World Health Organization

Methodological framework for WHO estimates of the global burden of foodborne disease

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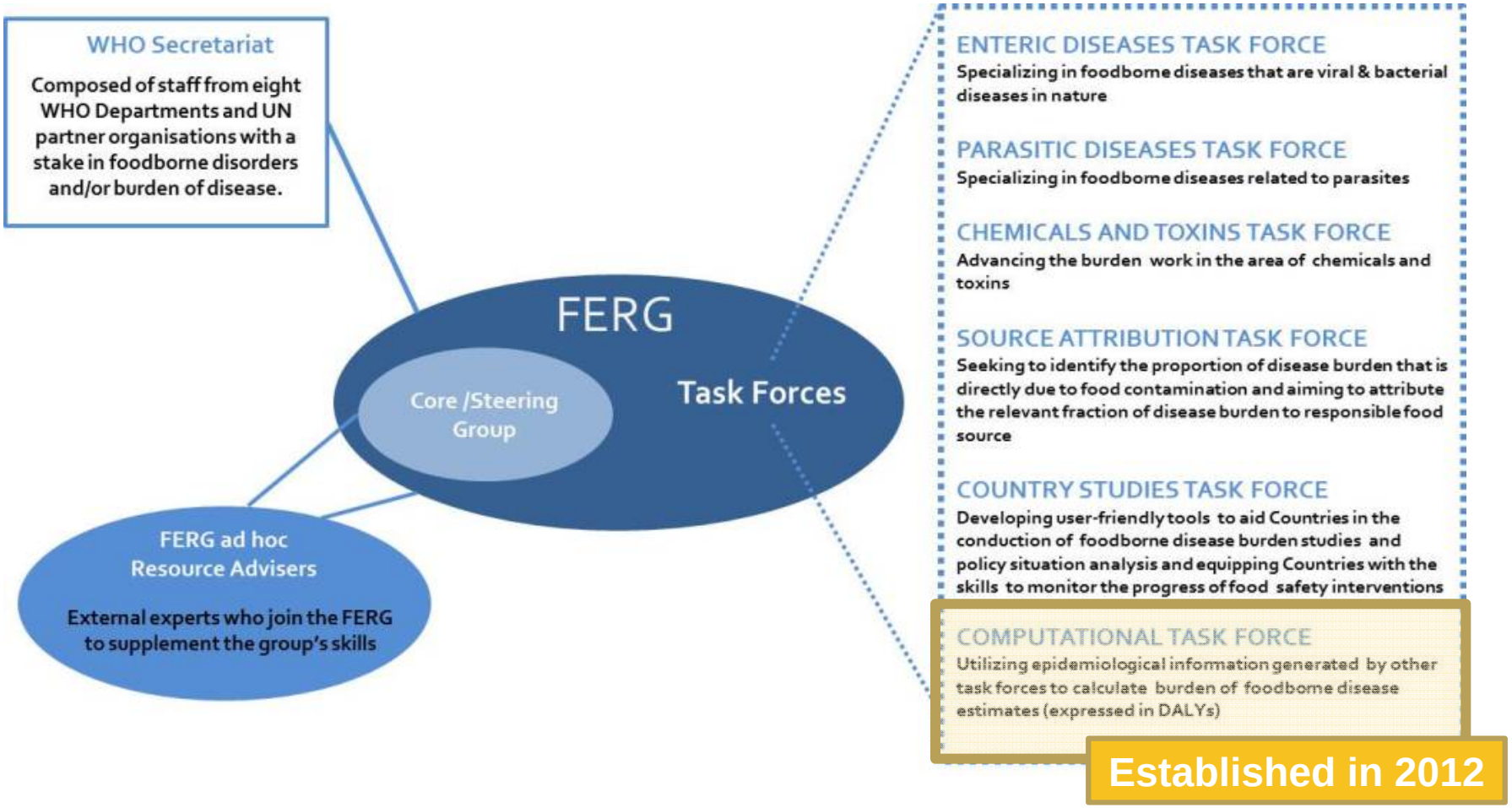
FERG Computational Task Force

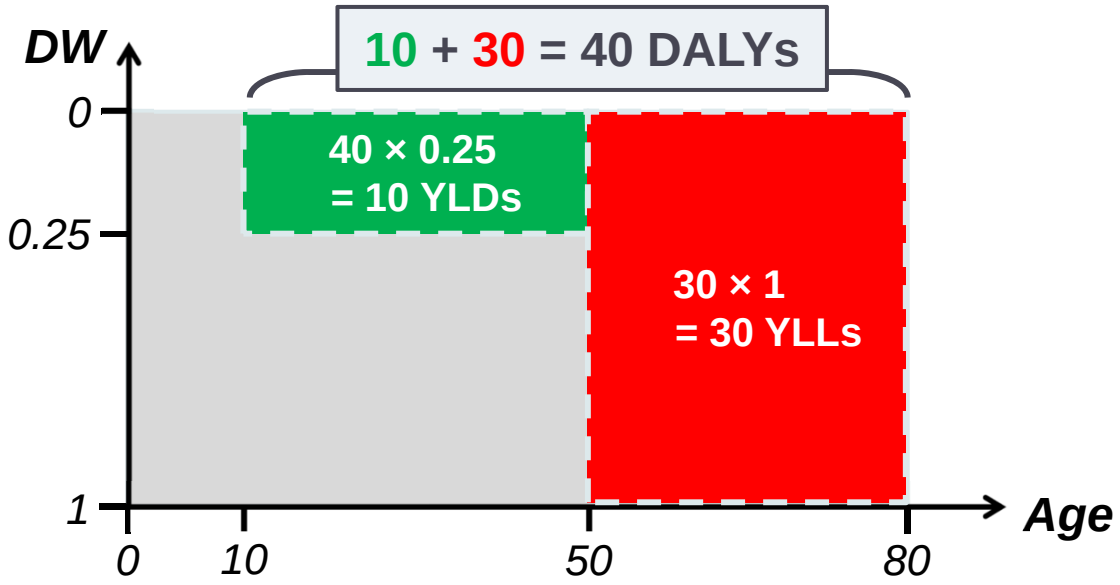


Methodological choices

Burden of foodborne disease

- Illnesses, deaths
- Disability-Adjusted Life Years (DALYs)
  - **1 DALY = 1 healthy life year lost**
  - Summary measure of population health
    - Morbidity + mortality
    - Disease occurrence + disease severity
  - DALY = YLD + YLL
    - YLD = Years Lived with Disability
      = Number of incident cases × Duration × Disability Weight
    - YLL = Years of Life Lost
      = Number of deaths × Residual Life Expectancy

