A sunset over the ocean with waves crashing on a beach. The sky is filled with soft, colorful clouds in shades of orange, yellow, and pink, reflecting on the water. The waves are white and foamy as they break on the shore.

# Overview of Site-Specific Criteria Guidance & Example QMRA

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# USEPA published guidance for site-specific recreational water quality criteria in 2014 (EPA-820-R-14-010)

- Establish alternative health relationships at sites
  - Epidemiology studies
  - **Modeling studies (Quantitative Microbial Risk Assessment, QMRA)**
  - Specific Technical Support Materials (TSMs) describing how to do this have not been publicly released
  - If scientifically defensible alternative health relationships can be established, site specific criteria can be approved
- Establish equivalency between new methods and methods used for criteria / standards
  - A TSM for this was released

# What is QMRA? A 4 step process

- Describe a “hazard” in ocean water
  - Raw sewage, bird feces, cow feces, stormwater with known concentrations of indicators and pathogens in the hazard (Example: Boehm and Soller 2020)
    - Estimate their concentrations in ocean water given dilution and/or decay
  - Measure concentrations of pathogens and indicators in the ocean water (Example: Viau et al. 2011)
- Describe an exposure scenario
  - Describe how much water a swimmer might ingest
- Calculate a dose of pathogens
  - Volume water ingested x concentration = Dose
- Estimate risk of illness
  - Use models describing risk of infection and illness given a dose of specific pathogens

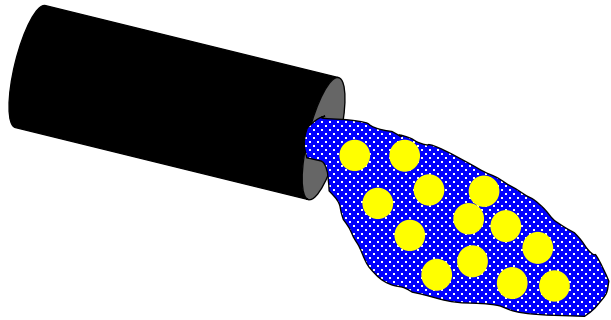


# Example QMRA application

Determine the risk-based threshold of HF183 if the source of HF183 and pathogens is raw sewage using a QMRA approach.

# QMRA hazard and exposure scenario

raw sewage with human markers and pathogens

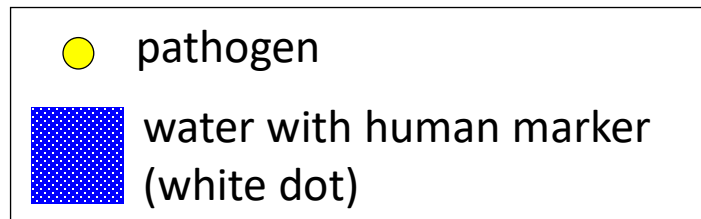


leaks into surface water

surface water with dilute sewage and human markers



*some time  $\tau$  later*  
swimmer exposed to human markers and pathogens



# QMRA scenario

1. Raw sewage discharged into surface water
  - raw sewage contains human marker HF183 and pathogens
2. Some time  $\tau$  passes
3. Swimmer is exposed to specified concentration of HF183
4. Concentration of HF183 is used to predict the amount of sewage in water
5. Pathogen concentration inferred from HF183 concentration and  $\tau$
6. Infection and illness risk predicted
  - dose-response equations
  - probability of illness given infection

# Example QMRA using point values

- Raw sewage has  $10^7$  copies / 100 ml human marker and  $10^5$  norovirus / 100 ml
- Human marker concentration is  $10^3$  copies / 100 ml at the beach when swimmer swims
- $\tau = 0$  days
- Assuming human marker comes from raw sewage, concentration of norovirus is 10 norovirus /100 mL at the beach.
- Swimmer consumes 30 ml water
- Swimmer consumes  $\sim 3$  norovirus
- Probability of infection is 0.4
- Probability of illness is 0.2

$$C_{i\_surface} = C_{meas} C_{i\_sewage} \exp((k_{hf} - k_i)\tau) / C_{hf\_sewage}$$

