Quantitative Microbial Risk Assessment for Contaminated Private Wells in the Fractured Dolomite Aquifer of Kewaunee County, Wisconsin

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Project Research Team

LIDE Team

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- Aaron D. Firnstahl (USGS)
- Joel P. Stokdyk (USGS)

L·I·D·E

LABORATORY FOR INFECTIOUS DISEASE AND THE ENVIRONMENT

Collaborators

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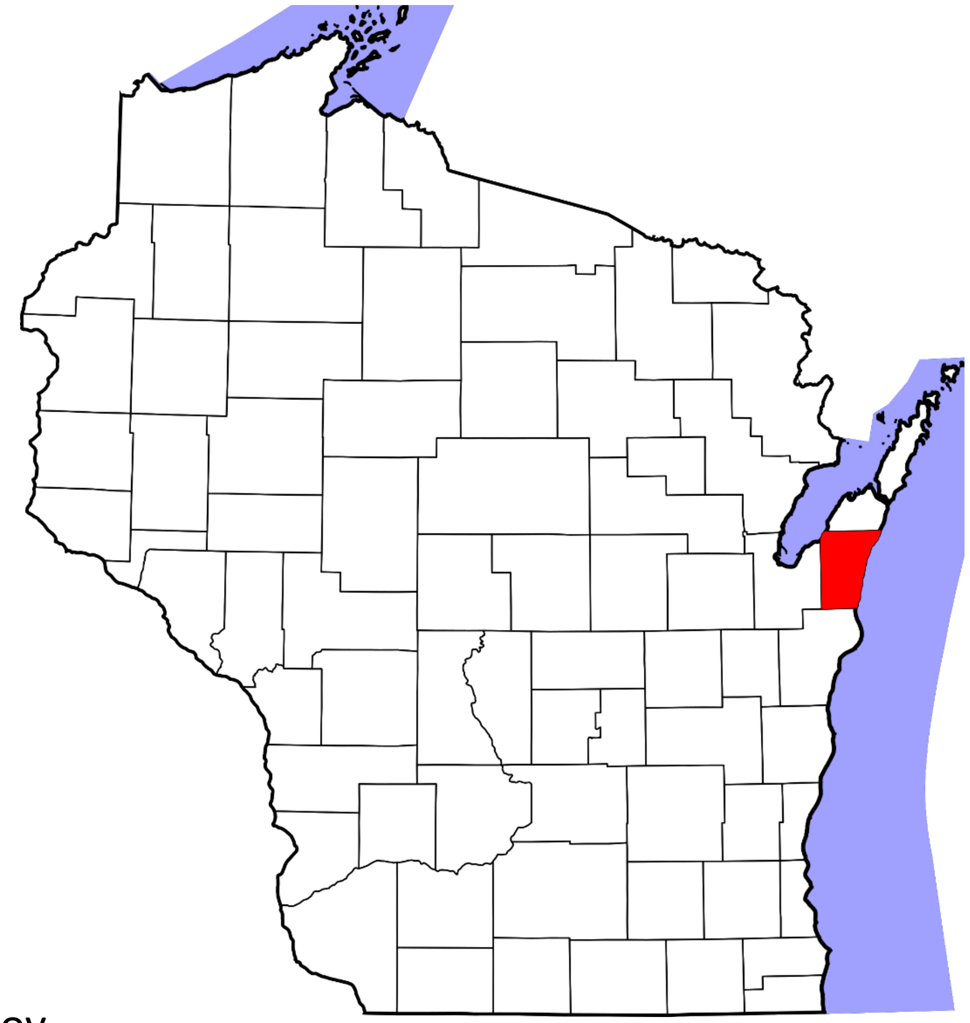
- Maureen A. Muldoon (Wisconsin Geological and Natural History Survey)
- Davina E. Bonness (Kewaunee County Department of Land and Water Conservation)
- Randall J. Hunt (USGS)

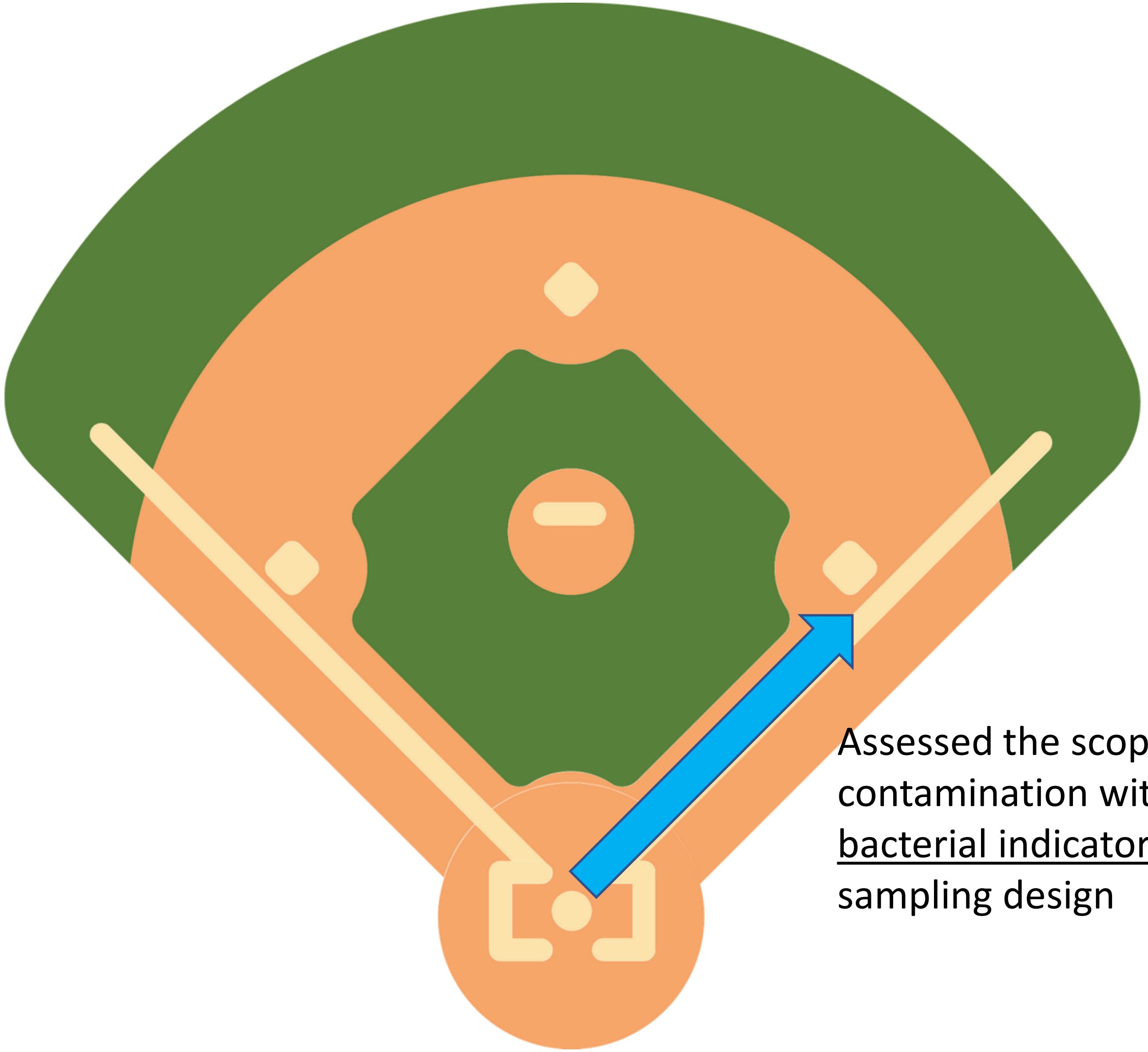
Kewaunee County – Background

- Population: 20,000+
  - 12,000 rely on private wells
- Thousands of private septic systems
- Tens of thousands of cattle, many on CAFOs
- Fractured Silurian dolomite aquifer



Map by David Benbennick using data from nationalatlas.gov.