Disability-Adjusted Life Years



DALY = YLD + YLL

- YLD = Years Lived with Disability = N × D × DW
- YLL = Years of Life Lost = M × RLE

Methodological choices

Burden of foodborne disease

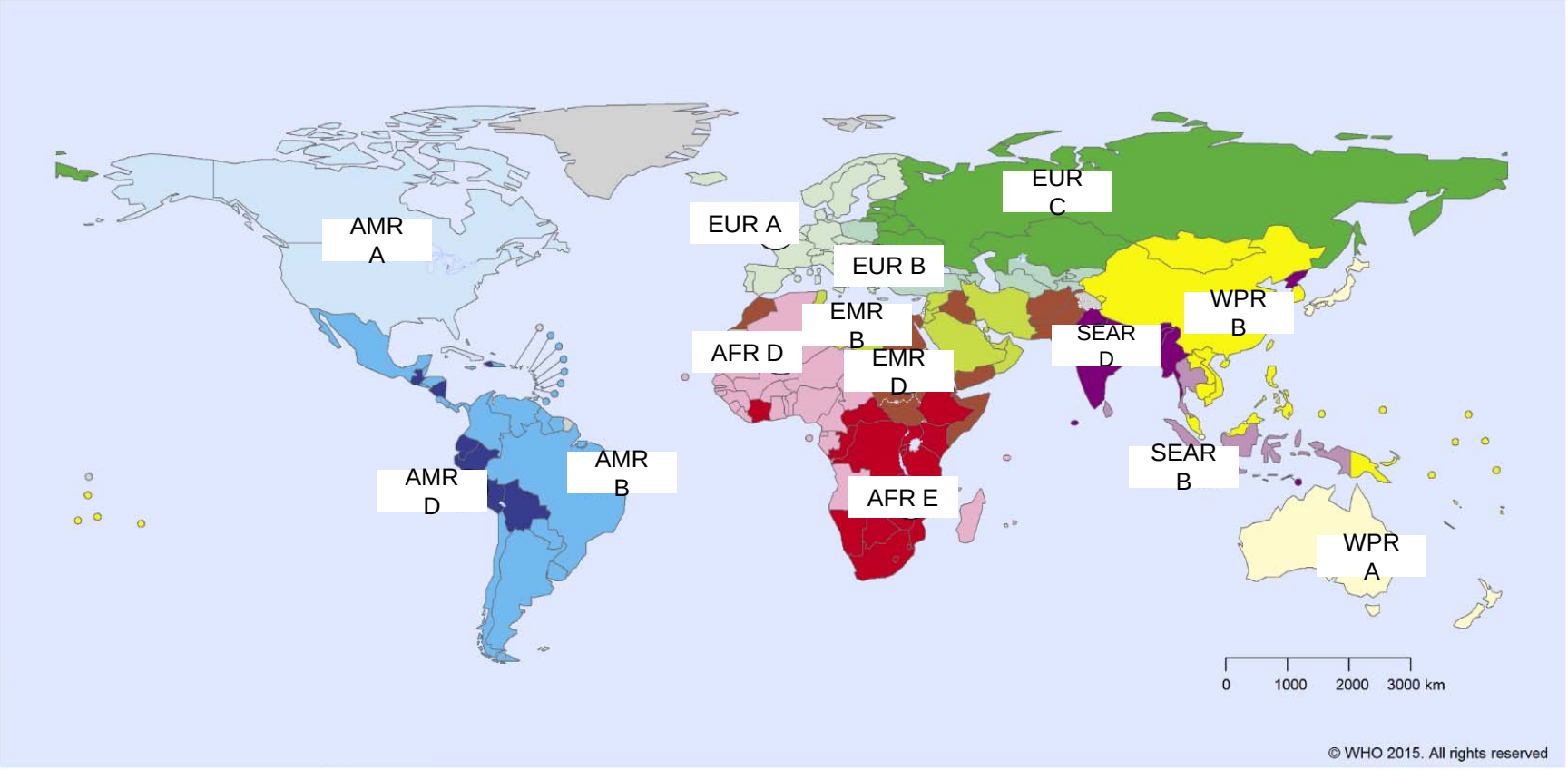
- Illnesses, deaths
- Disability-Adjusted Life Years (DALYs)
- Hazard-based
  - Burden of hazard = burden of causally related **health states**
    - Acute illness, chronic sequelae, death
    - Different severity levels
  - Represented by **disease model, outcome tree**
  - FERG: 31+6 hazards; 75 health states

Methodological choices

Burden of foodborne disease

- Illnesses, deaths
- Disability-Adjusted Life Years (DALYs)
- Hazard-based
- Incidence-based
  - Future burden resulting from current exposure
    - more sensitive to current epidemiological trends
    - more consistent with the estimation of YLLs
- Reference year 2010
  - Number of **incident** illnesses, deaths, DALYs **in 2010**
- Calculated at country level
  - Presented at subregion level (14)