$C_{i\_surface}$  = pathogen i concentration in surface water

$C_{i\_sewage}$  = pathogen i concentration in sewage

$C_{hf\_sewage}$  = human marker concentration in sewage

$k_{hf}$  = first order decay constant of human marker

$k_i$  = first order decay constant of pathogen i

$\tau$  = time

$C_{meas}$  = concentration of human marker measured



$$C_{i\_surface} = C_{meas} C_{i\_sewage} \exp((k_{hf} - k_i)\tau) / C_{hf\_sewage}$$

$C_{i\_surface}$  = pathogen i concentration in surface water

$C_{i\_sewage}$  = pathogen i concentration in sewage

$C_{hf\_sewage}$  = human marker concentration in sewage

$k_{hf}$  = first order decay constant of human marker

$k_i$  = first order decay constant of pathogen i

$\tau$  = time

$C_{meas}$  = concentration of human marker measured

use values from literature

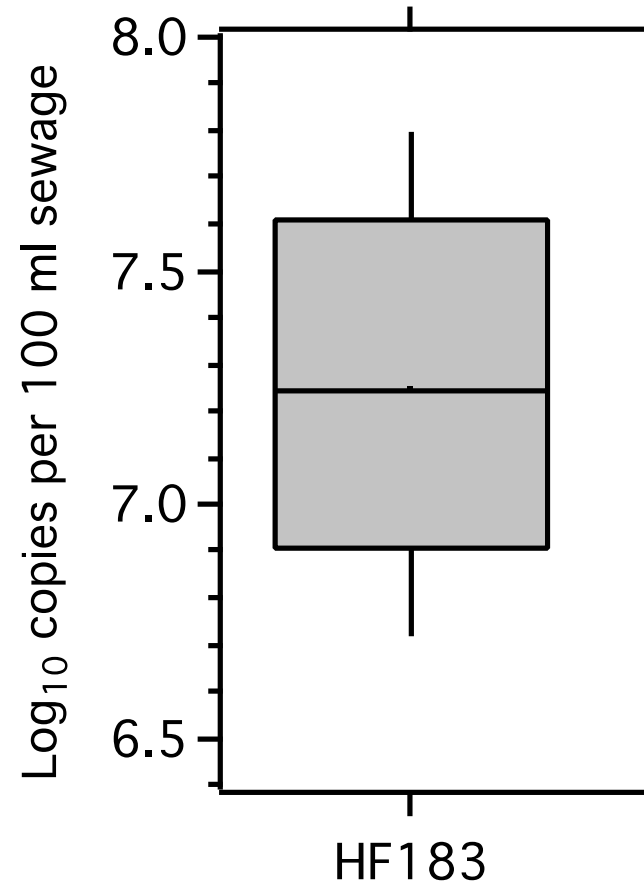
vary ourselves to preset values

# QMRA implementation

- Risk estimates for
  - $C_{\text{meas}}$  (human marker) at 1, 10, 100, 1000, 10000 copies/100 ml surface water
  - $\tau = 0, 0.5, 1, 1.5, 2, 2.5, 3$  days
- 10000 iterations per  $C_{\text{meas}}-\tau$  combo using Monte Carlo simulations
- Model requirements:
  - volume of water ingested
  - human marker & pathogen concentrations in raw sewage
  - k values for human marker and pathogens
  - dose-response models and  $P_{\text{ill}|\text{infected}}$
  - model parameters drawn from distributions
- 10000 model outputs for each  $C_{\text{meas}}-\tau$  combo:
  - $P_{\text{ill}_j}$  from each reference pathogen j
  - $P_{\text{ill}} = 1 - \prod(1 - P_{\text{ill}_j})$

