What Is Source Attribution for Foodborne Pathogens?

WHO Webinar: Source attribution method in the foodborne diseases estimates
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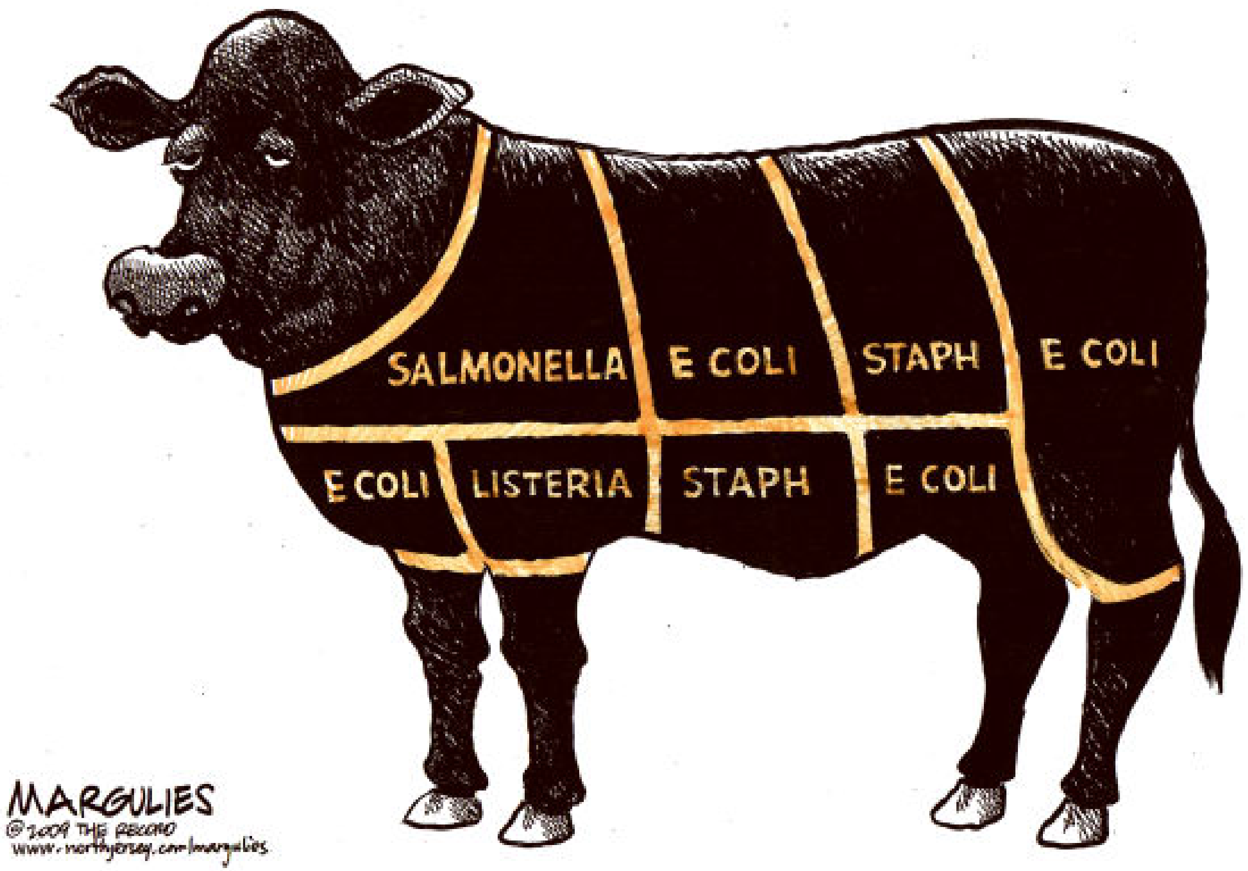
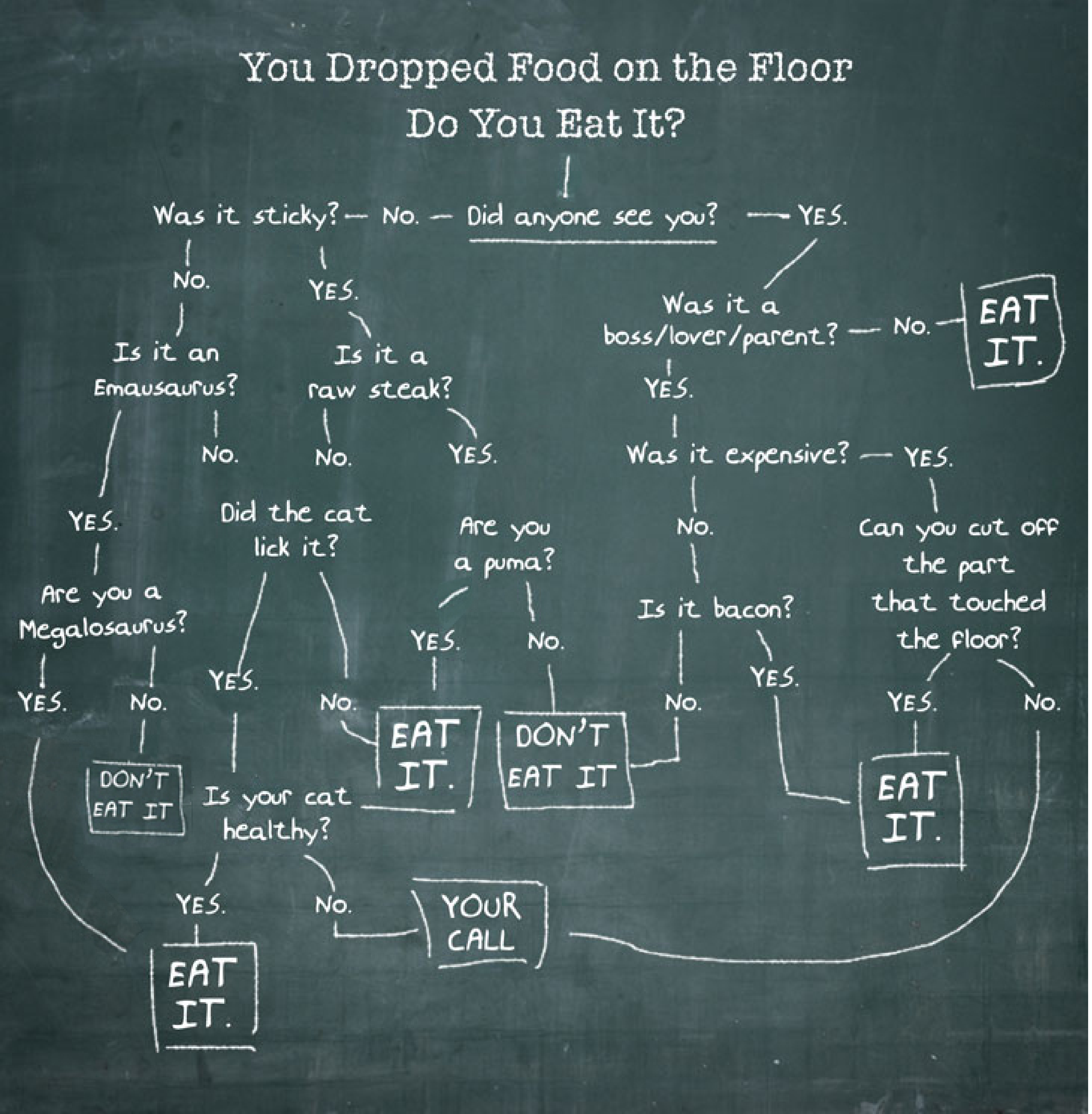