14 subregions



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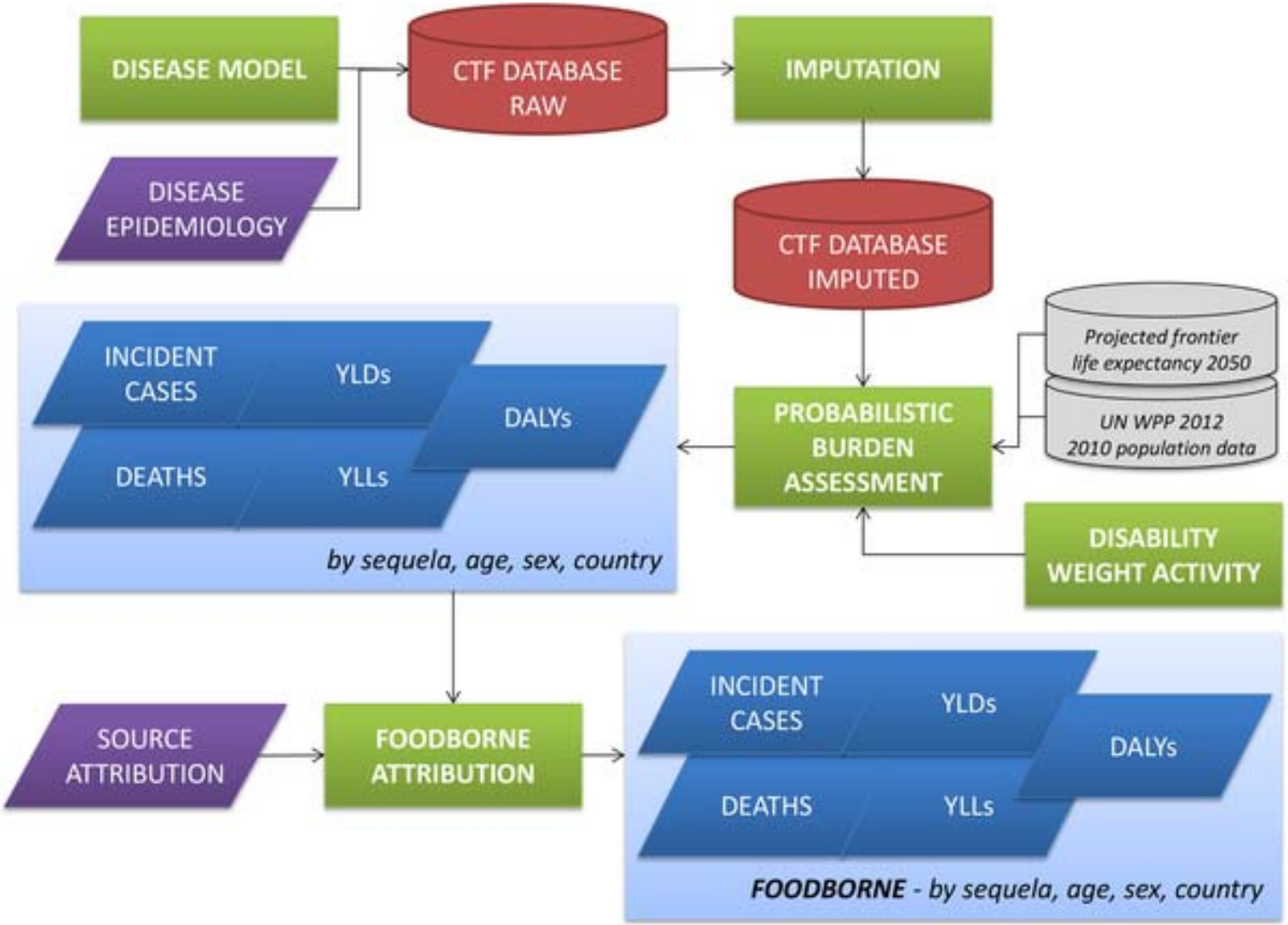
Map Production: Foodborne Disease Burden Epidemiology Reference Group (FERG), World Health Organization

Computational Task Force Workflow



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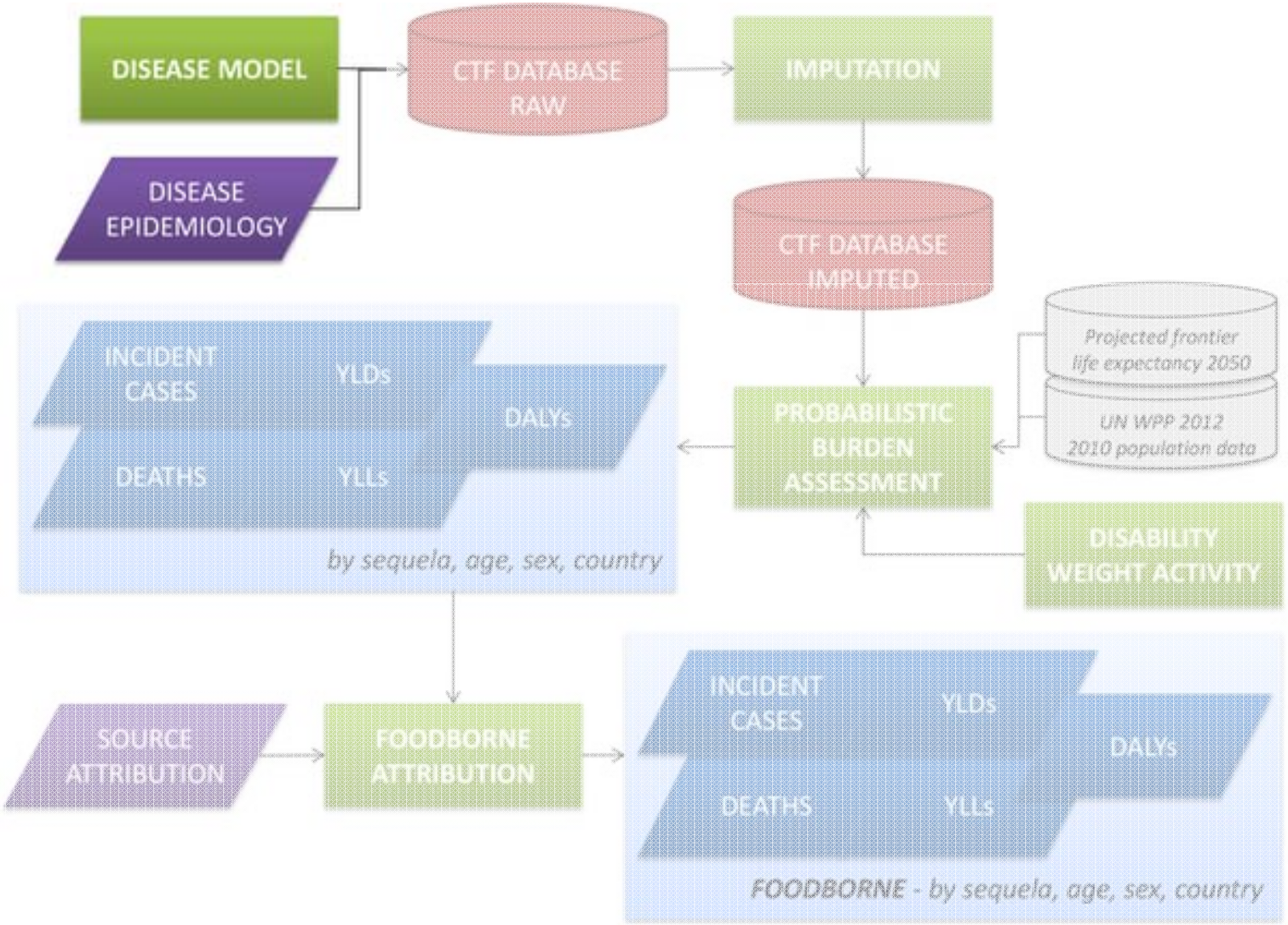