$C_{hf\_sewage}$

# HF183 in raw sewage



*These data are from 2011...  
more updated data?  
More localized data?*

54 samples of raw sewage from 37 states

# $C_{i\_sewage}$ and dose-response

Organism	$C_{sewage}$ range ( $\log_{10}$ per L)	$P_{inf}$	$P_{ill inf}$ (distribution)
<i>Salmonella spp.</i>	[0.5, 5]	$1 - (1 + \mu/2884)^{-0.3126}$	0.17-0.4 (uniform)
<i>Campylobacter</i>	[2.9, 4.6]	$1 - {}_1F_1(0.024, 0.024 + 0.011, -\mu)$	$1 - (1 + n\mu)^{-r}$
<i>E. coli</i> O157:H7	[-1, 3.3]	$1 - (1 + \mu/48.8)^{-0.248}$	0.2-0.6 (uniform)
<i>Cryptosporidium</i>	[-0.52, 4.7]	$1 - \exp(-0.09 \mu)$	0.3-0.7 (uniform)
<i>Giardia</i>	[0.51, 4.2]	$1 - \exp(-0.0199 \mu)$	0.2-0.7 (uniform)
Norovirus	[4.0, 1.1]*	$1 - {}_1F_1(0.04, 0.04 + 0.055, -\mu)$	0.6

\* log-normal distribution:  $\log_{10}$  mean and  $\log_{10}$  stdev

## Volume ingested during swimming

$\log_{10}$  normal with mean of 1.146 and standard deviation of 0.545 units of ml  
(Dufour et al. 2017)

*Distributions can be updated over time?*

*More localized data?*

# k values (d<sup>-1</sup>)

Target	N	log <sub>10</sub> - mean	log <sub>10</sub> - stdev	Geo- mean k
HF183	52	0.063	0.34	1.16
HumM2	15	0.050	0.37	1.12
BacHum-UCD	13	-0.038	0.43	0.92
Salmonella	84	-0.17	0.51	0.68
Campylobacter	41	0.28	0.84	1.91
E. coli O157:H7	84	-0.43	0.37	0.37
Giardia	14	-1.36	0.96	0.04
Cryptosporidium	22	-1.39	0.80	0.04
Virus	8*	-0.81	0.50	0.15

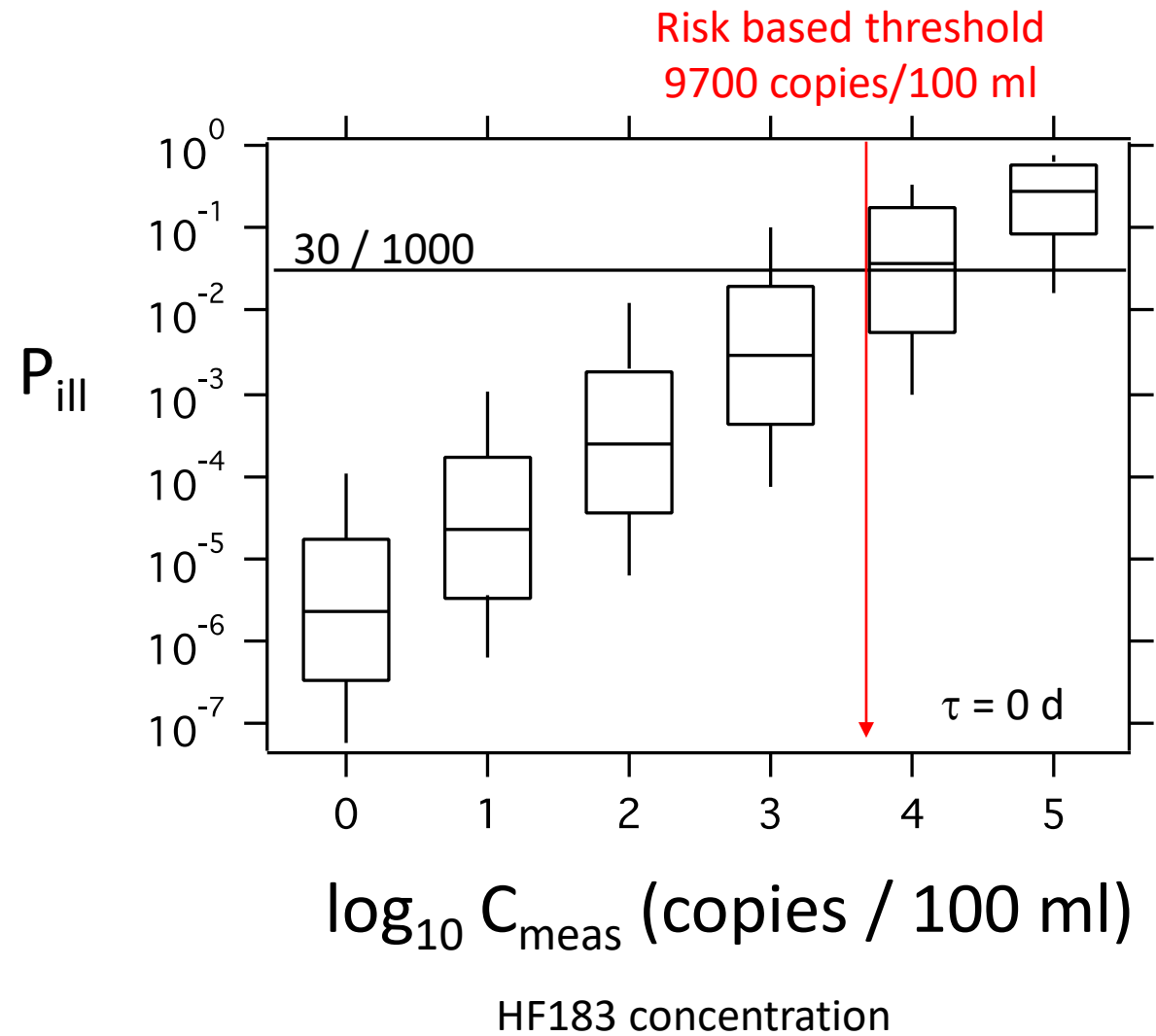
N = 2 for human norovirus, N = 4 for feline calicivirus, N = 2 for murine norovirus

