Pandemic Risk Modeling

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Financial Risk Management
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Topics for discussion

• What is the current environment with respect to pandemics?

• Which Milliman projects had a key pandemic modeling component?

• What makes this risk difficult to model?

• What methodology is being used to model pandemics?

• What data exists for calibrating the model?

• Are there any other models out there?

• How bad can it get?
Current environment

• In the past 25 years, at least 30 previously unknown diseases have emerged including HIV, SARS, Ebola, and Hepatitis C and E

• H5N1 of great concern because
  – it caused greatest number of human cases in recent years
  – it exhibits all features required to start a pandemic except the ability to efficiently transmit between humans

• As of May 2008 (according to WHO)
  – 383 laboratory confirmed cases
  – 241 deaths
  – 15 countries
Current environment - H5N1 timeline

- **Mid-2003**
  - Outbreaks of highly pathogenic H5N1 began in South-east Asia
- **July 2005**
  - Virus spreads to affect poultry in Russia and Kazakhstan
- **October 2005**
  - Virus is reported in Turkey, Romania and Croatia
- **March 2006**
  - WHO confirms five deaths in Azerbaijan
- **May 2006**
  - WHO confirms first case of infection in Africa (Djibouti)
- **February 2007**
  - WHO confirms first human death in Africa (Nigeria)
- **April 2008**
  - Japan reports H5N1 in wild swans
Current environment - Media
Milliman pandemic modeling projects

- Mortality catastrophe bond projects

<table>
<thead>
<tr>
<th>Company</th>
<th>Structure</th>
<th>Bond Notional</th>
<th>Countries Covered</th>
</tr>
</thead>
<tbody>
<tr>
<td>Swiss Re</td>
<td>VITA I</td>
<td>$400m</td>
<td>France, Italy, Switzerland, UK, US</td>
</tr>
<tr>
<td>Swiss Re</td>
<td>VITA II</td>
<td>$362m</td>
<td>Canada, Germany, Japan, UK, US</td>
</tr>
<tr>
<td>Swiss Re</td>
<td>VITA III</td>
<td>$2,000m</td>
<td>Canada, Germany, Japan, UK, US</td>
</tr>
<tr>
<td>AXA Gie</td>
<td>Osiris</td>
<td>$442m</td>
<td>France, UK, US</td>
</tr>
<tr>
<td>Scottish Re</td>
<td>Tartan</td>
<td>$155m</td>
<td>US</td>
</tr>
</tbody>
</table>

- With mortality catastrophe bonds, investors lose principal when general population mortality increases beyond pre-specified levels
- For mortality catastrophe bonds - bond design, risk analysis, rating agency presentations, investor road shows and calculation agent
- Economic capital modeling and mortality stress testing
Modeling difficulties

• What data is available for calibration?

• When does the pandemic start and when does it end?

• How lethal and infectious is the virus?

• How large is the affected region?

• What is the governmental response?

• How does individual behavior affect the pandemic?
Baseline Model
- Expected mortality
- Expected volatility
- Country specific time series models using historic data using pre-determined age/gender weights

Pandemic Model
- Additional mortality due to potential disease calamity
- Event frequency, severity modeled separately
- Same model for each country

Terrorism Model
- Additional mortality due to potential non-disease events
- Trinomial lattice model
- Same model for each country

Combined Model
- Combines baseline scenarios, disease scenarios and war scenarios for each country
- Converts country specific mortality to a country index for each scenario
- Combines country specific index into a combined index

Results Analyzer
Determines results:
1. Probability of loss
2. Probability of exhaustion
3. Expected loss
4. Average loss

Modeling methodology - Overview

250,000 simulations
Modeling methodology - Pandemic model

- Actuarial model based on a ‘frequency and severity’ approach
- Frequency and severity modeled separately based on historical occurrences of influenza epidemics
- Frequency set at 7.38% per annum based on 31 influenza epidemics over the last 420 years
- Disease epidemics occur in all countries at the same time with the same severity
- Severity curve reflects the age and gender distribution of the underlying cohort being modeled
- Severity modeled using an exponential curve
Modeling methodology - Frequency data

- Pandemics in the past
  - 31 in the last 420 years
  - 4 in the last 100 years

- Pandemic does not become more likely because a long time has passed since the last one - virus mutation is a random process

- Debate as to whether current risk level is elevated due to H5N1 prevalence in bird populations