Disease models and epidemiological data

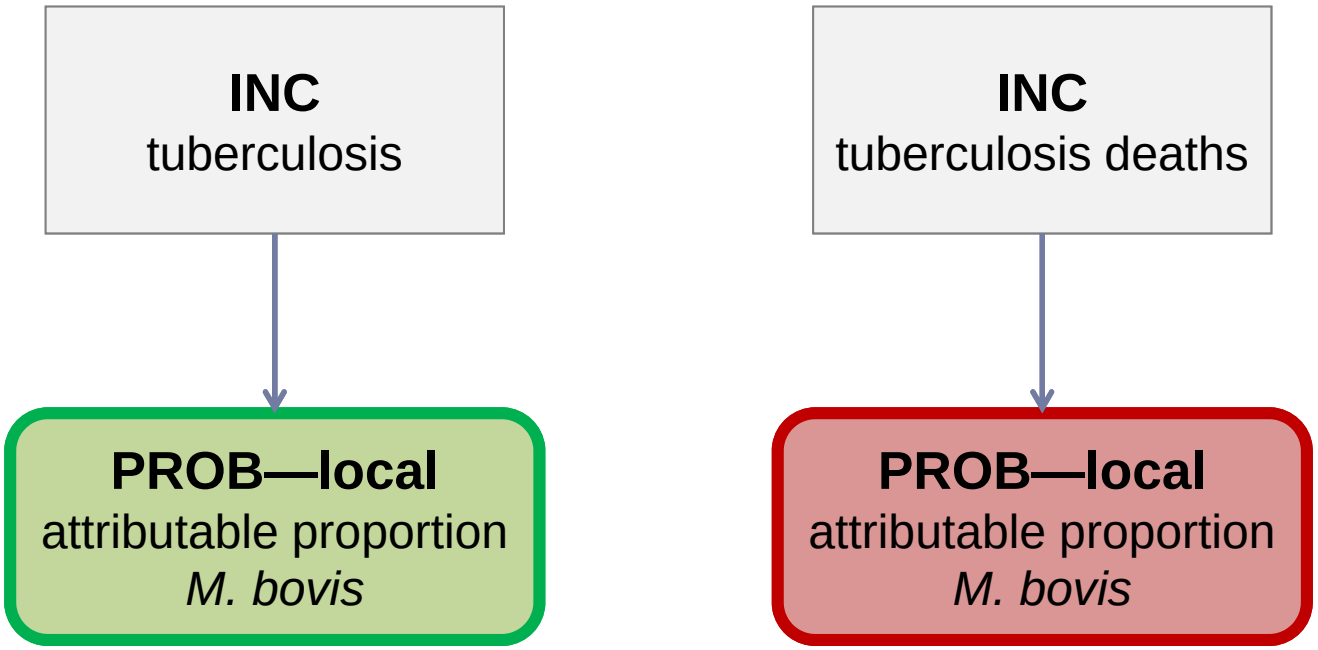
- Hazard-based task forces: systematic reviews
- **Computational** disease model
  - Disease biology + Data availability
  - Directed acyclic graphs (nodes and arrows)
- Quantifying hazard disease burden
  - Categorical attribution
  - Counterfactual analysis
  - Risk assessment

Disease models and epidemiological data

- Hazard-based task forces: systematic reviews
- Computational disease model
- Quantifying hazard disease burden
  - **Categorical attribution**
    - Outcome identifiable as caused by hazard in individual cases
    - All viral, bacterial and parasitic hazards; cyanide in cassava, peanut allergen
    - Attributional model: symptom → hazard attribution
    - Transitional model: infection/exposure → symptom

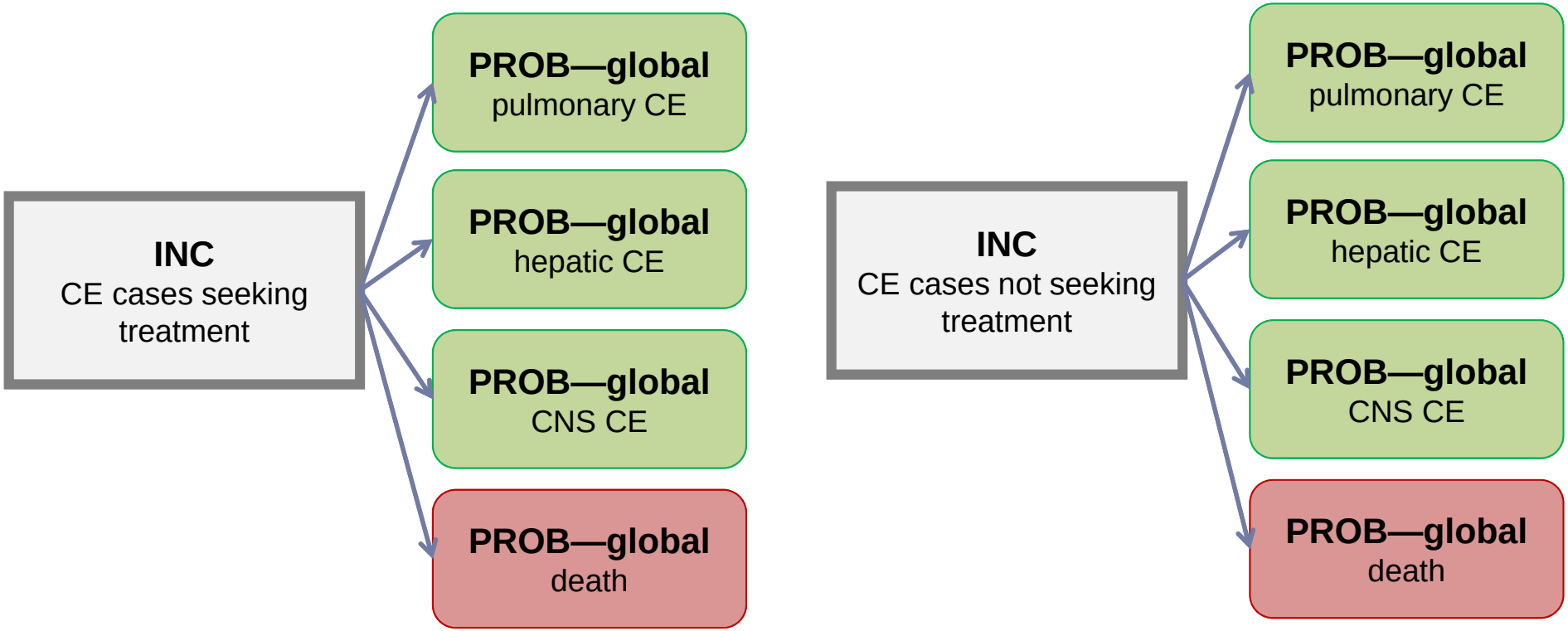
Categorical attribution; Attributional model