Homerun Scored for Private Well Research



Assessed the scope of private well contamination with nitrate and bacterial indicators using sophisticated sampling design

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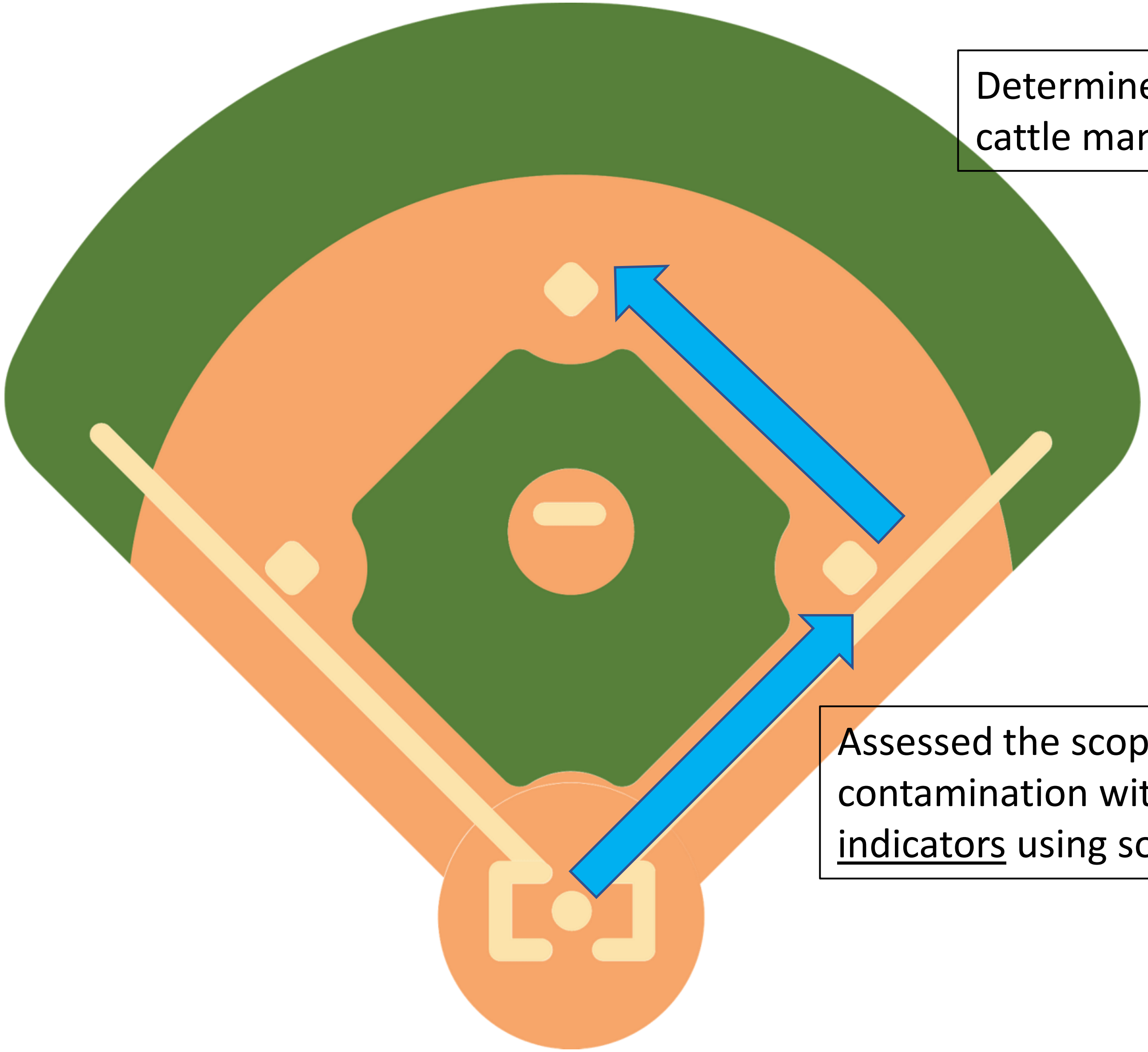
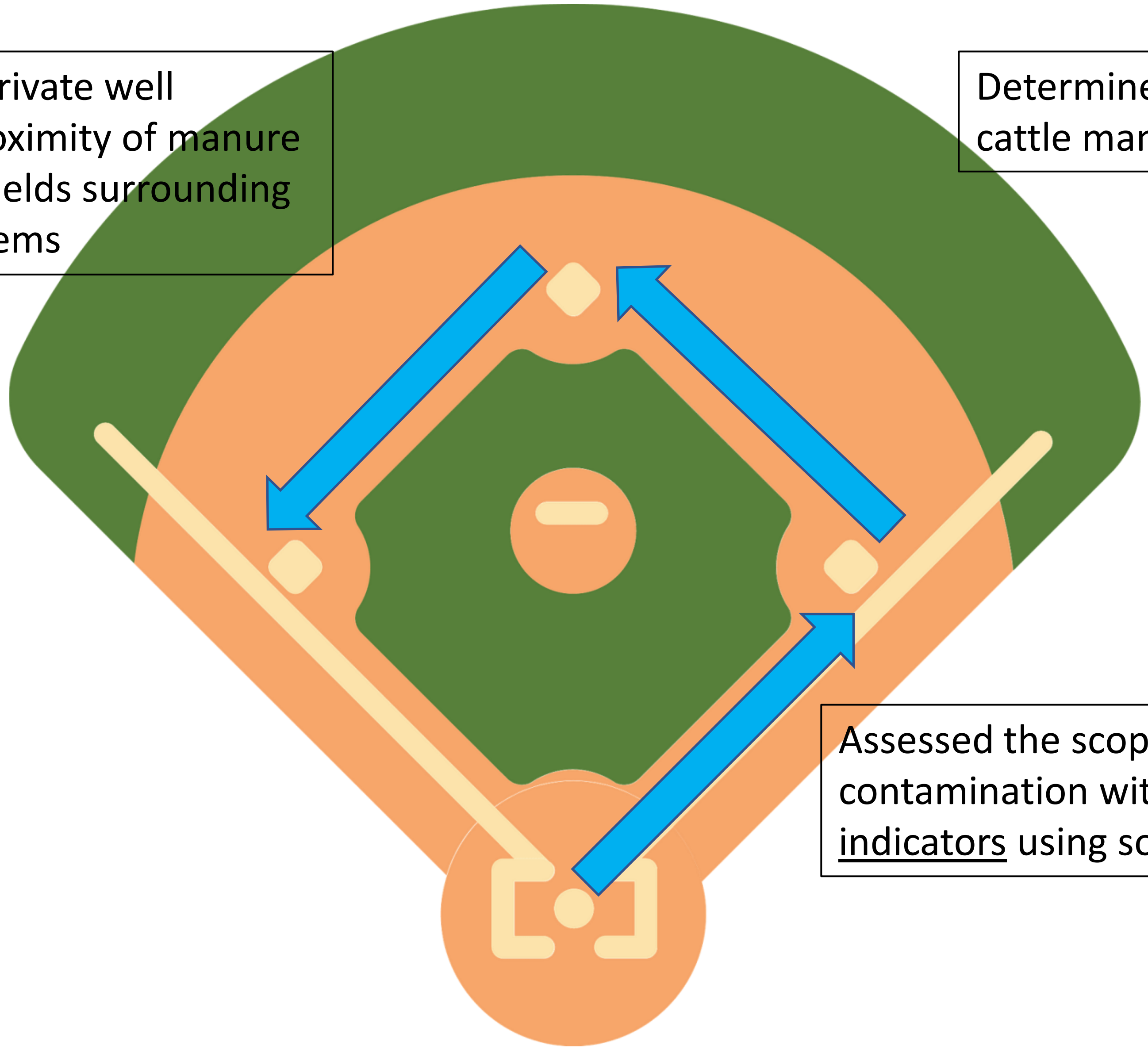