Foodborne illness source attribution

the relative contribution of different food sources to human illness

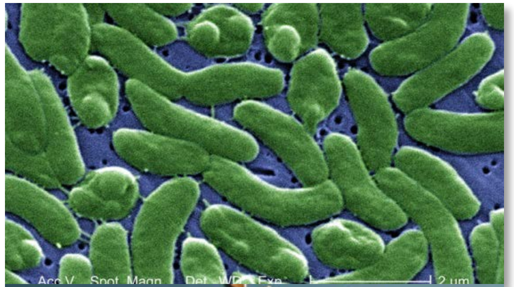


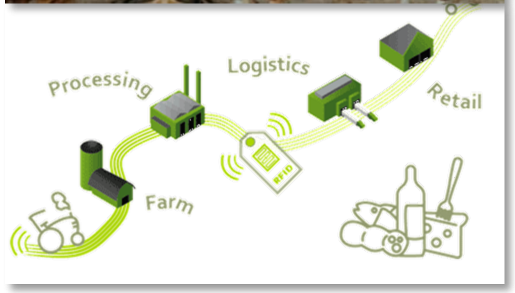
Why?

- A risk-based approach to food safety allocates limited resources to the biggest problems, and those we can do the most about
- Attribution informs broad priority setting and targeted risk management decisions, and can be used to evaluate the public health impacts of regulatory activities

How do we target resources?

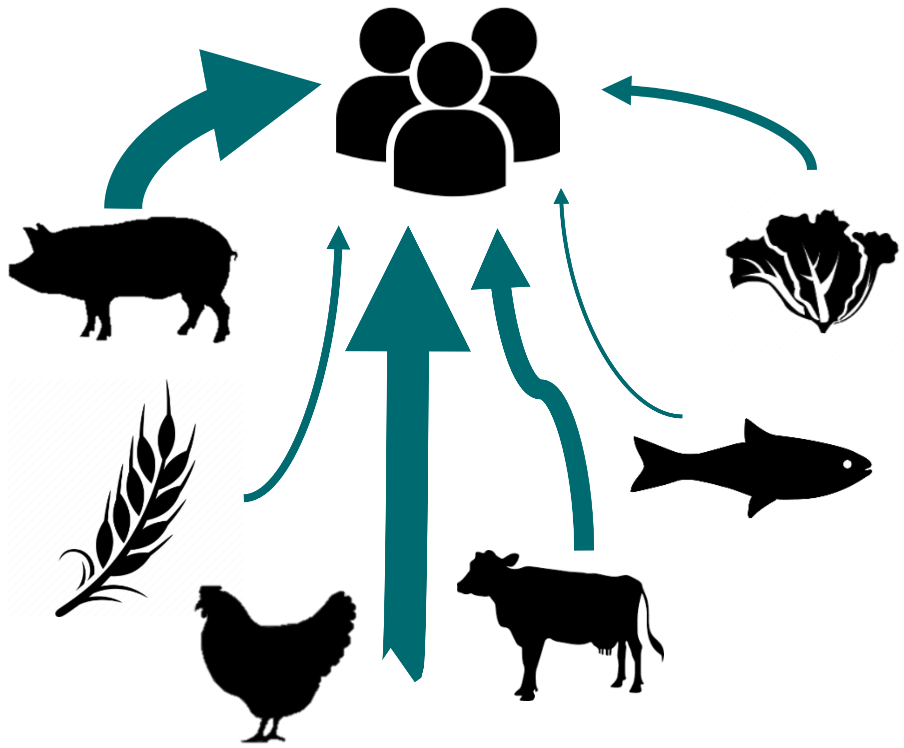
- **By pathogen**
  - *Salmonella*, *E. coli* O157:H7, etc.
- **By food**
  - Beef, pork, chicken, dairy, eggs, seafood, fruits, vegetables, etc.
- **By point in the farm to fork spectrum**
  - Seeds/feed, pre-harvest, post-harvest/slaughter, packaging, distribution, retail/wholesale, restaurants/caterers
- **By origin** (domestic vs. imported)
- **By level of processing** (fresh, frozen, canned, cured)





A more formal definition…

- "Source attribution of foodborne diseases is defined as the partitioning of the human cases caused by foodborne pathogens among their animal, food, and environmental reservoirs and/or transmission routes."