Mycobacterium bovis
Disease Model



Categorical attribution; Transitional model

Echinococcus granulosus Disease Model

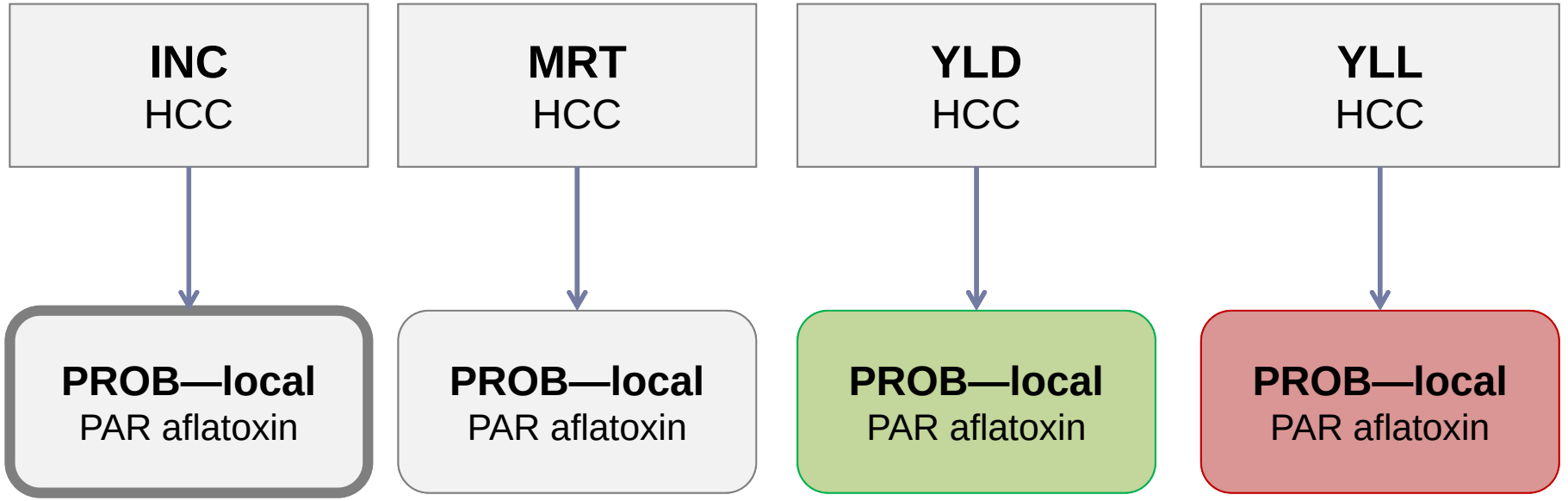


Disease models and epidemiological data

- Hazard-based task forces: systematic reviews
- Computational disease model
- Quantifying hazard disease burden
  - Categorical attribution
  - **Counterfactual analysis**
    - Causal attribution cannot be made on an individual basis
    - Aflatoxin and hepatocellular carcinoma
    - Statistical association: Population Attributable Risk (PAR)
    - Attributional model: symptom → hazard attribution

Counterfactual analysis; Attributional model

Aflatoxin
Disease Model



Disease models and epidemiological data

- Hazard-based task forces: systematic reviews
- Computational disease model
- Quantifying hazard disease burden
  - Categorical attribution
  - Counterfactual analysis
  - **Risk assessment**
    - Combining exposure and dose-response data
    - Not necessarily consistent with existing health statistics
    - Dioxin and impaired fertility, hypothyroidy

Note: underreporting

- Not explicitly addressed in CTF framework
- Captured by framework
  - Attributional models: corrected envelopes
  - Use of survey instead of surveillance data
  - Underreporting factor included in disease model

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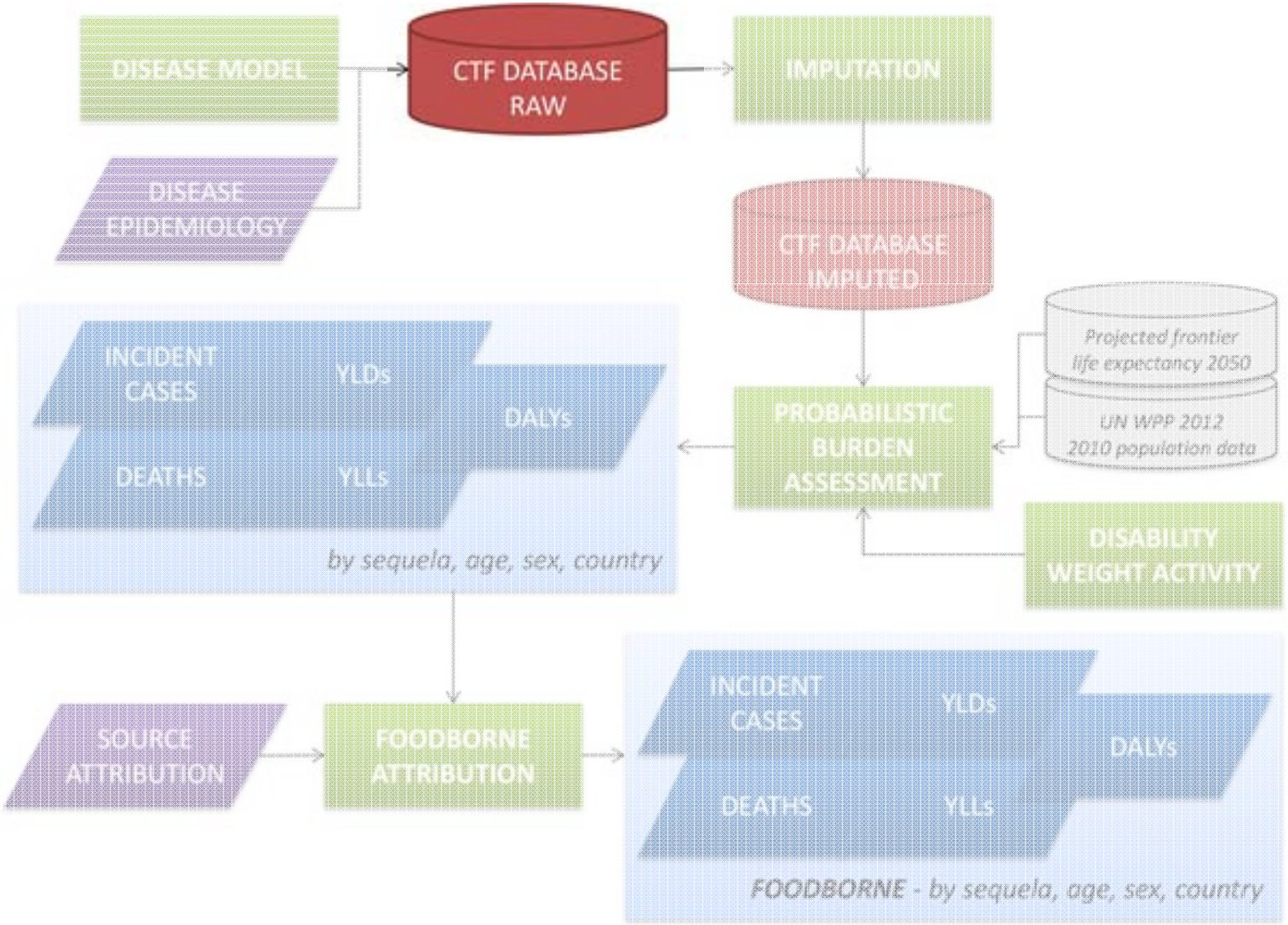