Determined sources of fecal contamination, cattle manure or septic systems

Assessed the scope of private well contamination with nitrate and bacterial indicators using sophisticated sampling design

Homerun Scored for Private Well Research

Identified risk factors for private well contamination, such as proximity of manure lagoons, area of cropped fields surrounding well, density of septic systems



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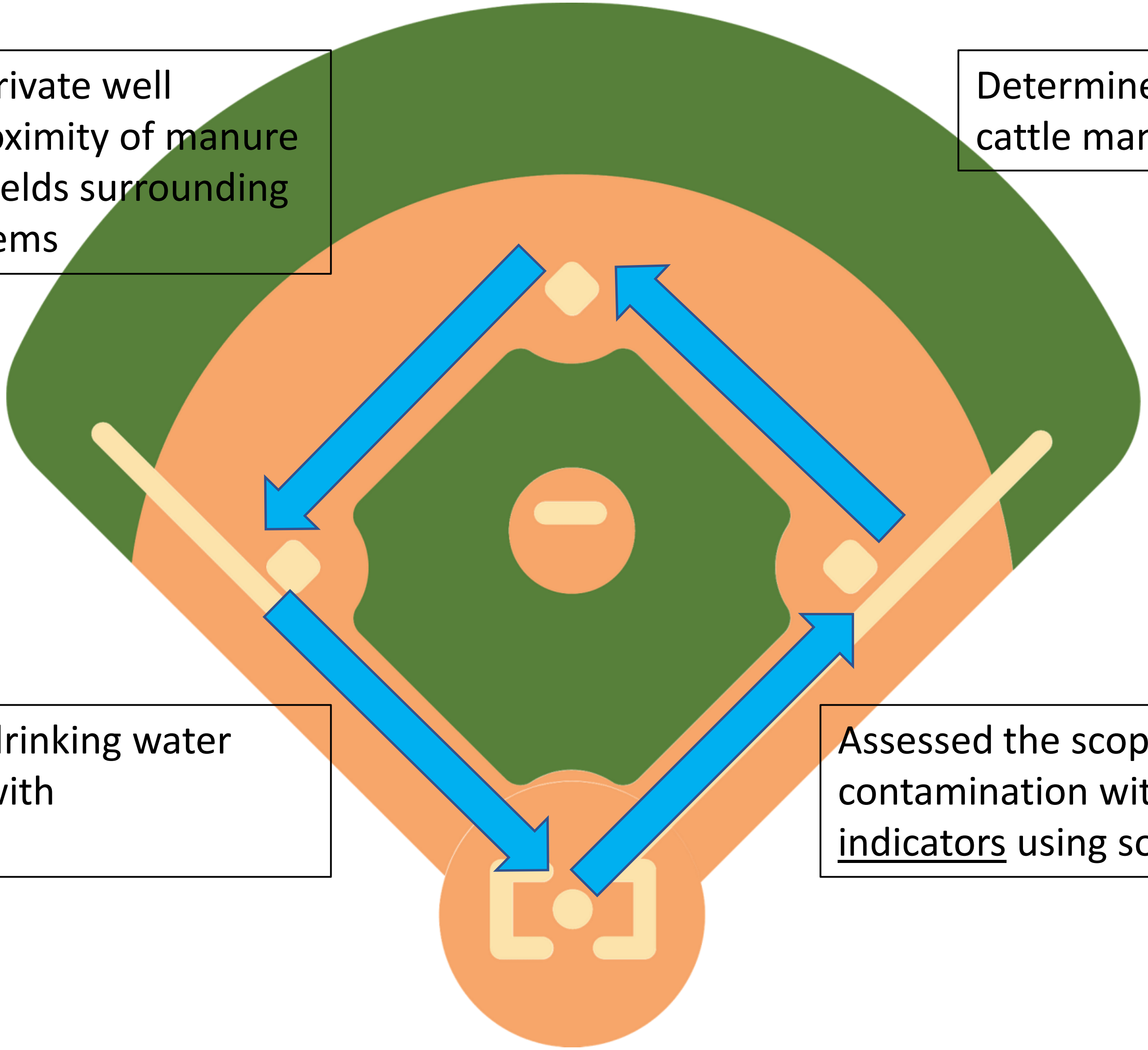

Estimate health risk from drinking water from wells contaminated with gastrointestinal pathogens

Assessed the scope of private well contamination with nitrate and bacterial indicators using sophisticated sampling design

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Research

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Sources and Risk Factors for Nitrate and Microbial Contamination of Private Household Wells in the Fractured Dolomite Aquifer of Northeastern Wisconsin

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Research

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Quantitative Microbial Risk Assessment for Contaminated Private Wells in the Fractured Dolomite Aquifer of Kewaunee County, Wisconsin

Tucker R. Burch,[1] Joel P. Stokdyk,[2] Susan K. Spencer,[1] Burney A. Kieke Jr.,[3] Aaron D. Firnstahl,[2] Maureen A. Muldoon,[4] and Mark A. Borchardt[1]

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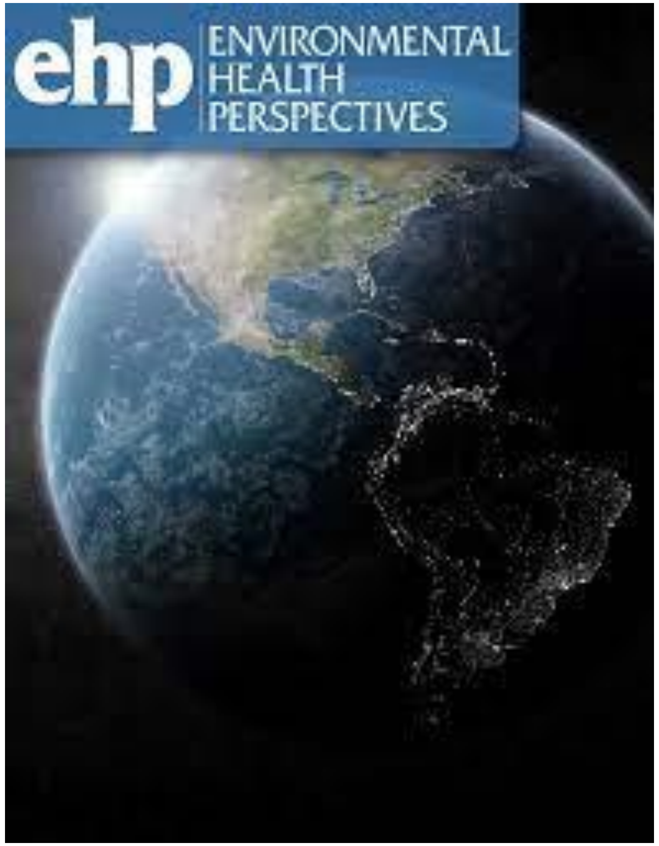
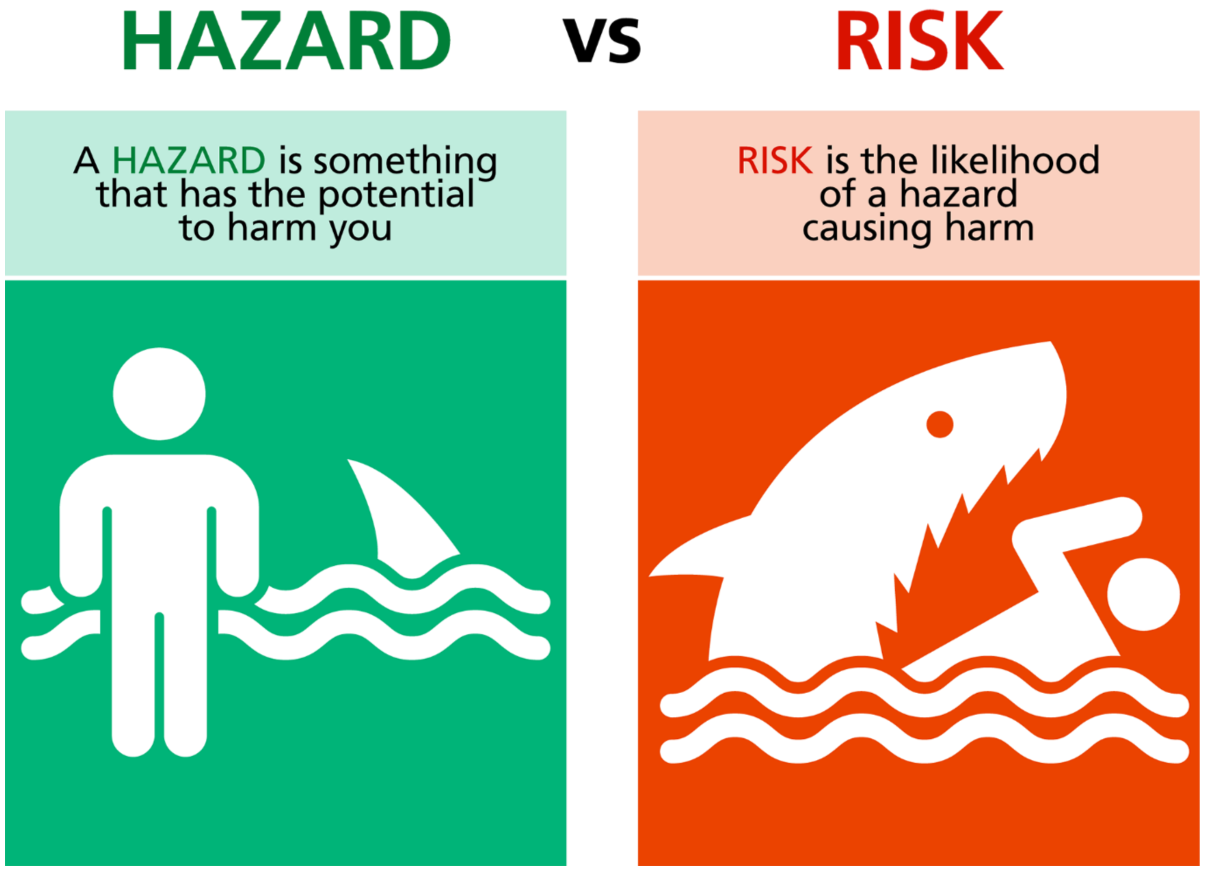