Definition: Mughini-Gras, et al. 2019. https://doi.org/10.3389/fmicb.2019.02578

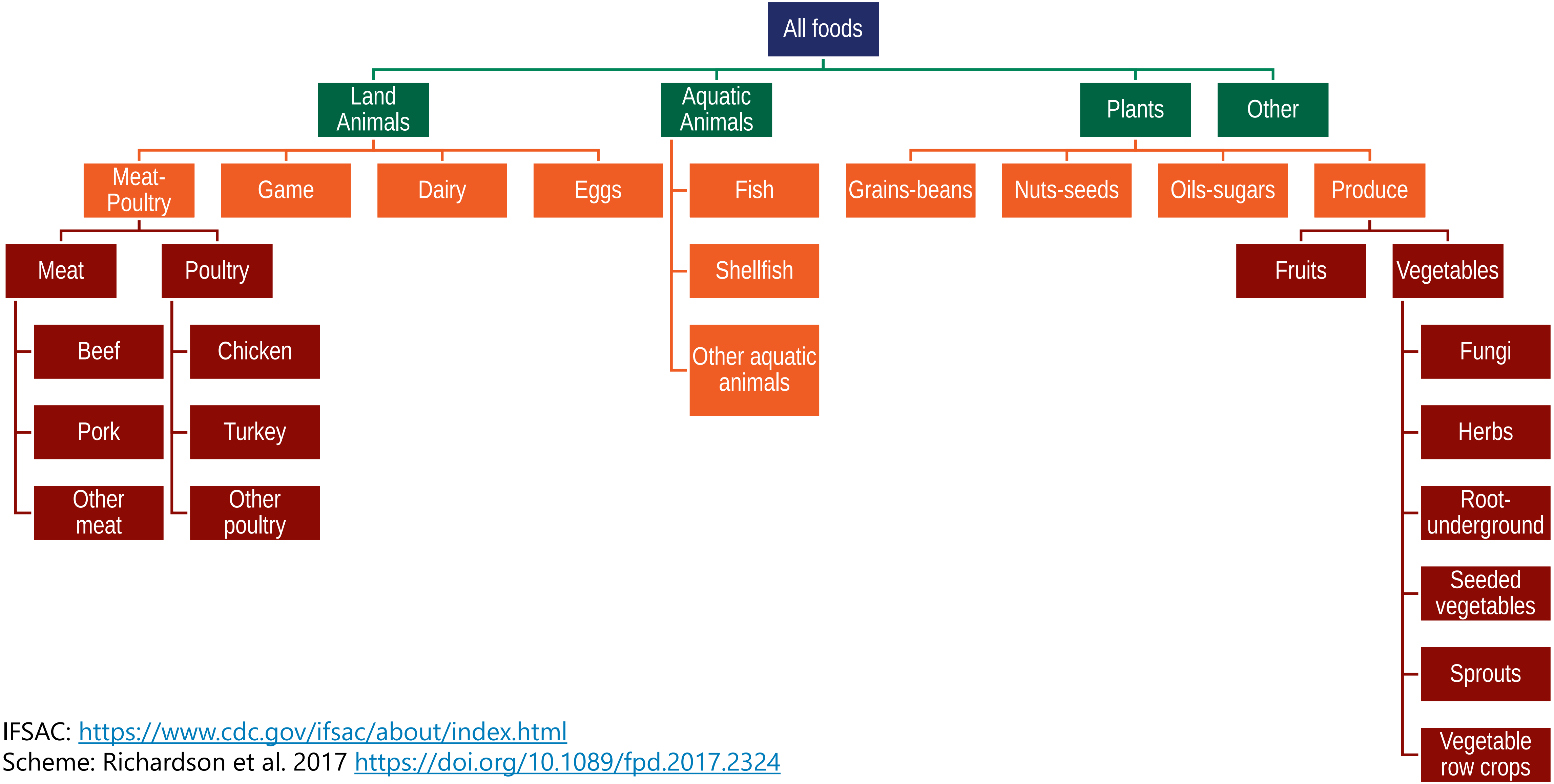
Granularity of categories

- **Studies differ in how broadly diseases are partitioned**
  - Major transmission routes (percent foodborne)
  - Animal reservoirs (percent due to cows)
  - Food categories (percent of foodborne due to beef)
  - Specific foods and/or risk factors (percent due to consumption of undercooked burgers)

- **Foodborne illness source attribution usually means estimating one of two things:**
  - Fraction of illnesses that are foodborne
  - Fraction of foodborne illnesses due to major food categories