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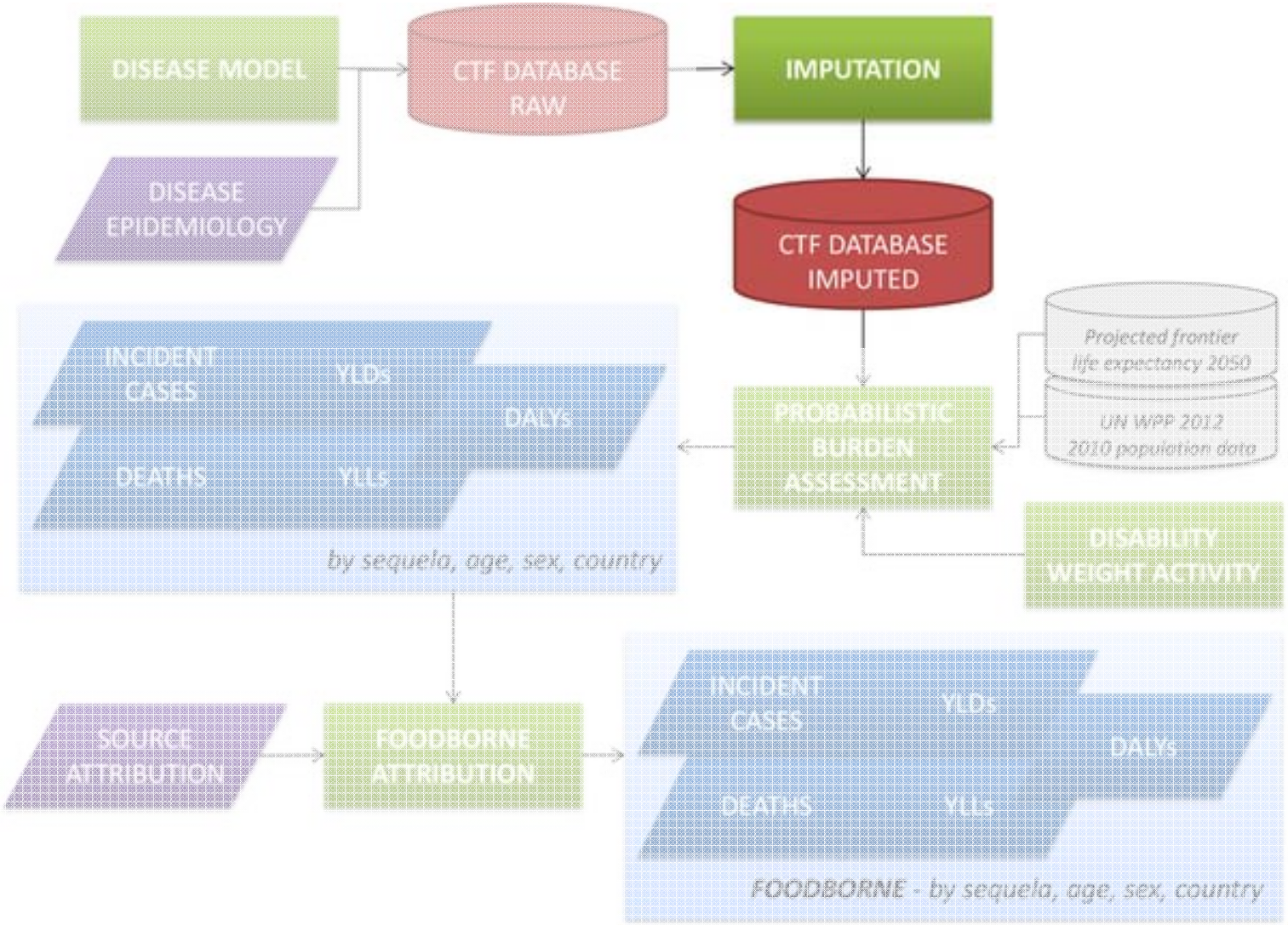
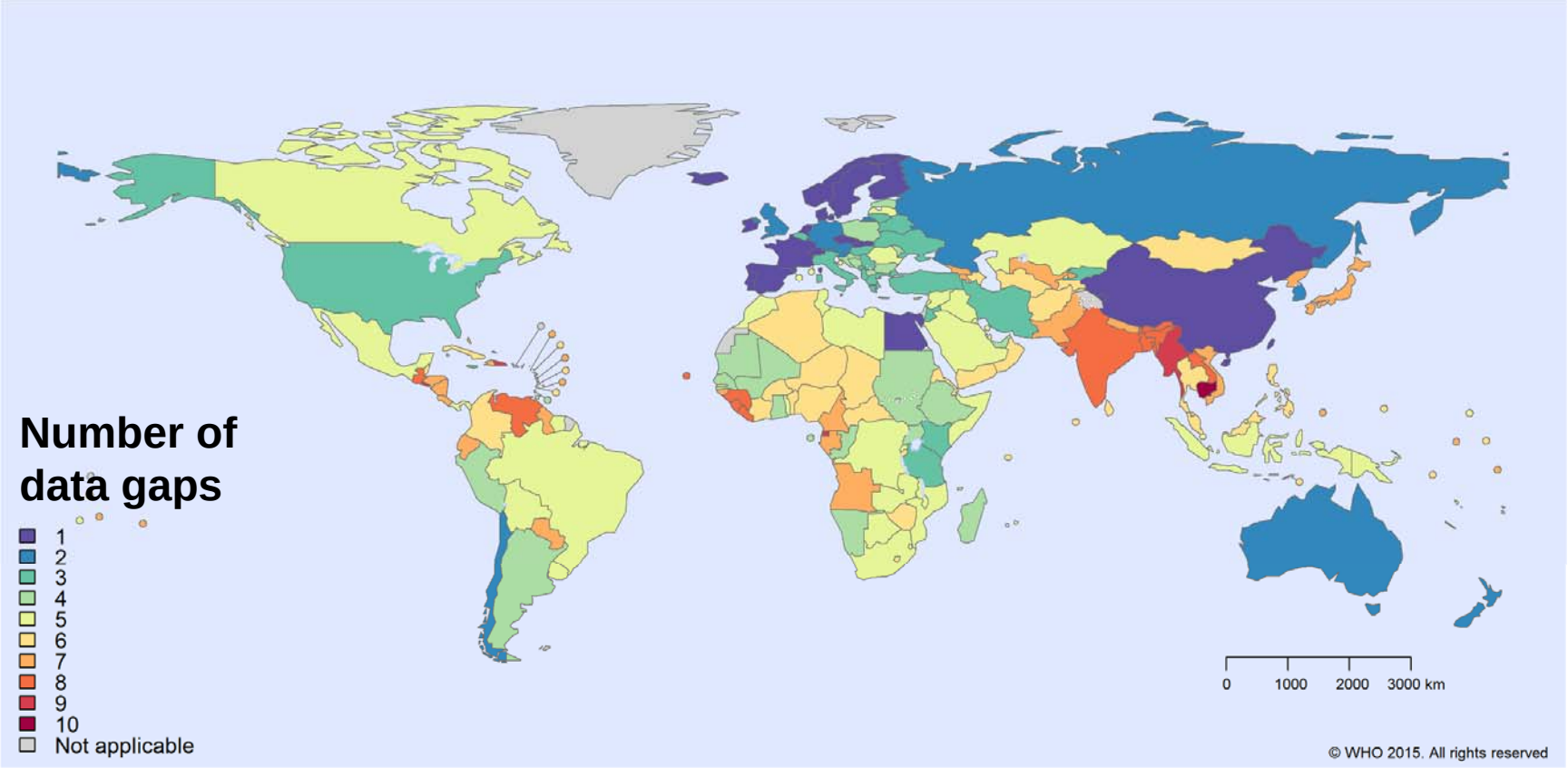