What is risk?

- Dictionary definition: the possibility of loss or injury

Probability

Damage



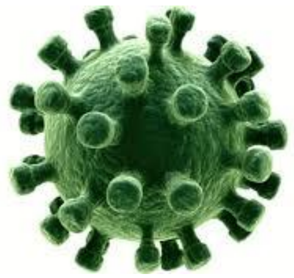
$\boxed{\text{Risk} = \text{Probability} \times \text{Damage}}$

What is quantitative microbial risk assessment (QMRA)?

- Estimation of risk (Probability × Damage) for microbial hazards
- Hazards – often foodborne or waterborne gastrointestinal pathogens (e.g., *Salmonella*, *Cryptosporidium*)
- Damage (i.e., health outcomes)
  - Infections – carriage of pathogen in gastrointestinal tract
  - Symptomatic illness – acute gastrointestinal illness (AGI): some combination of vomiting, diarrhea, and other symptoms
  - AGI is often self-limiting, but can be severe in immuno-compromised and other susceptible hosts (e.g., the very young or very old)

Conducting a QMRA – 4 steps

1. Hazard identification
   - Which pathogens? Which exposure routes?
2. Exposure assessment
   - Define dose: quantify frequency and magnitude of exposure
3. Dose-response assessment
   - Standard models for each pathogen
   - Extrapolated from experimental feeding study and/or outbreaks
4. Risk characterization
   - e.g., which outcome? Infection? Illness?
   - What role does variability/uncertainty play?



QMRA = mathematical predictions

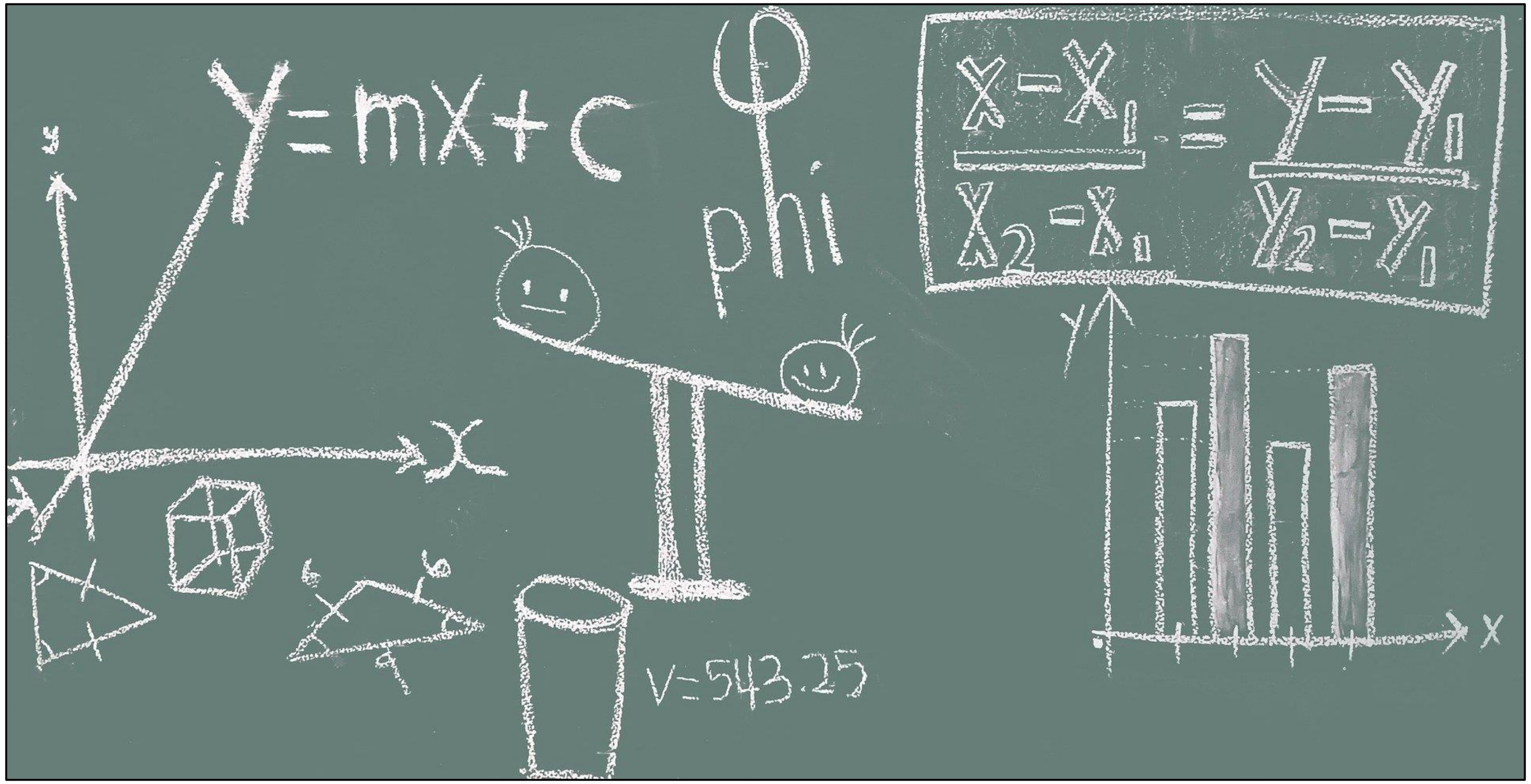
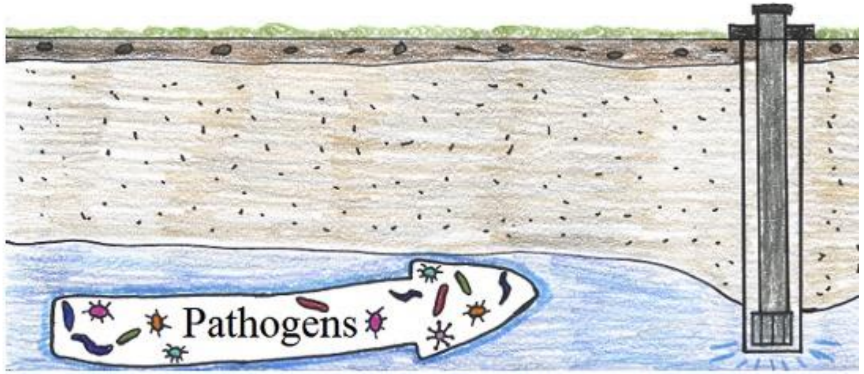


Image by Chuk Yong from Pixabay: https://pixabay.com/?utm_source=link-attribution&utm_medium=referral&utm_campaign=image&utm_content=1547018.