Food categorization example

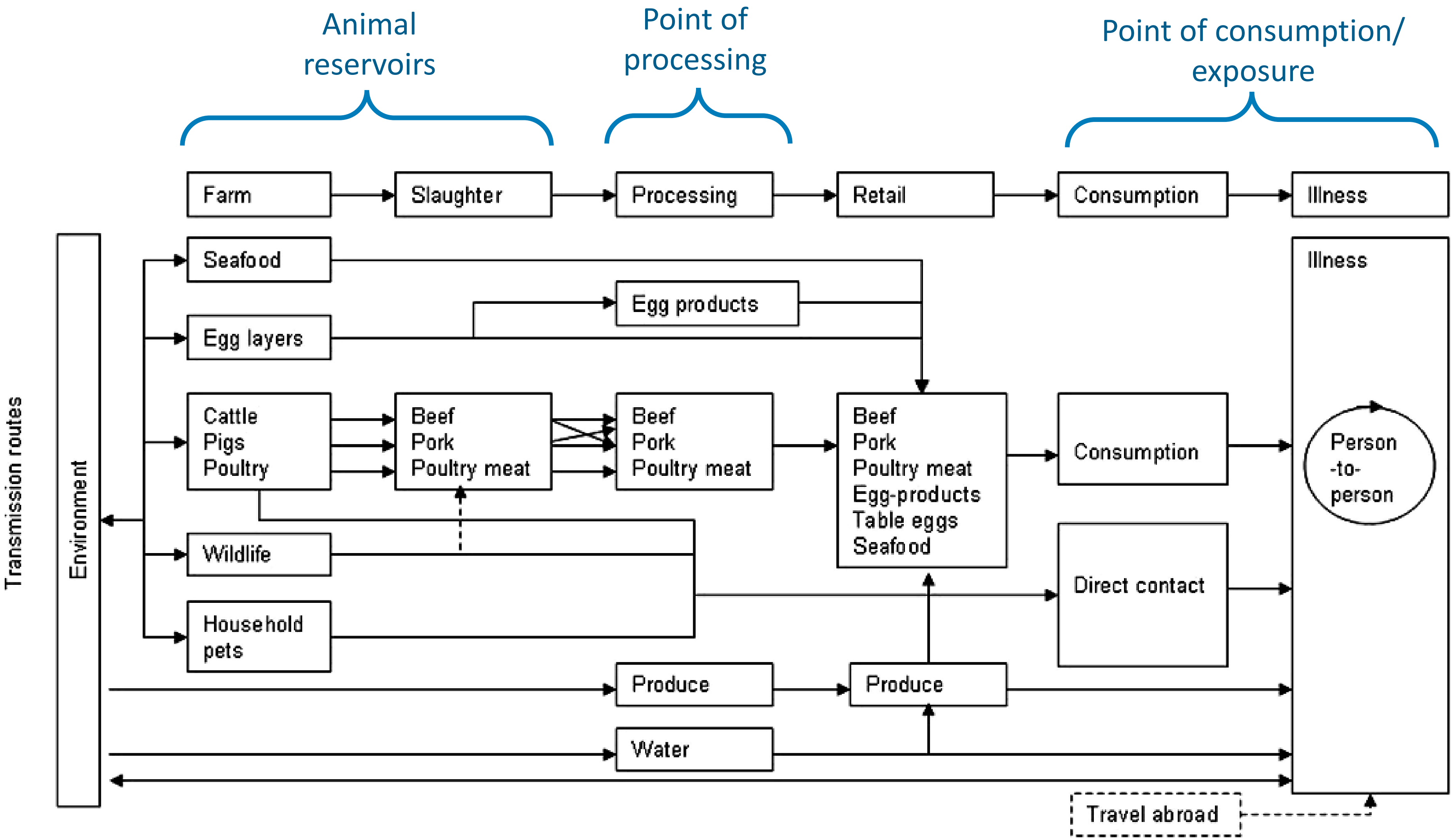
Interagency Food Safety Analytics Collaboration (IFSAC) scheme for categorizing foodborne outbreaks



- All foods
  - Land Animals
    - Meat-Poultry
      - Meat
        - Beef
        - Pork
        - Other meat
      - Poultry
        - Chicken
        - Turkey
        - Other poultry
    - Game
    - Dairy
    - Eggs
  - Aquatic Animals
    - Fish
    - Shellfish
    - Other aquatic animals
  - Plants
    - Grains-beans
    - Nuts-seeds
    - Oils-sugars
    - Produce
      - Fruits
      - Vegetables
        - Fungi
        - Herbs
        - Root-underground
        - Seeded vegetables
        - Sprouts
        - Vegetable row crops
  - Other

IFSAC: https://www.cdc.gov/ifsac/about/index.html
Scheme: Richardson et al. 2017 https://doi.org/10.1089/fpd.2017.2324

Point of attribution



Source: Pires, et al. 2009 https://doi.org/10.1089/fpd.2008.0208

Overview of Source Attribution Methods

Source Attribution Methods

- Retrospective analysis of surveillance data
- Epidemiological studies of sporadic disease
- Microbial subtype modeling
- Predictive microbiology
- Intervention studies/natural experiments
- Structured expert judgment

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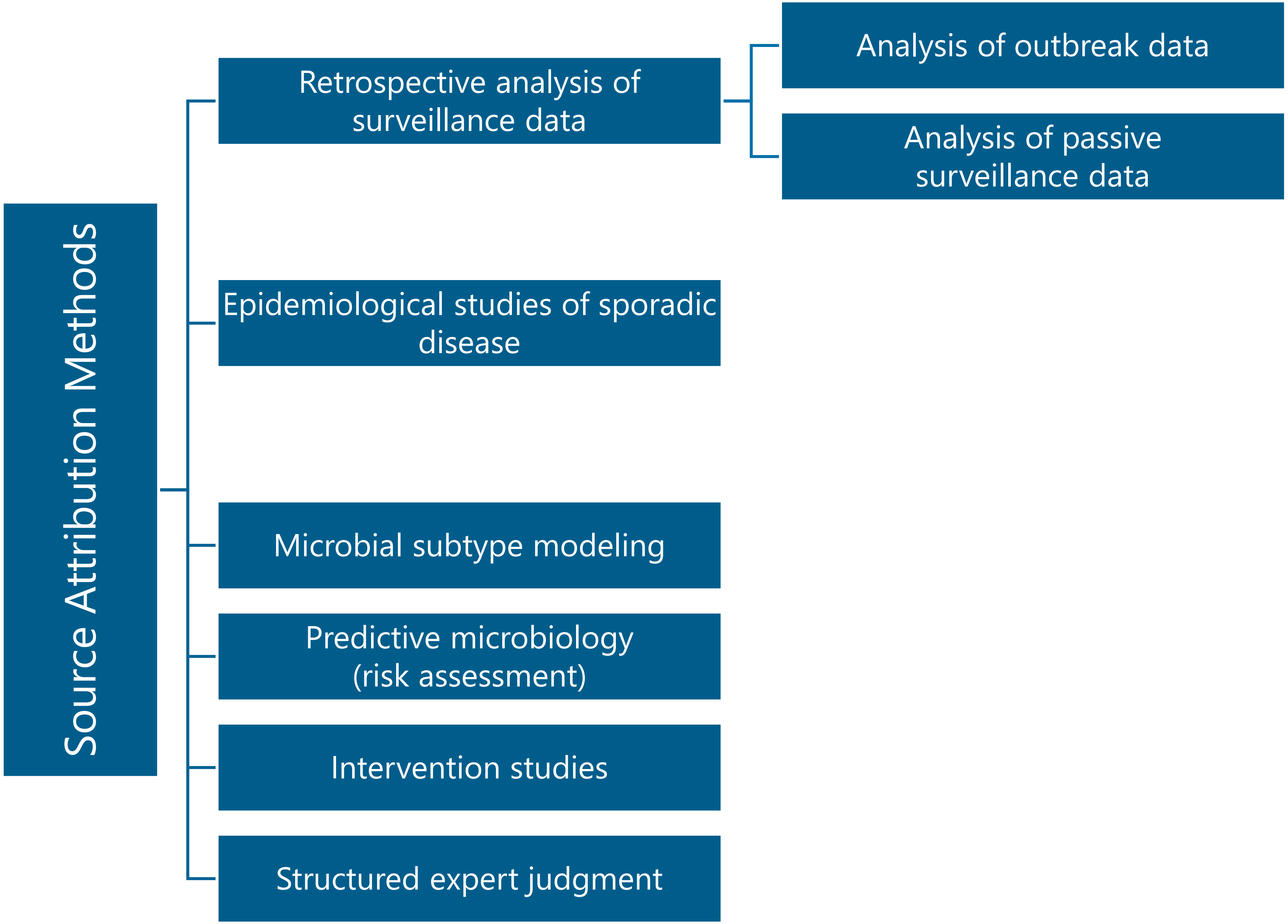