Need for imputation



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Imputation model

- Provide reasonable value + uncertainty range
- Bayesian random effects log-Normal regression model

$$\log(\theta_{ij}) \sim Normal(\mu_i, \sigma_w^2)$$
$$\mu_i \sim Normal(\mu_0, \sigma_b^2)$$

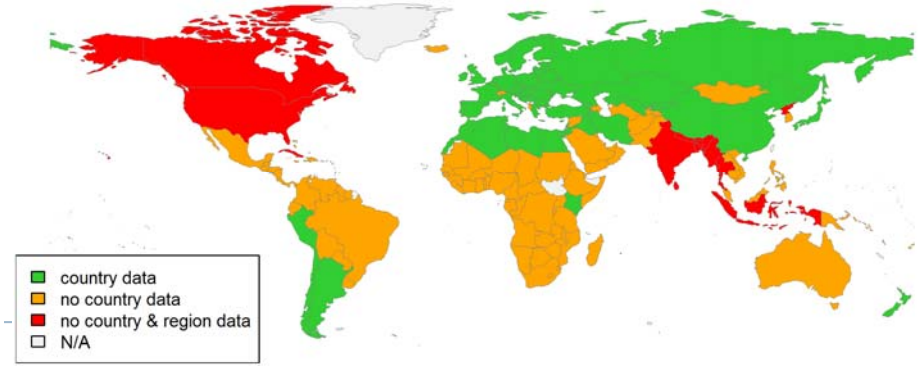
θ_{ij} = incidence in country j belonging to region i

μ_i = regional mean; μ_0 = global mean

σ_w^2 = within-region variance; σ_b^2 = between-region variance

Imputation model

- Provide reasonable value + uncertainty range
- Bayesian random effects log-Normal regression model
  - **green** countries: no imputation
  - **orange** countries: $LN(\mu_i, \sigma_w^2)$
    - "random" country within concerned subregion
    - UI describes variability within subregions
  - **red** countries: $LN(\mu_0, \sigma_b^2 + \sigma_w^2)$
    - "random" country within a "random" subregion
    - UI describes variability between and within subregions



Imputation model

- Provide reasonable value + uncertainty range
- Bayesian random effects log-Normal regression model
- Only when data from different subregions available
  - If not: no imputation, no global estimates
  - *Bacillus cereus, Clostridium perfringens, Clostridium botulinum, Staphylococcus aureus*, and peanut allergens