QMRA – research question



1. Waterborne pathogens in private wells.

2. Consumers drink water.

3. Do illnesses result?

QMRA Approach for Kewaunee County

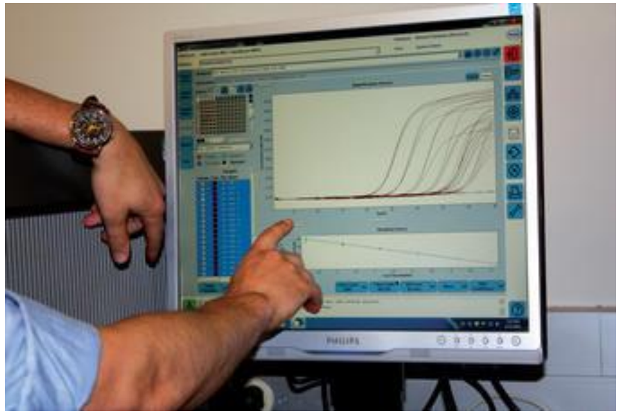
1. Hazard identification
2. Exposure assessment
3. Dose-response assessment
4. Risk characterization

QMRA Approach for Kewaunee County

1. Hazard identification
2. Exposure assessment
3. Dose-response assessment
4. Risk characterization

Unique to county

Photo credit: K. Abbott, Iowa County LCD. Public domain.



Concentration measurements via quantitative PCR.

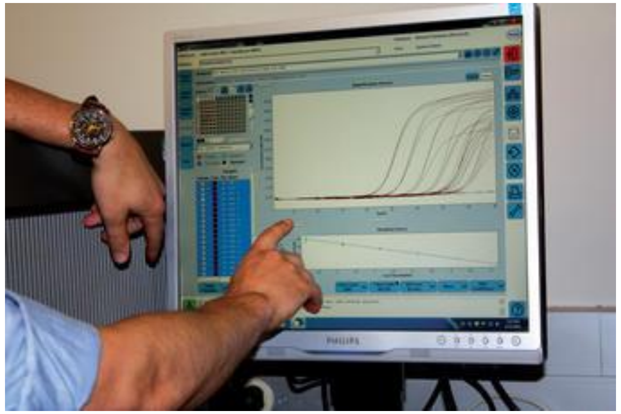
QMRA Approach

1. Hazard identification

<u>Pathogens included in QMRA:</u>
Adenovirus
Campylobacter jejuni
Enteropathogenic *E. coli* (EPEC)
Non-typhoidal *Salmonella*
Cryptosporidium hominis
Cryptosporidium parvum
Ungenotyped *Cryptosporidium* spp.
Giardia duodenalis

*Norovirus was never detected

Photo credit: K. Abbott, Iowa County LCD. Public domain.



Concentration measurements via quantitative PCR.

QMRA Approach

1. Hazard identification
2. Exposure assessment

Calculations for exposure assessment stratified by:
1. Depth to bedrock
   (< 20 ft. or > 20 ft.)
2. Fecal source
   (bovine, human, unknown)

Supports policy and management decisions

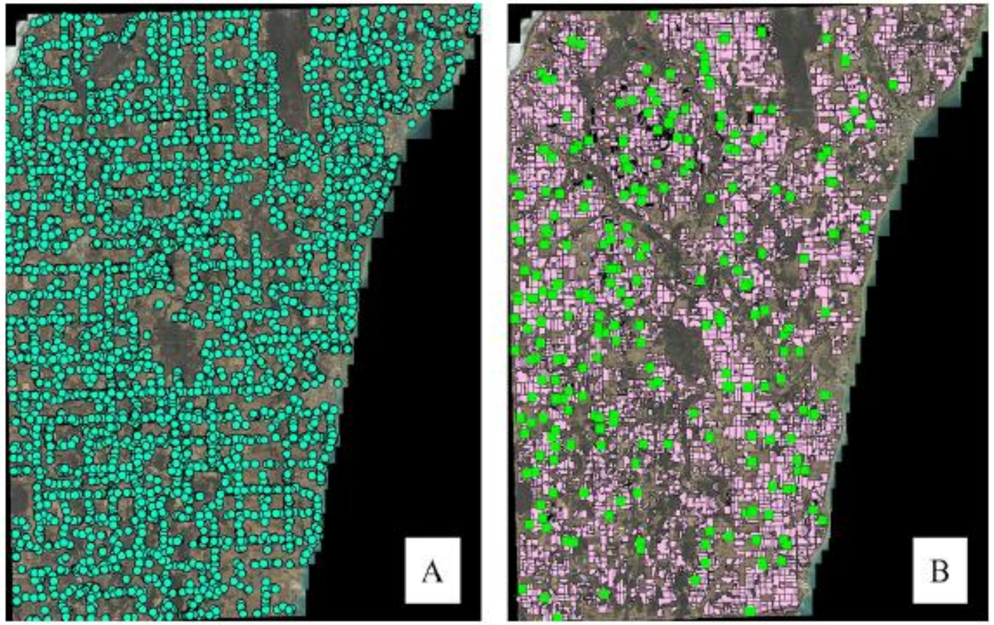


Figure Fecal sources of interest in Kewaunee County including (A) private septic systems, with each green dot representing a single septic system and (B) sources of cattle manure; each green square represents a storage facility (e.g., manure lagoon), and pink shading represents fields with approved nutrient management plans (i.e., those fields on which manure is likely to be spread). Produced using Geographic Information System data layers maintained by the Kewaunee County government and ArcMap software (version 10.3.1, ESRI).

Results – Outline

1. Exposure Assessment – People exposed per day
2. Exposure Assessment – Average daily doses
3. Risk – Predicted annual cases of illness
4. Context and implications

People exposed per day

Table Intermediate QMRA results for calculating exposure of Kewaunee residents to contaminated private wells (n, people per day), stratified by depth-to-bedrock and contamination source.

Depth to bedrock	Contamination source	Number of wells, *W*	Contaminated proportion, *F*	Source-associated proportion, *S*	People per well, *T*	People per day, *n*
≤6.1 m	Bovine feces	680 (510, 850)	0.41 (0.33, 0.50)	0.21 (0.13, 0.32)	2.4 (2.2, 2.6)	140 (70, 250)
	Human feces			0.26 (0.16, 0.36)		160 (90, 270)
	Unknown			0.53 (0.41, 0.64)		350 (220, 510)
>6.1 m	Bovine feces	4,170 (3,980, 4,330)	0.24 (0.19, 0.30)	0.29 (0.19, 0.41)		690 (420, 1,070)
	Human feces			0.098 (0.044, 0.18)		230 (100, 450)
	Unknown			0.60 (0.49, 0.71)		1,440 (1,010, 1,950)

Notes:
* 6.1 m = 20 ft.
** Point estimates are presented with 95% confidence intervals (in parentheses).
*** *W* and *T* estimated from county-specific public data; *F* and *S* estimated from companion groundwater study.