# Now we can run our model!

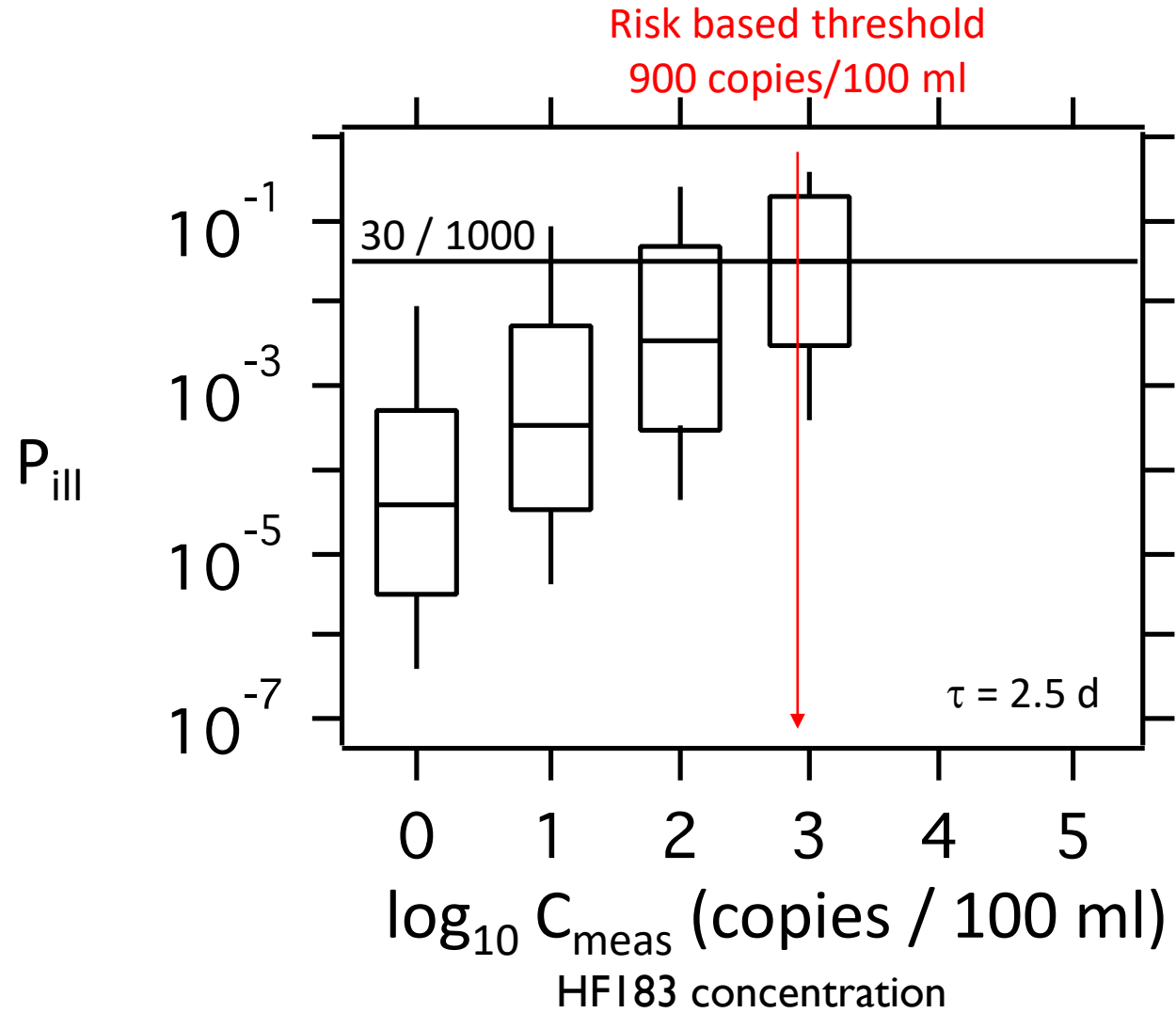
1. Modeler specifies  $C_{\text{meas}}$  (HF183 conc.) and  $\tau$
2. Run model in Matlab and R
3. Output: 10000  $P_{\text{ill}}$  estimates that consider the range of model parameters



