'per week'
```

```
 set transmission-rate 0.00083 / ( 52 / 12 ) * number-people
 set recruitement-rate ( 10 / ( 1500 / number-people ) ) / ( 52 / 12 )

 ;;To maintain a steady population
 set maturation-rate ( 1 / ( number-people / recruitement-rate) )

 ;; boredom-rate-list [ (2 * (52 / 12)) (1 / ((52 / 12) * 2)) (1 / ((52 / 12) * 6)) (1 / ((52 / 12) * 24)) (1 /
((52 / 12) * 120)) ]
 set boredom-rate-list [ 0.46153846153846153846153846153846
0.11538461538461538461538461538462 0.03846153846153846153846153846154
0.00961538461538461538461538461538 0.00192307692307692307692307692308 ]

 if boredom-rate = "2 weeks" [ set boredom-rate-value item 0 boredom-rate-list ]
 if boredom-rate = "2 months" [ set boredom-rate-value item 1 boredom-rate-list ]
 if boredom-rate = "6 months" [ set boredom-rate-value item 2 boredom-rate-list ]
 if boredom-rate = "2 years" [ set boredom-rate-value item 3 boredom-rate-list ]
 if boredom-rate = "10 years" [ set boredom-rate-value item 4 boredom-rate-list ]

 ;;Media arrays are hardcoded, with three options (Absence of media, Normal media and Positive peak
followed by negative) each using an array for positive and negative media
 ;;The arrays contain data for 10 years, with as unit 'story week^-1'
 ;;ARRAYS ARE INITIALIZED, OMITTED DUE TO THE SIZE OF THE ARRAYS
 set positive-media [ [;;absence_array] [;;normal_array] [;;positive_peak_negative_array] ]
 set negative-media [ [;;absence_array] [;;normal_array] [;;positive_peak_negative_array] ]

if media-coverage = "Absence" [ set media-type 0 ]
 if media-coverage = "Normal" [ set media-type 1 ]
 if media-coverage = "Positive-peak-negative" [ set media-type 2 ]

 set positive-media-rate-list item media-type positive-media
 set negative-media-rate-list item media-type negative-media
end

;; We create a variable number of turtles of which 1% are infected and and distribute them randomly
to setup-turtles
 create-turtles number-people
   [ setxy random-xcor random-ycor
     set size 1.2  ;; easier to see
     get-susceptible ]
 ask n-of ceiling( 0.01 * number-people ) turtles
   [ get-infected ]
end

to get-susceptible ;; turtle procedure
 set infected? false
 set recovered? false
end

to get-infected ;; turtle procedure
 set infected? true
end

to get-recovered ;; turtle procedure
 set infected? false
```

```
 set recovered? true
end

to update-global-variables
 if count turtles > 0
  [ set %infected (count turtles with [ infected? ] / count turtles) * 100
    set #infected (count turtles with [ infected? ] )
    set %recovered (count turtles with [ recovered? ] / count turtles) * 100
    set #recovered (count turtles with [ recovered? ] ) ]
end

to update-display
 ask turtles
  [ if shape != turtle-shape [ set shape turtle-shape ]
    set color ifelse-value infected? [ red ] [ ifelse-value recovered? [ green ] [ grey ] ] ]
end

;; Multiply media arrays by their effectiveness ε and use modulo to loop them
to go
 set positive-media-rate item ( ticks mod length positive-media-rate-list ) positive-media-rate-list * ε *
0.05
 set negative-media-rate item ( ticks mod length positive-media-rate-list ) negative-media-rate-list * (
1 - ε ) * 0.05

 ask turtles [
  move
  if infected? [ recover-or-susceptible ]                    ;;evaluate whether or not to
change state
  if infected? [ infect ]                    ;;if still infected, evaluate whether or
not to infect direct neighbors
  ifelse recovered? [ if positive-media-rate > random-float 1 [ get-susceptible ] ]
  [ if not infected? [                    ;;if susceptible
      ;;Evaluate which of three flows gets the chance to change the state of the agent:
      ifelse transmission-rate * random-float 1 > negative-media-rate * random-float 1 or positive-
media-rate * random-float 1 > negative-media-rate * random-float 1
      [ ifelse transmission-rate * random-float 1 > positive-media-rate * random-float 1
        [ if transmission-rate > random-float 1 [ get-infected ] ]
        [ if positive-media-rate > random-float 1 [ get-infected ] ] ]
      [ if negative-media-rate > random-float 1 [ get-recovered ] ] ] ]
  if maturation-rate > random-float 1 [ die ]                    ;;Evaluate whether agent exits
the model
 ]

 if recruitement-rate > random-float 1 [
  create-turtles ( 1 )                    ;;New susceptible entering the population, as
determined by value π (pi) in the model
  [ setxy random-xcor random-ycor
    ;;set age random lifespan
    set size 1.2  ;; easier to see
    get-susceptible ]]
 update-global-variables
 update-display
 tick
end
```

```
;; Turtles move about at random.
to move ;; turtle procedure
 rt random 100
 lt random 100
 fd 1
end

to recover-or-susceptible ;; turtle procedure
 ifelse boredom-rate-value * random-float 1 > negative-media-rate * random-float 1
   [ if boredom-rate-value > random-float 1 [ get-recovered ] ]
   [ if negative-media-rate > random-float 1 [ get-susceptible ] ]
end

to infect ;; turtle procedure
 ask other turtles-here with [ not infected? and not recovered? ]
   [ if transmission-rate > random-float 1 [ get-infected ] ]
end

to startup
 setup-constants ;; so that carrying-capacity can be used as upper bound of number-people slider
end
```