Source Attribution Methods

- Retrospective analysis of surveillance data
  - Analysis of outbreak data
  - Analysis of passive surveillance data
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Outbreak-based Attribution

- **Summaries of compiled foodborne outbreak data have long been used to extrapolate the pathogens, food vehicles, and risk factors associated with foodborne disease**
  - Early example: Bryan 1978 https://doi.org/10.4315/0362-028X-41.10.816
- Assumes outbreak risks reflect those of sporadic infections
- Requires large multi-year compilations of data that must be cleaned and processed for analysis
- Useful to partition foodborne risks, but less useful for major transmission routes due to limitations in data collection
- Recent example: US estimates by the Interagency Food Safety Analytics Collaboration (IFSAC): https://www.cdc.gov/ifsac/php/annual-reports/index.html

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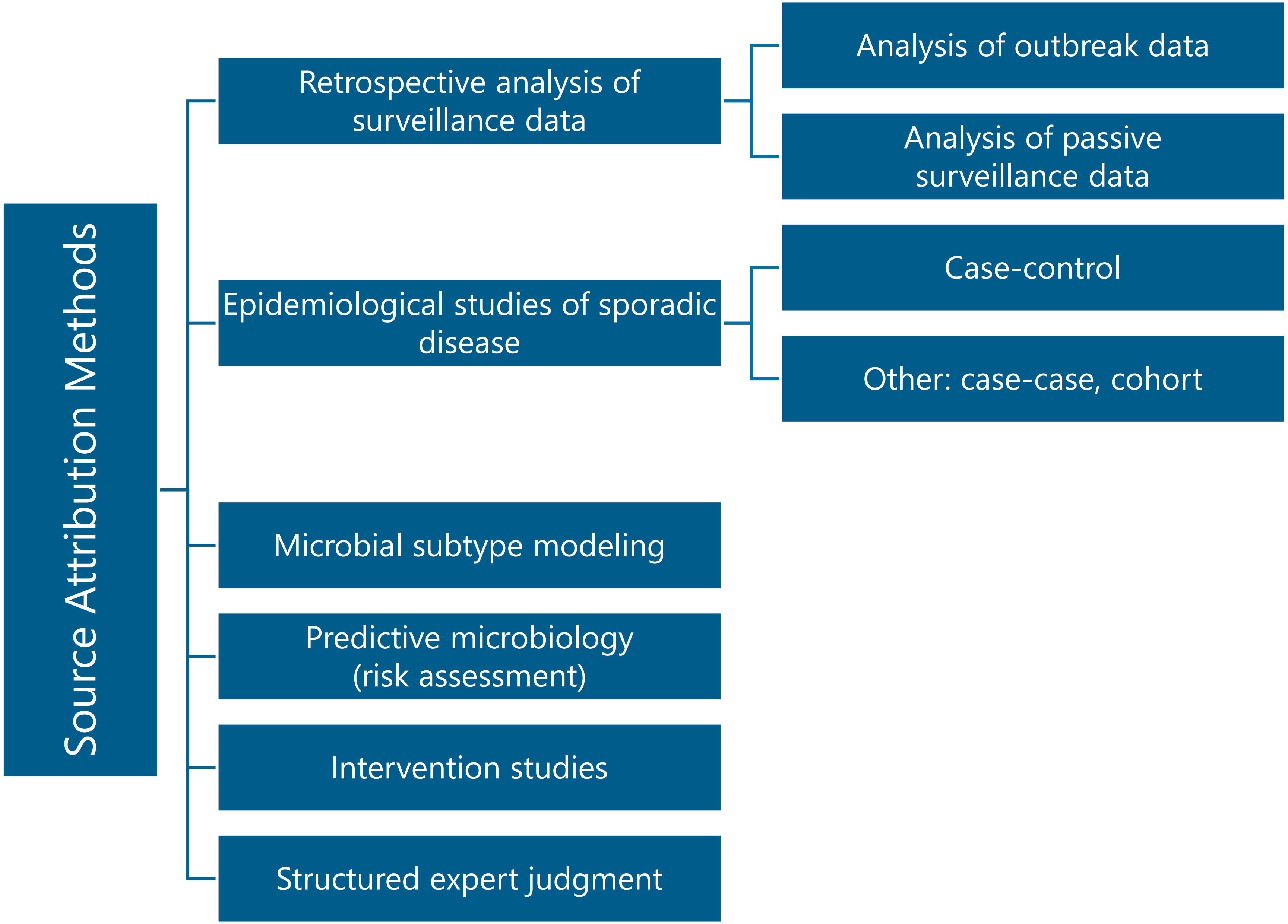

