Rubella Report

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April 5, 2020

1 Model

Let us define a k-age group compartmental SIRV model for the infection dynamics of the diseases covered by the MMR vaccine. This model takes the form of a system of four vectorised ordinary differential equations. Each of the k vector entries then corresponds to a given age subgroup with span $m_i, \quad i \in 1...k$. Each equation then governs the dynamics what proportion of the subpopulations is susceptible, infected, recovered, or has been vaccinated.

$$\frac{d\mathbf{s}}{dt} = \mathbf{B} - (\mathbf{V} - \mathbf{D})\mathbf{s} - \mathbf{s} * (\beta(t)\mathbf{i}) + \delta_{t_{end}}(t)\mathbf{Ms}$$

$$\frac{d\mathbf{i}}{dt} = \mathbf{s} * (\beta(t)\mathbf{i}) - (\mathbf{D} - \mathbf{d} - \gamma)\mathbf{i} + \delta_{t_{end}}(t)\mathbf{Mi}$$

$$\frac{d\mathbf{r}}{dt} = \gamma\mathbf{i} - \mathbf{Dr} + \delta_{t_{end}}(t)\mathbf{Mr}$$

$$\frac{d\mathbf{v}}{dt} = \mathbf{Vs} - \mathbf{Dv} + \delta_{t_{end}}(t)\mathbf{Mv}$$

$\mathbf{s} * \mathbf{i}$ *Denotes the elementwise product*
Where:

$\mathbf{s}, \mathbf{i}, \mathbf{r}, \mathbf{v} \in \mathbb{R}^k$	are k-age group classes of susceptible, infected, recovered
$\mathbf{B} \in \mathbb{R}^{k \times k}, \mathbf{B} := diag(B, 0, ..., 0)$	Birth rate
$\mathbf{V} \in \mathbb{R}^{k \times k}, \mathbf{V} := diag(V_1, ..., V_k)$	Vaccination rates
$\mathbf{D} \in \mathbb{R}^{k \times k}, \mathbf{D} := diag(D_1, ..., D_k)$	Death rates due to other causes
$\mathbf{d} \in \mathbb{R}^{k \times k}, \mathbf{d} := diag(d_1, ..., d_k)$	Death rates due to disease
$\beta(t) : \mathbb{R} \to \mathbb{R}^{k \times k}$	The (potentially time-dependent) contact rate
$\gamma \in \mathbb{R}$	Recovery rate
$\mathbf{M} \in \mathbb{R}^{k \times k}$	The age group transition matrix

where **M** has the structure

$$\mathbf{M} = \begin{bmatrix} -m_1^{-1} & & & & \\ m_1^{-1} & -m_2^{-1} & & & \\ & m_2^{-1} & -m_3^{-1} & & \\ & & \ddots & \ddots & \\ & & & m_{k-1}^{-1} & 0 \end{bmatrix}$$

2 Data

Epidemiologic age structured data for Rubella can be obtained from either Health Protection Agency archives [1] or from ECDC Atlas of Infectious Diseases [4].

Immunisation is available from the NHS COVER reports [2].

As a starting point for contact rate matrices, the POLYMOD study [3] can utilised.

This data should enable us to parametrise and fit an age stratified SIRV model for years 1998-2019. Adding gender structure should be explored as well in the case of rubella as the primary concern is cogenital rubella syndrome in newborns.

References

[1] Health Protection Agency. *Epidemiological Data*. Archive Location: UK Library Catalog: webarchive.nationalarchives.gov.uk Publisher: Health Protection Agency, 151 Buckingham Palace Road, London, SW1W 9SZ, 020 7811 7000, webteam@hpa.org.uk. URL: `https://webarchive.nationalarchives.gov.uk/20140505133414/http://www.hpa.org.uk/Topics/InfectiousDiseases/InfectionsAZ/Rubella/EpidemiologicalData/` (visited on 04/05/2020).

[2] *Childhood Vaccination Coverage Statistics - England 2018-19*. NHS Digital. Library Catalog: digital.nhs.uk. URL: `https://digital.nhs.uk/data-and-information/publications/statistical/nhs-immunisation-statistics/england-2018-19` (visited on 04/02/2020).

[3] Joël Mossong et al. "Social Contacts and Mixing Patterns Relevant to the Spread of Infectious Diseases". In: *PLOS Medicine* 5.3 (Mar. 25, 2008). Publisher: Public Library of Science, e74. ISSN: 1549-1676. DOI: `10.1371/journal.pmed.0050074`. URL: `https://journals.plos.org/plosmedicine/article?id=10.1371/journal.pmed.0050074` (visited on 04/02/2020).

[4] *Surveillance Atlas of Infectious Diseases*. URL: `https://www.ecdc.europa.eu/en/surveillance-atlas-infectious-diseases` (visited on 04/02/2020).