Quantitative Microbial Risk Assessment (QMRA)
Why Health Risk Models (like QMRA)?

• Human health risk models are not new

• Risk models are much cheaper than epidemiology studies

• But nobody has used one for regulating body contact regulation
Three Basic Steps to a QMRA

- Source identification
- Pathogen loading
- Dose-response modeling
- [translating results into site-specific water quality criteria]
SCCWRP Has Conducted Three QMRAs

• Hobie/Kiddie Beaches, Ventura Harbor
  - Stopped at source identification

• Inner Cabrillo Beach, Los Angeles Harbor
  - Stopped at source identification

• Ocean/Tourmaline Beaches, San Diego
  - QMRA model being used in regulatory decision making right now
Phased Source Identification Approach Works Best

- Mine historical data, reconnaissance
- Intensive beach sampling for indicator bacteria
  - Gradients give clues to potential sources
- More expensive sampling and/or analysis for confirmation
  - Genetic source markers
  - Circulation, fate & transport studies
Enterococcus

Frequency of Exceedence

Percent Exceedence

Site
Presence of Human qPCR markers

Site
1 2 3 4 5 6 7 8

Percent of Samples

HumM2
HF 183
**Enterococcus**

**Gull Marker**

**Human Marker**

**Source Tracking Results:**
Inner Cabrillo Beach  
(Summer 2016)
Surfer Health Study: Empirical and Model

- Epidemiology study collects water quality AND health effects data
  - Wet weather, >10,000 surf exposures, 12 symptoms

- Measured estimate of risk ground-truths model estimates

- Source identification focused on the wet weather discharge
Cumulative Incidence of Gastrointestinal Illness

- **Unexposed Dry Weather Exposure**: 18.0
- **Dry Weather Exposure**: 25.0
- **Wet Weather Exposure**: 30.2

**Excess Risk** 12.2 per 1000

**USEPA Risk** 32 per 1000
Three Basic Steps to a QMRA

• Source identification
• Pathogen loading
• Dose-response modeling
• [translating results into site-specific water quality criteria]
Wet Weather at Ocean Beach
Log Enterococcus (cfu/100 ml)
### Wet Weather Discharge Pathogen Loading: Detection Frequency for Pathogens and Human Markers

<table>
<thead>
<tr>
<th></th>
<th>Norovirus</th>
<th>Adenovirus</th>
<th>Enterovirus</th>
<th>Campylobacter</th>
<th>Salmonella</th>
<th>Human Marker (HF183)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>San Diego River</strong></td>
<td>96%</td>
<td>22%</td>
<td>0%</td>
<td>100%</td>
<td>25%</td>
<td>86%</td>
</tr>
<tr>
<td><strong>Tourmaline Creek</strong></td>
<td>72%</td>
<td>9%</td>
<td>0%</td>
<td>45%</td>
<td>9.5%</td>
<td>95%</td>
</tr>
</tbody>
</table>
Dose-Response Modeling Factors

- Pathogen concentration
  - Dilution

- Volume of water ingested*

- Relationship between number of pathogens ingested and probability of infection*

- Number of infections that result in illness*  
  *Literature values
QMRA Results: Probability of GI Illness

The image displays a box plot showing the probability of GI illness for different pathogens. The y-axis represents the probability of illness on a logarithmic scale, ranging from $10^{-7}$ to $10^{1}$. The x-axis lists the pathogens: Norovirus, Adenovirus, Campylobacter, Salmonella, and Combined. The boxes indicate the interquartile range of the probability, with the central line representing the median. The whiskers show the range of the data, and any points outside the whiskers are considered outliers.
QMRA Results: Probability of GI Illness
QMRAs Can Work

• Currently only mechanism for setting site specific criteria for indicator bacteria

• Based on human health risk
  - Primary hurdle for Natural Source Exclusion

• Technical challenges remain, but primary obstacles are non-technical