Source Attribution Methods

- Retrospective analysis of surveillance data
  - Analysis of outbreak data
  - Analysis of passive surveillance data
- Epidemiological studies of sporadic disease
  - Case-control
  - Other: case-case, cohort
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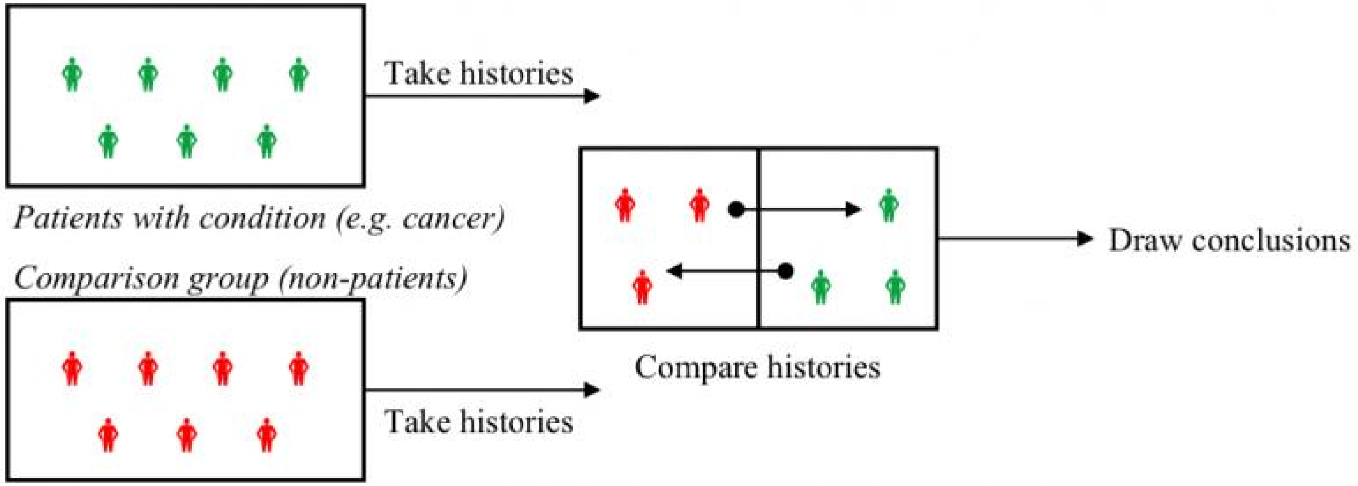
Analysis of sporadic illness



- **In case-control studies, cases and matched controls are interviewed about risk behavior; statistical analysis quantifies deviations between the groups**
- Reflects risks at the point of consumption (not reservoirs)
- Can capture food and non-food exposures
- Requires careful design to avoid biases; time and resource intensive, but likely better reflects risk factors for sporadic disease than outbreak data; newer methods may address biases and resource needs

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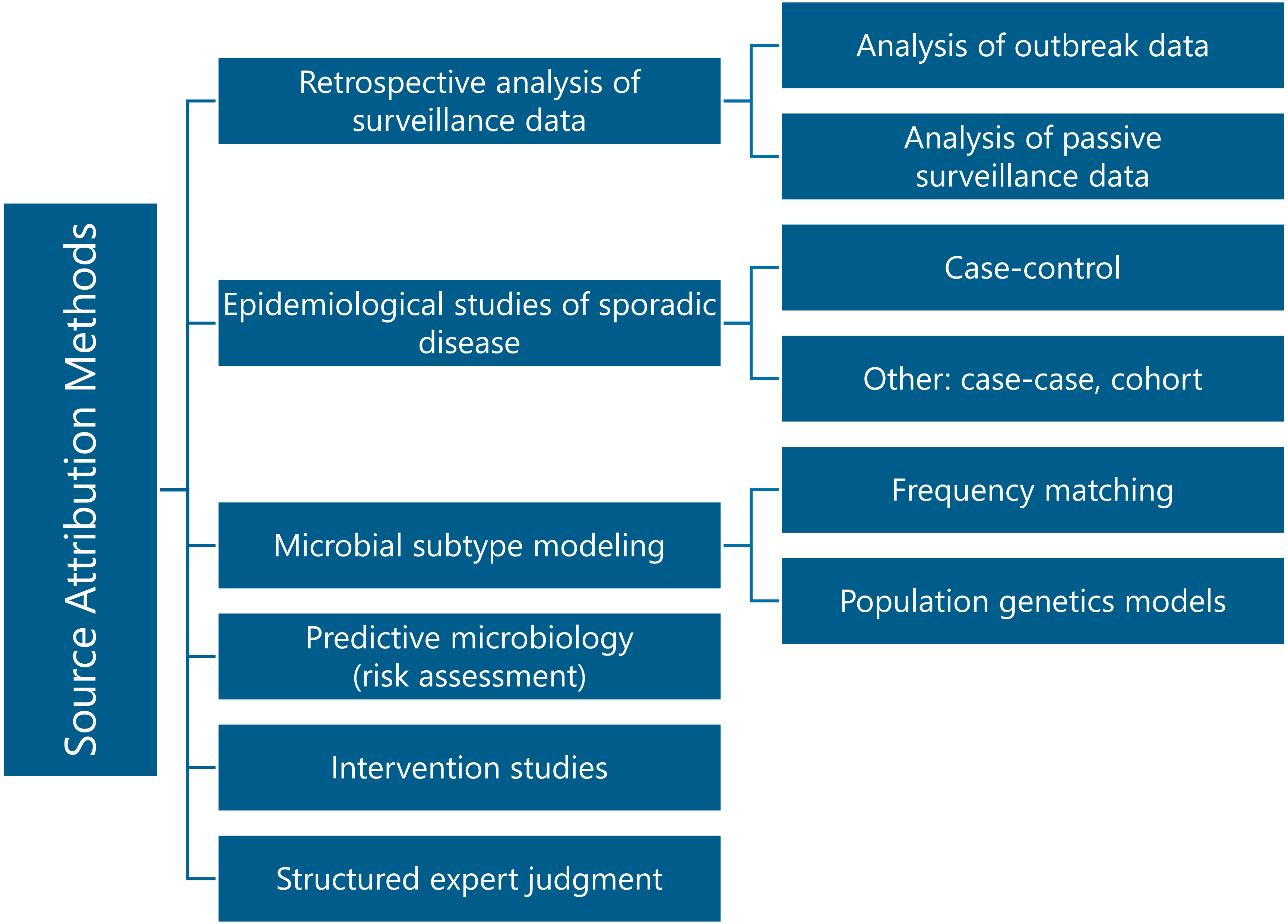