# Model output for $\tau=0$



# Model output for t=2.5 d



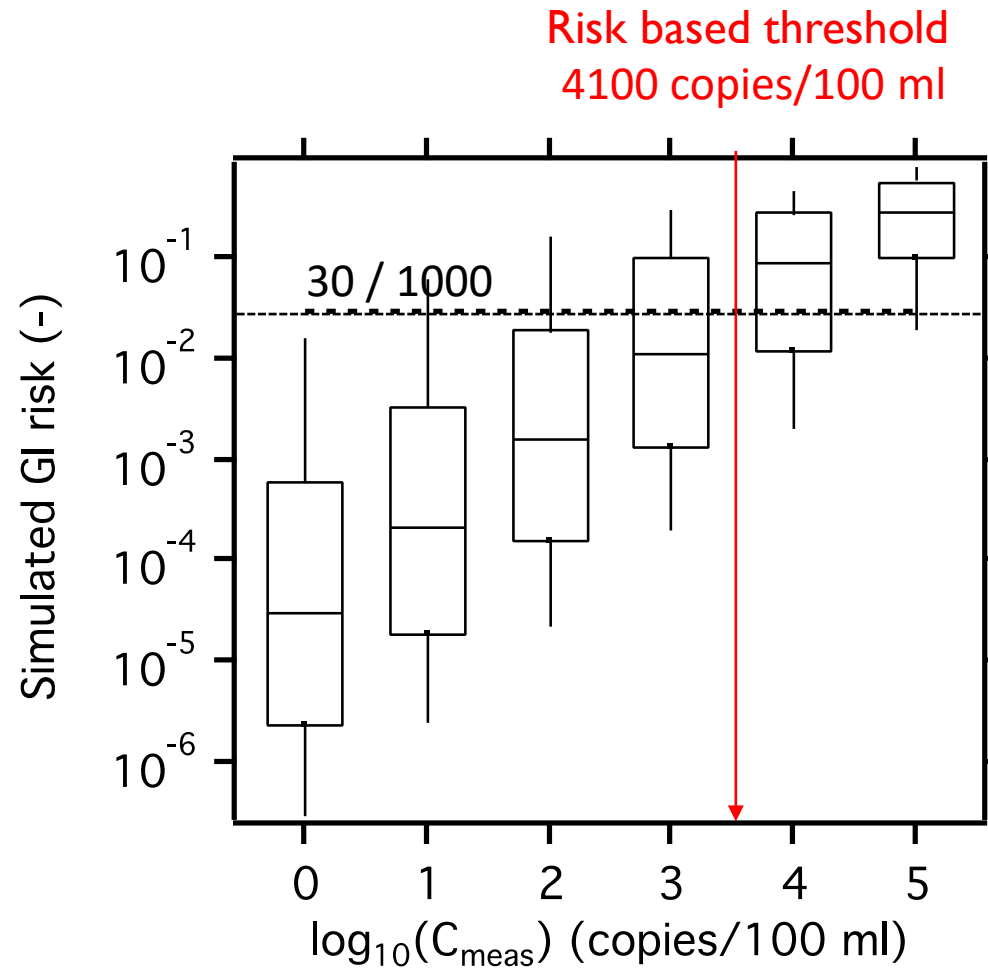


# What risk based threshold should we use?

## We don't know t!

- Re-ran QMRA
- Specify  $C_{\text{meas}}$
- Draw t from a uniform distribution from 0 to a maximum realistic value (varies with  $C_{\text{meas}}$ ) because we don't know t
  - If you measure a specific HF183 value and you know how fast it decays and the source has a specific concentration of HF183, then you can constrain how old it can possibly be
- All other methods the same

# Results for $\tau$ unknown



# Can We Swim Yet? Systematic Review, Meta-Analysis, and Risk Assessment of Aging Sewage in Surface Waters

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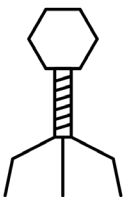
## Supporting Information

**ABSTRACT:** This study investigated the risk of gastrointestinal illness associated with swimming in surface waters with aged sewage contamination. First, a systematic review compiled 333 first order decay rate constants ( $k$ ) for human norovirus and its surrogates feline calicivirus and murine norovirus, *Salmonella*, *Campylobacter*, *Escherichia coli* O157:H7, *Giardia*, and *Cryptosporidium*, and human-associated indicators in surface water. A meta-analysis investigated effects of sunlight, temperature, and water matrix on  $k$ . There was a relatively large number of  $k$  for bacterial pathogens and some human-associated indicators ( $n > 40$ ), fewer for protozoan and ( $n = 14–22$ ), and few for human norovirus and its *Caliciviridae* surrogates ( $n = 2–4$ ). Average  $k$  ranked: *Campylobacter* > human-associated markers > *Salmonella* > *E. coli* O157:H7 > norovirus and its surrogates > *Giardia* > *Cryptosporidium*. Compiled  $k$  values were used in a quantitative microbial