Sum = 3,010 people/day across all depth-to-bedrock and fecal source categories

People exposed per day

Table Intermediate QMRA results for calculating exposure of Kewaunee residents to contaminated private wells (n, people per day), stratified by depth-to-bedrock and contamination source.

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Notes:
* 6.1 m = 20 ft.
** Point estimates are presented with 95% confidence intervals (in parentheses).
*** *W* and *T* estimated from county-specific public data; *F* and *S* estimated from companion groundwater study.

Sum = 2,360 people/day
for > 20 ft. depth-to-bedrock

Average daily doses

Table Predicted daily exposure doses for all modeled pathogens, stratified by depth-to-bedrock and contamination source.

Pathogen	≤6.1 m depth to bedrock: Bovine feces	≤6.1 m depth to bedrock: Human feces	≤6.1 m depth to bedrock: Unknown	>6.1 m depth to bedrock: Bovine feces	>6.1 m depth to bedrock: Human feces	>6.1 m depth to bedrock: Unknown
Adenovirus A ($TCID_{50}$)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	1.4×10^{-4} (0.0, 4.3×10^{-4})	0.0 (0.0, 0.0)
Campylobacter jejuni (CFU)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	5.7×10^{-3} (0.0, 1.5×10^{-2})	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)
EPEC (CFU)	0.0 (0.0, 1.4×10^{-1})	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	4.8×10^{-3} (0.0, 1.8×10^{-2})
Salmonella (CFU)	3.0×10^{-1} (0.0, 8.3×10^{-1})	6.9×10^{-2} (0.0, 6.6×10^{-1})	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 2.1×10^{-2})
Cryptosporidium hominis (oocysts)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 2.7×10^{-4})	0.0 (0.0, 0.0)
Cryptosporidium parvum (oocysts)	1.9×10^{-2} (2.3×10^{-4}, 4.8×10^{-2})	7.4×10^{-5} (0.0, 1.2×10^{-3})	8.3×10^{-5} (0.0, 2.3×10^{-4})	5.4×10^{-2} (9.4×10^{-3}, 1.2×10^{-1})	0.0 (0.0, 0.0)	1.9×10^{-4} (0.0, 4.8×10^{-2})
Cryptosporidium spp. (oocysts)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	3.9×10^{-3} (0.0, 1.3×10^{-2})	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)
Giardia duodenalis (cysts)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 4.3×10^{-3})	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 3.9×10^{-3})

Notes:
* 6.1 m = 20 ft.
** Point estimates are presented with 95% confidence intervals (in parentheses).
*** Point estimates and 95% CIs determined using 2-dimensional Monte Carlo simulation.

Average daily doses

Table Predicted daily exposure doses for all modeled pathogens, stratified by depth-to-bedrock and contamination source.

	$\leq$6.1 m depth to bedrock			>6.1 m depth to bedrock		
Pathogen	Bovine feces	Human feces	Unknown	Bovine feces	Human feces	Unknown
Adenovirus A ($TCID_{50}$)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	1.4×10^{-4} (0.0, 4.3×10^{-4})	0.0 (0.0, 0.0)
Campylobacter jejuni (CFU)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	5.7×10^{-3} (0.0, 1.5×10^{-2})	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)
EPEC (CFU)	0.0 (0.0, 1.4×10^{-1})	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	4.8×10^{-3} (0.0, 1.8×10^{-2})
Salmonella (CFU)	3.0×10^{-1} (0.0, 8.3×10^{-1})	6.9×10^{-2} (0.0, 6.6×10^{-1})	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 2.1×10^{-2})
Cryptosporidium hominis (oocysts)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 2.7×10^{-4})	0.0 (0.0, 0.0)
Cryptosporidium parvum (oocysts)	1.9×10^{-2} (2.3×10^{-4}, 4.8×10^{-2})	7.4×10^{-5} (0.0, 1.2×10^{-3})	8.3×10^{-5} (0.0, 2.3×10^{-4})	5.4×10^{-2} (9.4×10^{-3}, 1.2×10^{-1})	0.0 (0.0, 0.0)	1.9×10^{-4} (0.0, 4.8×10^{-2})
Cryptosporidium spp. (oocysts)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	3.9×10^{-3} (0.0, 1.3×10^{-2})	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)
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Notes:
* 6.1 m = 20 ft.
** Point estimates are presented with 95% confidence intervals (in parentheses).
*** Point estimates and 95% CIs determined using 2-dimensional Monte Carlo simulation.

Predicted annual cases of illness

Table 3. Predicted AGI cases per year among private well users in Kewaunee County, stratified by depth-to-bedrock and contamination source.

	≤6.1 m depth to bedrock			>6.1 m depth to bedrock			
Pathogen	Bovine feces	Human feces	Unknown	Bovine feces	Human feces	Unknown	Total by pathogen
Adenovirus A	0 (0, 0)	0 (0, 0)	0 (0, 0)	0 (0, 0)	2 (0, 10)	0 (0, 0)	2 (0, 10)
Campylobacter jejuni	0 (0, 0)	0 (0, 0)	2 (0, 20)	0 (0, 0)	0 (0, 0)	0 (0, 0)	2 (0, 20)
EPEC	0 (0, 270)	0 (0, 0)	0 (0, 0)	0 (0, 0)	0 (0, 0)	7 (0, 500)	7 (0, 770)
Salmonella	30 (0, 120)	10 (0, 100)	0 (0, 0)	0 (0, 0)	0 (0, 0)	0 (0, 30)	40 (0, 180)
Cryptosporidium hominis	0 (0, 0)	0 (0, 0)	0 (0, 0)	0 (0, 0)	0 (0, 7)	0 (0, 0)	0 (0, 7)
Cryptosporidium parvum	10 (0.005, 90)	0.2 (0, 1)	0.1 (0, 1)	130 (0.2, 1,080)	0 (0, 0)	50 (0, 540)	190 (2, 1,380)
Cryptosporidium spp.	0 (0, 0)	0 (0, 0)	0 (0, 0)	60 (0, 470)	0 (0, 0)	0 (0, 0)	60 (0, 470)
Giardia duodenalis	0 (0, 0)	0 (0, 0)	0 (0, 10)	0 (0, 0)	0 (0, 0)	0 (0, 40)	0 (0, 40)
Total by contamination source (within depth-to-bedrock)	40 (0.5, 410)	10 (0, 110)	2 (0.006, 30)	190 (2, 1,200)	2 (0, 10)	57 (0.009, 910)	301 (80, 2,200)
Total by depth to bedrock		52 (10, 450)			249 (30, 1,800)		

Notes:
* AGI: acute gastrointestinal illness
** 6.1 m = 20 ft.
*** Point estimates are presented with 95% confidence intervals (in parentheses), determined using 2-dimensional Monte Carlo simulation.