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  - Frequency matching
  - Population genetics models
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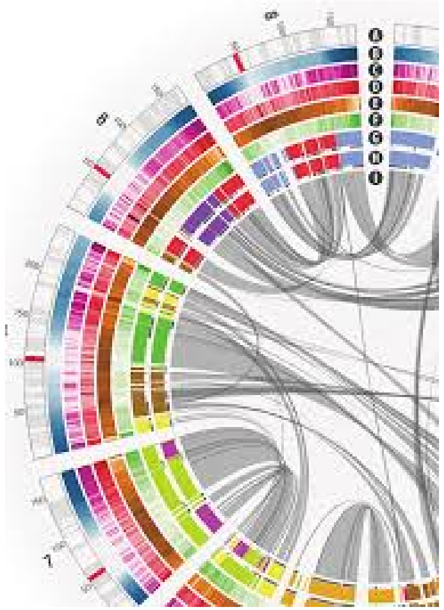
Microbial subtyping methods

- **Microbial subtyping approaches use different methods to describe the similarities and differences of pathogen strains, and then use those subtypes to link isolates from human cases to those from food, animals, and other sources**
- Most methods focus on reservoirs, so not as useful for transmission routes (subtypes from beef may reach humans via animal contact, meat consumption, fecal contamination of water, etc.)
- A very diverse and fast-moving area of research that reflects many different subtyping methods, AND many different modeling methods of those subtypes
  - WGS methods reflect the majority today
- Require large libraries of isolates and sophisticated tools



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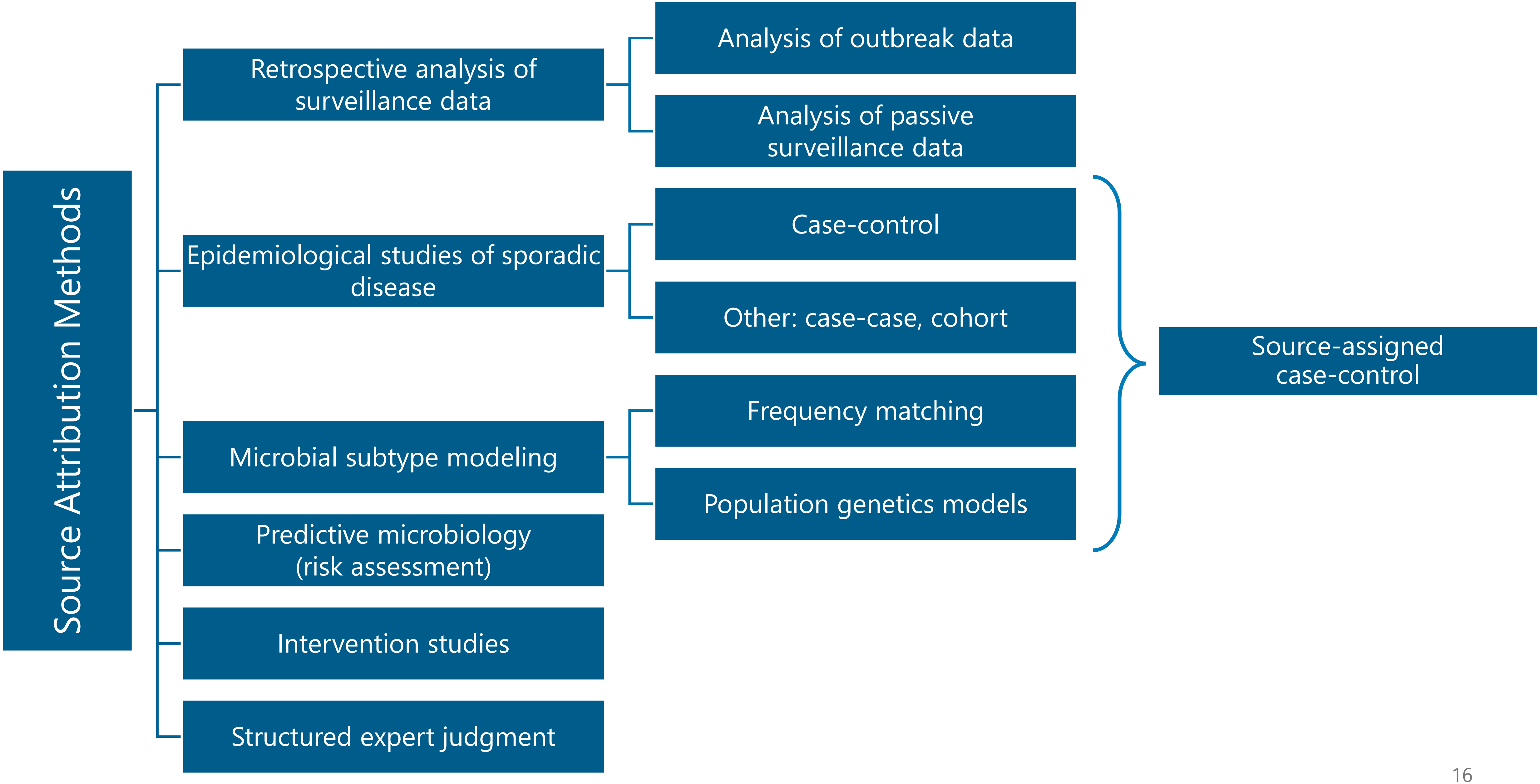

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Frequency matching

Population genetics models

Source-assigned case-control

Predictive microbiology (risk assessment)