<table>
<thead>
<tr>
<th>Year</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>1580</td>
<td>First recorded influenza pandemic began in Europe</td>
</tr>
<tr>
<td>1700's</td>
<td>Influenza pandemics in 1729-1730, 1732-1733 and 1781-1782</td>
</tr>
<tr>
<td>1800's</td>
<td>Influenza pandemics in 1830-1831, 1833-1834 and 1889-1890</td>
</tr>
<tr>
<td>1918</td>
<td>Spanish Flu</td>
</tr>
<tr>
<td>1957</td>
<td>Asian Flu</td>
</tr>
<tr>
<td>1968</td>
<td>Hong Kong Flu</td>
</tr>
</tbody>
</table>
Modeling methodology - Severity data

- Data points used for the severity curve: 1918, 1957, 1968, 1977 and SARS 2003

- Severity curve data is sourced from the CDC (except SARS 2003)

- Severity data is based on US population experience and applied proportionately to other countries

- Seasonality element is modeled using a multiple-state model based on epidemiological progression of influenza during a typical influenza season
Modeling methodology - Model results

<table>
<thead>
<tr>
<th>Percentile</th>
<th>Probability</th>
<th>Mortality Increase</th>
<th>Number of US Deaths</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Model 1</td>
<td>Model 2</td>
</tr>
<tr>
<td>0.1</td>
<td>1 in 13,500 years</td>
<td>420%</td>
<td>427%</td>
</tr>
<tr>
<td>0.5</td>
<td>1 in 2,700 years</td>
<td>42%</td>
<td>45%</td>
</tr>
<tr>
<td>1.0</td>
<td>1 in 1,350 years</td>
<td>37%</td>
<td>39%</td>
</tr>
<tr>
<td>3.2</td>
<td>1 in 420 years</td>
<td>27%</td>
<td>29%</td>
</tr>
<tr>
<td></td>
<td></td>
<td>9,660k</td>
<td>9,820k</td>
</tr>
<tr>
<td></td>
<td></td>
<td>970k</td>
<td>1,040k</td>
</tr>
<tr>
<td></td>
<td></td>
<td>860k</td>
<td>900k</td>
</tr>
<tr>
<td></td>
<td></td>
<td>620k</td>
<td>670k</td>
</tr>
</tbody>
</table>

Distribution of Maximum Additional Mortality

<table>
<thead>
<tr>
<th>Range</th>
<th>Proportion of Scenarios</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>98.53%</td>
</tr>
<tr>
<td>1</td>
<td>0.91</td>
</tr>
<tr>
<td>2</td>
<td>0.33</td>
</tr>
<tr>
<td>3</td>
<td>0.15</td>
</tr>
<tr>
<td>4</td>
<td>0.04</td>
</tr>
<tr>
<td>5</td>
<td>0.01</td>
</tr>
<tr>
<td>7</td>
<td>0.01</td>
</tr>
<tr>
<td>100+</td>
<td>0.02</td>
</tr>
</tbody>
</table>

- Results are sensitive to age and gender distribution
- Higher increases for Model 2 due to younger age weighting for Model 2 cohort
Other models - Swiss Re internal model

• Combination of actuarial and epidemiological model

• Model starts by estimating excess mortality rates using data from 20th century pandemics

• Excess rates are then adjusted for health changes since prior pandemics, vaccines, etc.

• For a 1-in-500 year event Swiss Re Internal Model estimates excess US deaths of 300k (Milliman Model = 650k)

• Swiss Re defines recurrence of 1918 pandemic as a 1-in-500 year event
Other models - Lancet 2006 article

- Model published in The Lancet, Volume 368, December 2006
- Statistical model relates excess mortality to per-head income and absolute latitude
- Model calibrated to vital registration data for the 1918 pandemic only
- Model projects excess mortality rates for several countries
- Recurrence of 1918 pandemic would cause 380k US deaths
- Model does not specify the probability of the recurrence of a 1918 pandemic
Other models - RMS model

• Epidemiological model

• Model based on
  – medical research
  – medical trials
  – clinical data
  – published government containment plans

• Model projects
  – virus infectiousness and lethality
  – effects of human behavior and containment plans
How bad can it get?

• In most analyses 1918 pandemic sets the upper limit

• Why was it so bad?
  – No antibiotics, vaccines, etc. were available
  – World War I
  – Outbreaks of contagious disease

• Why it could be worse
  – No biological or logical reason why not
  – Random genetic mutation could produce a more lethal virus

• Why it may not be worse
  – Medical management has improved
  – Virological research and knowledge has grown rapidly
  – Surveillance networks have been established
  – Vaccines have been available since the 1950’s