Predicted annual cases of illness

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Campylobacter jejuni	0 (0, 0)	0 (0, 0)	2 (0, 20)	0 (0, 0)	0 (0, 0)	0 (0, 0)	2 (0, 20)
EPEC	0 (0, 270)	0 (0, 0)	0 (0, 0)	0 (0, 0)	0 (0, 0)	7 (0, 500)	7 (0, 770)
Salmonella	30 (0, 120)	10 (0, 100)	0 (0, 0)	0 (0, 0)	0 (0, 0)	0 (0, 30)	40 (0, 180)
Cryptosporidium hominis	0 (0, 0)	0 (0, 0)	0 (0, 0)	0 (0, 0)	0 (0, 7)	0 (0, 0)	0 (0, 7)
Cryptosporidium parvum	10 (0.005, 90)	0.2 (0, 1)	0.1 (0, 1)	130 (0.2, 1,080)	0 (0, 0)	50 (0, 540)	190 (2, 1,380)
Cryptosporidium spp.	0 (0, 0)	0 (0, 0)	0 (0, 0)	60 (0, 470)	0 (0, 0)	0 (0, 0)	60 (0, 470)
Giardia duodenalis	0 (0, 0)	0 (0, 0)	0 (0, 10)	0 (0, 0)	0 (0, 0)	0 (0, 40)	0 (0, 40)
Total by contamination source (within depth-to-bedrock)	40 (0.5, 410)	10 (0, 110)	2 (0.006, 30)	190 (2, 1,200)	2 (0, 10)	57 (0.009, 910)	301 (80, 2,200)
		17%			**83%**		
Total by depth to bedrock		52 (10, 450)			249 (30, 1,800)		

Notes:

* AGI: acute gastrointestinal illness

** 6.1 m = 20 ft.

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Campylobacter jejuni	0 (0, 0)	0 (0, 0)	2 (0, 20)	0 (0, 0)	0 (0, 0)	0 (0, 0)	2 (0, 20)
EPEC	0 (0, 270)	0 (0, 0)	0 (0, 0)	0 (0, 0)	0 (0, 0)	7 (0, 500)	7 (0, 770)
Salmonella	30 (0, 120)	10 (0, 100)	0 (0, 0)	0 (0, 0)	0 (0, 0)	0 (0, 30)	40 (0, 180)
Cryptosporidium hominis	0 (0, 0)	0 (0, 0)	0 (0, 0)	0 (0, 0)	0 (0, 7)	0 (0, 0)	0 (0, 7)
Cryptosporidium parvum	10 (0.005, 90)	0.2 (0, 1)	0.1 (0, 1)	130 (0.2, 1,080)	0 (0, 0)	50 (0, 540)	190 (2, 1,380)
Cryptosporidium spp.	0 (0, 0)	0 (0, 0)	0 (0, 0)	60 (0, 470)	0 (0, 0)	0 (0, 0)	60 (0, 470)
Giardia duodenalis	0 (0, 0)	0 (0, 0)	0 (0, 10)	0 (0, 0)	0 (0, 0)	0 (0, 40)	0 (0, 40)
Total by contamination source (within depth-to-bedrock)	$\boxed{40 (0.5, 410)}$	$\boxed{10 (0, 110)}$	2 (0.006, 30)	$\boxed{190 (2, 1,200)}$	$\boxed{2 (0, 10)}$	57 (0.009, 910)	301 (80, 2,200)
Total by depth to bedrock		52 (10, 450)			249 (30, 1,800)		

Notes:
* AGI: acute gastrointestinal illness
** 6.1 m = 20 ft.
*** Point estimates are presented with 95% confidence intervals (in parentheses), determined using 2-dimensional Monte Carlo simulation.

Is risk high or low?

Short answer – defining "acceptable" risk is a subjective and collective process.

Is risk high or low?

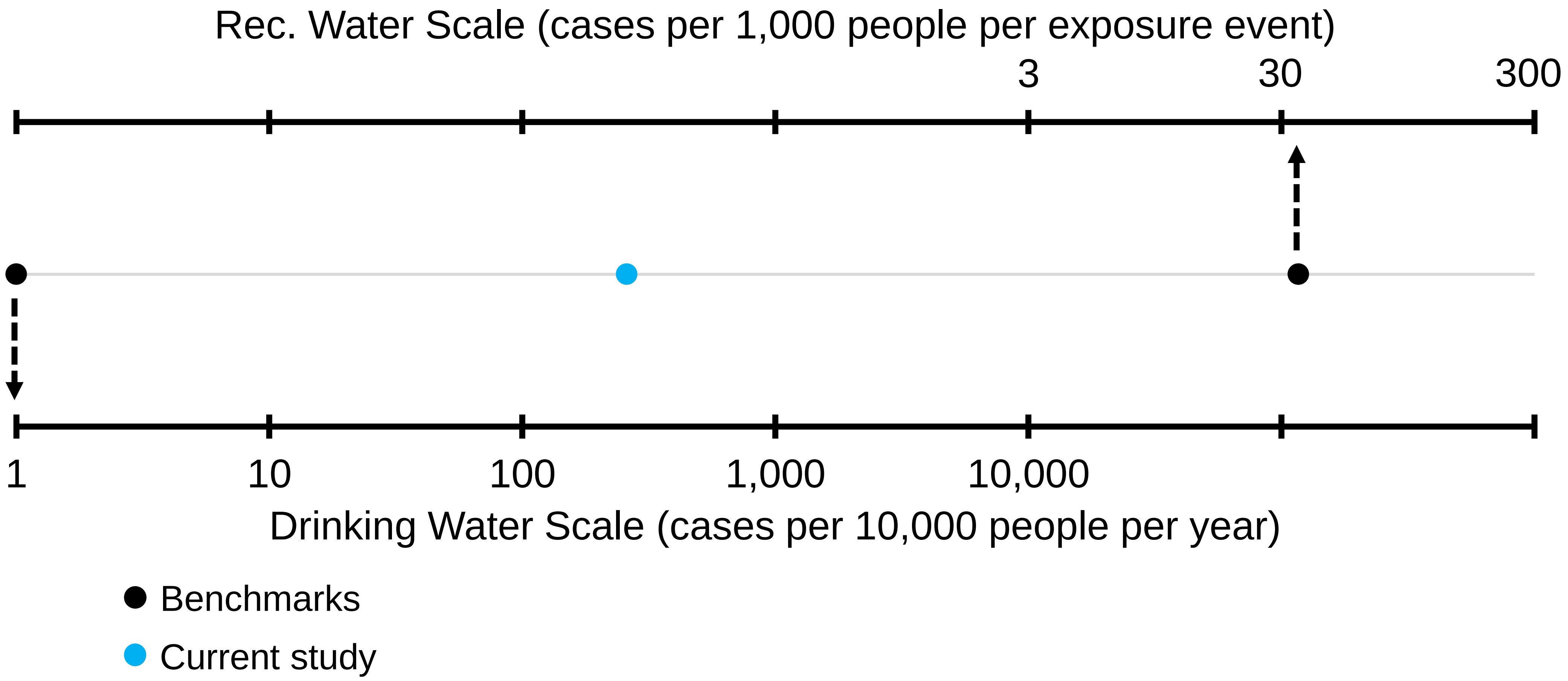
Short answer – defining “acceptable” risk is a subjective and collective process.

There is no standard acceptable risk for private wells in the U.S.