risk assessment (QMRA) to simulate gastrointestinal illness risk associated with swimming in water with aged sewage contamination. The QMRA used human-associated fecal indicator HF183 as an index for the amount of sewage present and thereby provided insight into how risk relates to HF183 concentrations in surface water. Because exposure to norovirus contributed the majority of risk, and HF183  $k$  is greater than norovirus  $k$ , the risk associated with exposure to a fixed HF183 concentration increases with the age of contamination. Swimmer exposure to sewage after it has aged  $\sim 3$  days results in median risks less than 30/1000. A risk-based water quality threshold for HF183 in surface waters that takes into account uncertainty in contamination age is derived to be 4100 copies/100 mL.



# Summary of work to date

Indicator (source)	Risk-based threshold (copy/100 mL)	Reference	Notes
HF183 (raw sewage, uncertain age)	4100 copy/100 mL	Boehm et al. 2018	This example
HF183 (raw sewage, uncertain age)	525 copy/100 mL	Boehm and Soller 2020	Updated k values (to be temperature dependent), updated pathogen distributions in sewage
F+ coliphage (raw sewage, uncertain age)	~1 PFU/100 mL	Boehm 2020	For 15-25°C water
Somatic coliphage (raw sewage, uncertain age)	~1-10 PFU/100 mL	Boehm 2020	For 15-25°C water



# Things to remember



1. QMRA models require defining the hazard (pathogens) and the exposure
2. The pathogen levels can be modeled from a specific source (like sewage)
  - Carefully choose model inputs
  - Understand assumptions
3. Pathogen levels can also be measured (Viau et al. example)
4. Colleagues and I have published a number of risk-based thresholds for different indicators over the years and established a framework for doing so

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