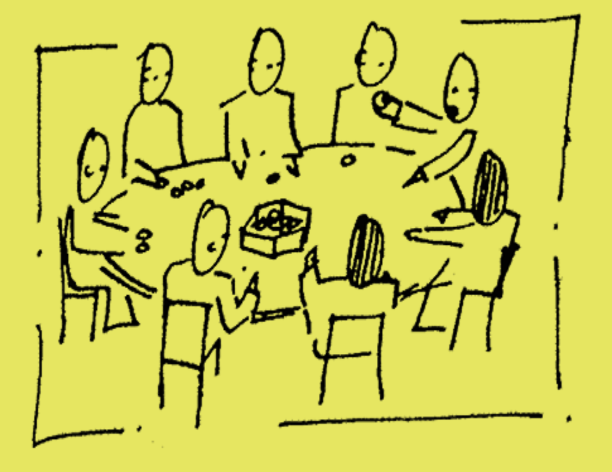
Intervention studies

Structured expert judgment

Predictive microbiology

- **Quantitative microbiological risk assessments (QMRA) start with data on the contamination of food ingredients, and predict pathogen movement and growth through subsequent stages to consumption and illness**
- Requires detailed and representative data on contamination, and is very resource intensive
- More useful to understand/estimate risks associated with specific food products than overall system risks

Structured expert judgement



- **Estimates of attribution fractions are elicited using one of several established, structured protocols**
- Can be useful when data is thin, or when literature is substantial but inconclusive:
  - The literature often includes competing estimates, but major differences in methods and data sources makes formal meta-analyses difficult or impossible
- Can be used for both major transmission routes and specific food vehicles
- Often reflect snapshots based on a set of people at a certain time
- Can have serious biases in study design and expert recruitment; formal methods attempt to address these or minimize their influence

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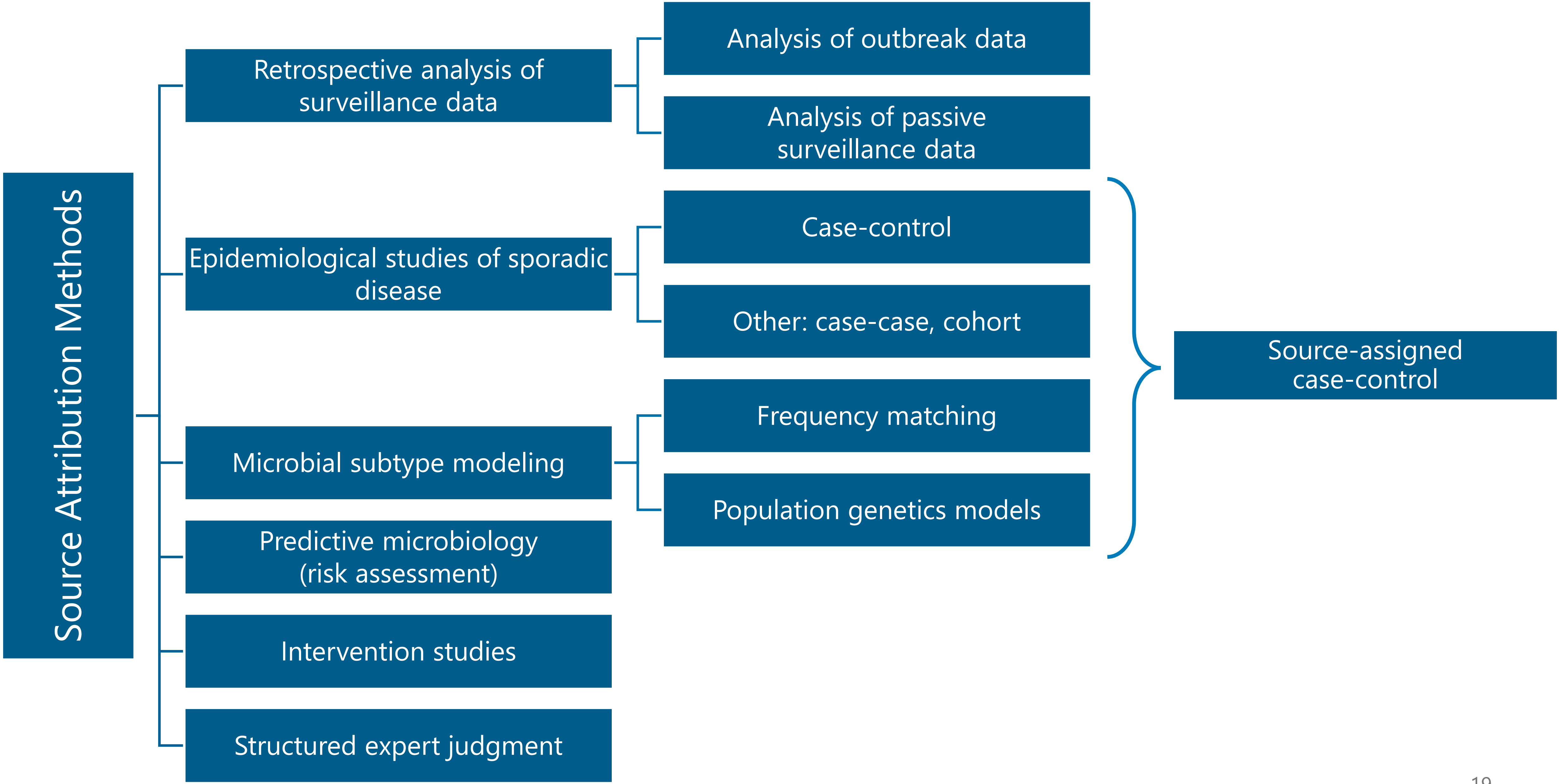

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Choice of Method

- Some methods suited for estimating the relative roles of major transmission pathways and others suited to estimating attribution of illnesses to specific food exposures or reservoirs
- The biggest driver of choice of source attribution method is often the availability and reliability of public health surveillance systems and associated data for a given country or region
- Computing resources and analytical expertise are also a critical issue
- Sporadic epidemiological studies and microbial subtyping methods are powerful approaches for specific pathogens and situations, but are often not feasible given data and resource requirements

Thank you!

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