Two acceptable risk benchmarks commonly cited in U.S. research literature

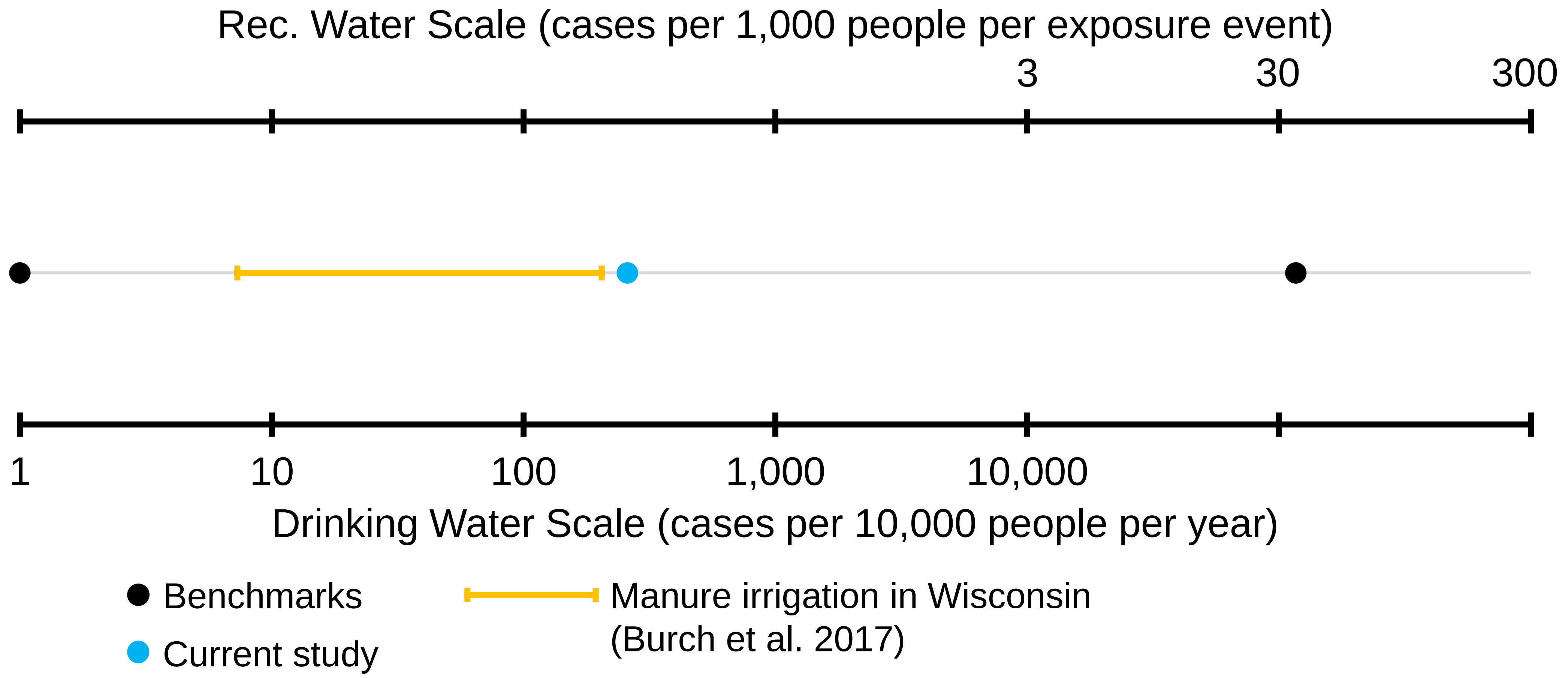
1. For <u>public</u> drinking water systems in U.S. – 1 infection per 10,000 people per year.
2. For recreational water in U.S. – 32 illnesses per 1,000 people per exposure event (e.g., per daily swimming event)

Risk estimates in context



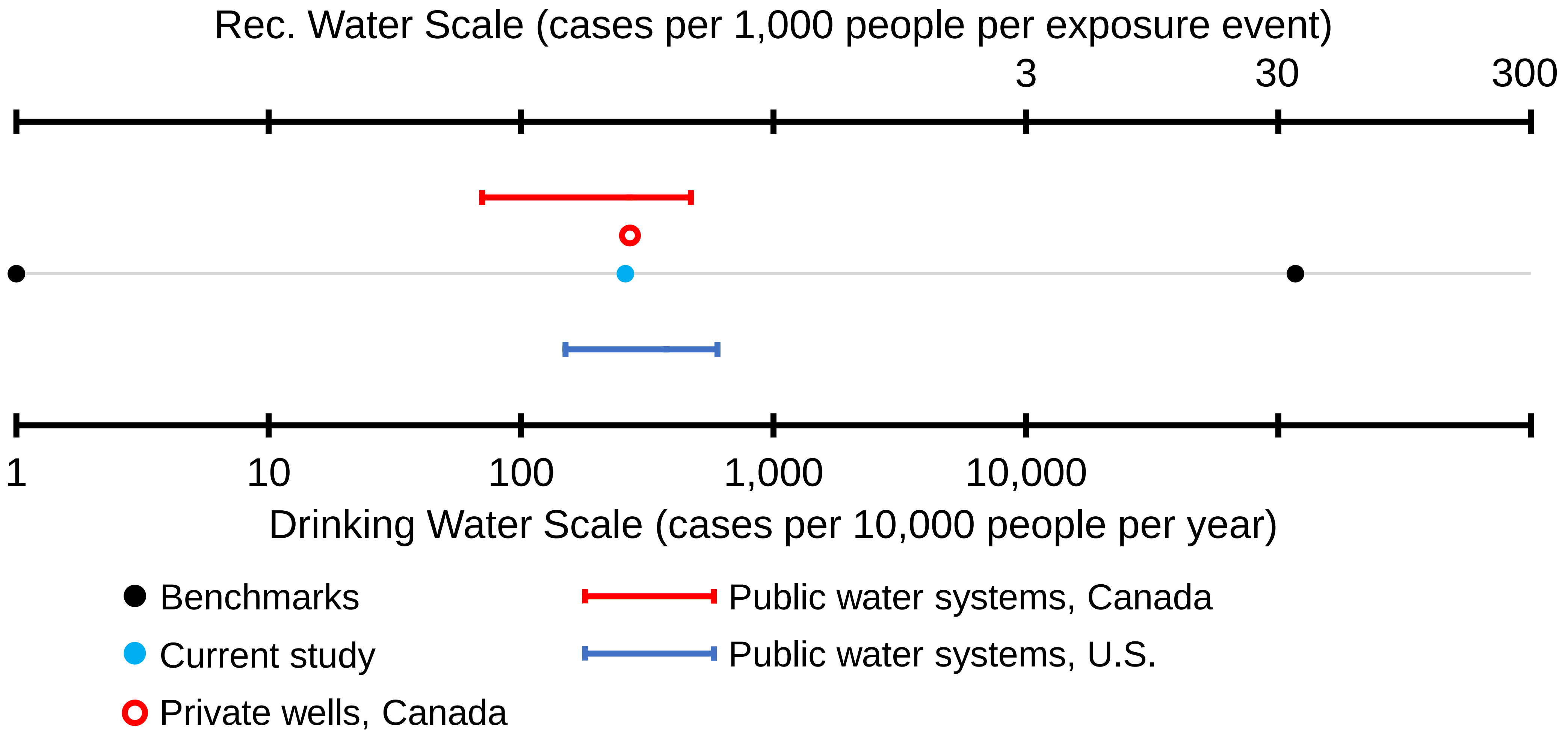
Note: 365 drinking water exposure events per year (i.e., 1 “event” = 1 day)

Risk estimates in context



Note: 1–8 manure irrigation exposures per year at ~ 900 ft setback distance.

Risk estimates in context



Are risk estimates realistic?

Yes. Two lines of evidence:

1. Comparison to AGI rates for all sources/transmission routes (e.g., foodborne, person-to-person, animal contact, etc.)

    a) U.S. data suggest expected rate of 650 cases per 1,000 people per year (Roy et al. 2006)
    b) 650 × 12 = ~ 7,800 AGI cases among Kewaunee private well users per year
    c) 301 / 7,800 = ~ 4% of cases associated with waterborne transmission

Consistent with national estimates: 3% - 20%

Are risk estimates realistic?

Yes. Two lines of evidence:

2. Comparison to reportable disease data for Kewaunee County

Cryptosporidiosis example:

a) Reported cryptosporidiosis cases: < 5
   (2015 data, close to annual averages; Wi. Dept. of Health Services, 2017)
b) Under-reporting factor for cryptosporidiosis: 100
   (U.S. Centers for Disease Control and prevention, in Scallan et al. 2011)
c) Accounting for under-reporting: 5 ×100 = 500 (or fewer) cases per year
d) We predicted 250 among private well users, which is less than total of 500

Implications for risk mitigation

Largest priorities based on risk estimates in this study:

1. Private wells constructed in > 20 ft. depth-to-bedrock
   - 83% of total predicted AGI cases
2. Private wells contaminated with bovine fecal markers
   - 76% of total predicted AGI cases
3. Private wells contaminated with *Cryptosporidium parvum*
   - 63% of total predicted AGI cases

Conclusions

Drinking water from private wells in Kewaunee County presents risk of AGI

- Falls between two available benchmarks for “acceptable” risk
- Consistent with national-level estimates for drinking water exposures in U.S. and Canada

Priority areas with most potential for risk mitigation:

a) Wells constructed in deeper depths-to-bedrock
b) Wells contaminated with bovine fecal material
c) Wells contaminated with *Cryptosporidium parvum*
d) Or any combination of a-c

Q & A

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