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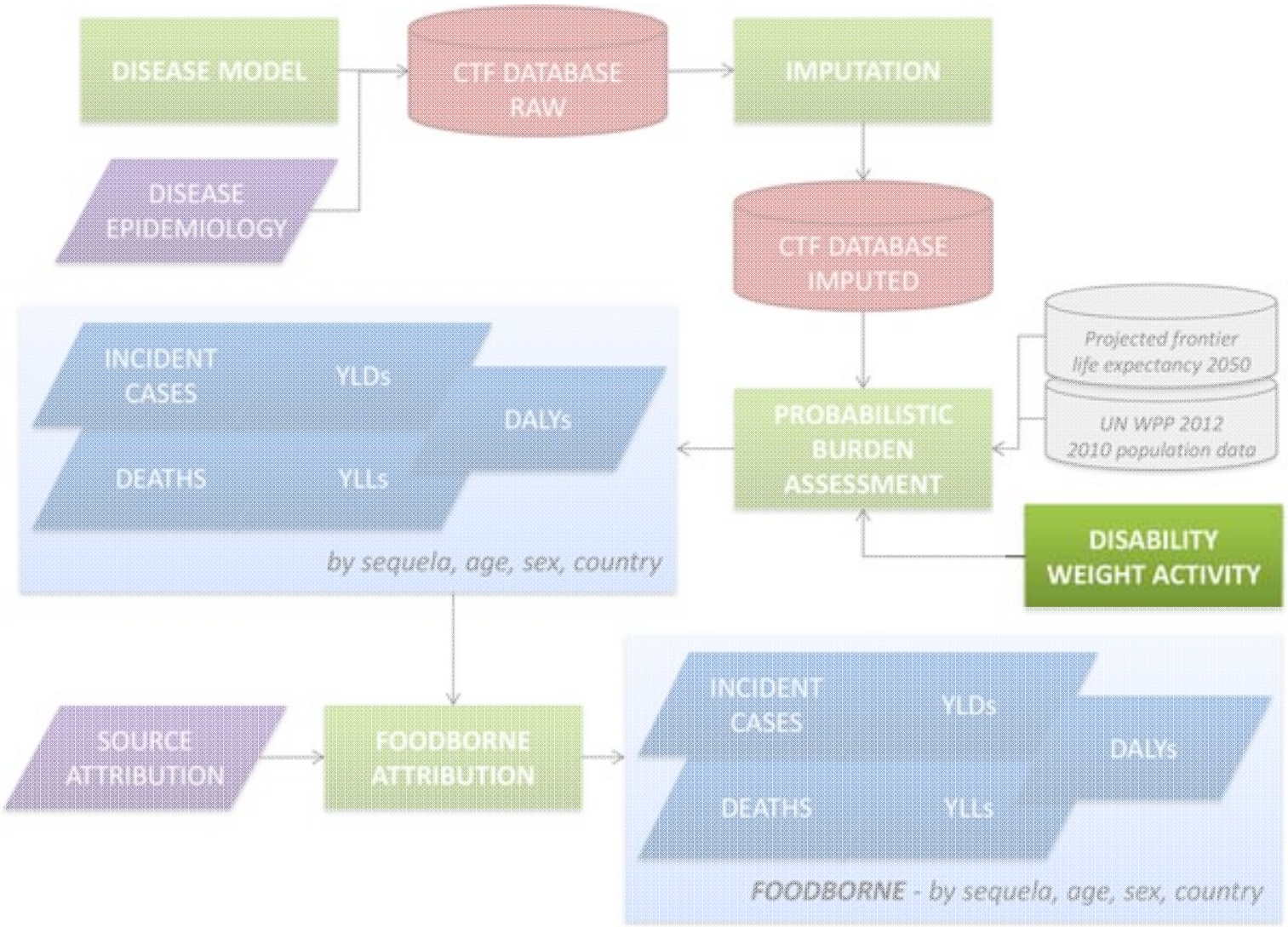
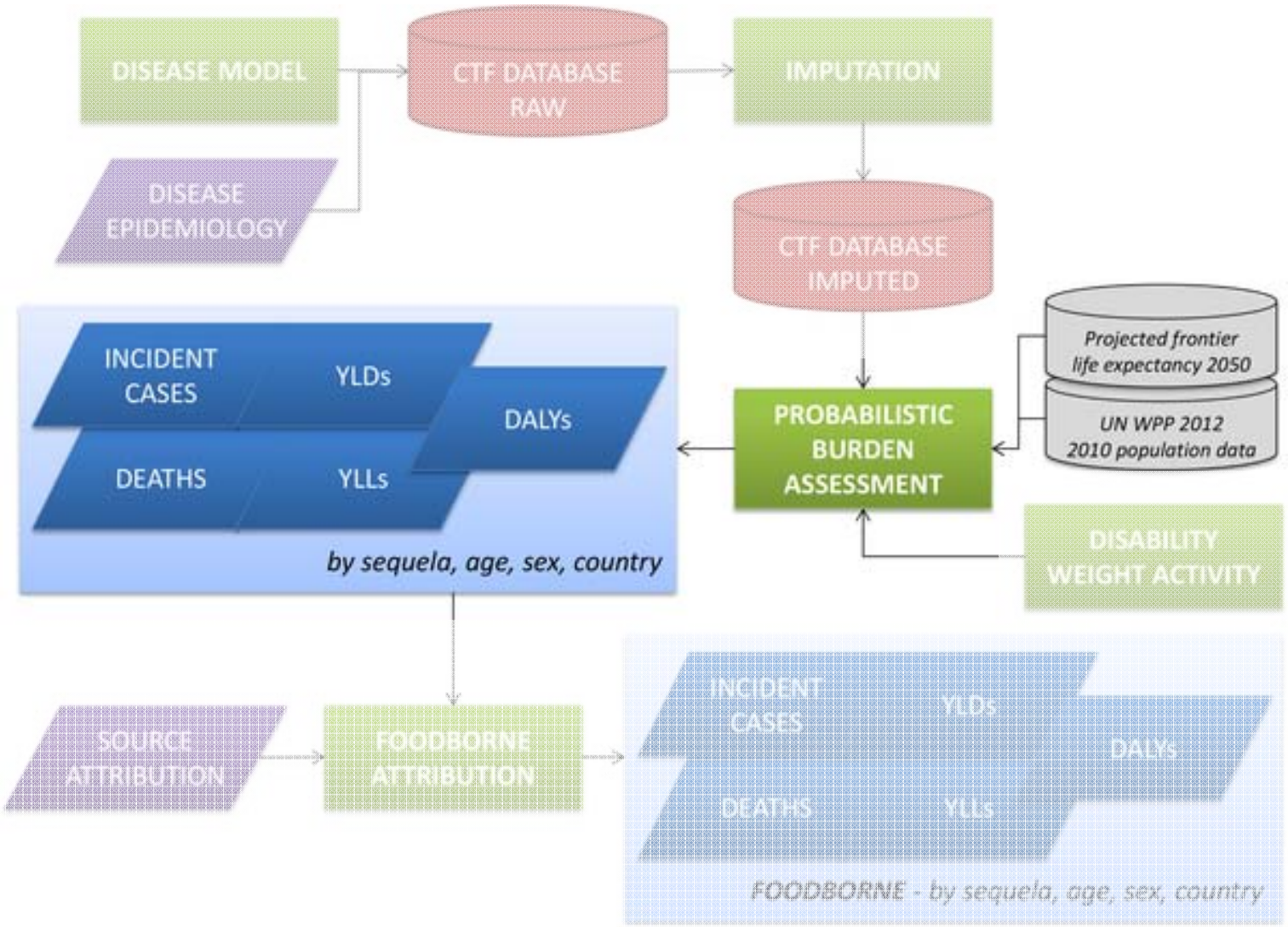


Disability weights

- Severity of health states, relative reduction in health
  - 0 = perfect health
  - 1 = death
- Adopted from WHO Global Health Estimates
  - Based on GBD 2010, except:
    - Primary infertility: alternative value
    - Hypothyroidy: GBD 2013
  - Direct mapping or proxy health state(s)
- Severity levels (mild, moderate, severe)
  - Included in disease model as distinct health states
  - Weighted average, based on epidemiological data

Computational Task Force Workflow

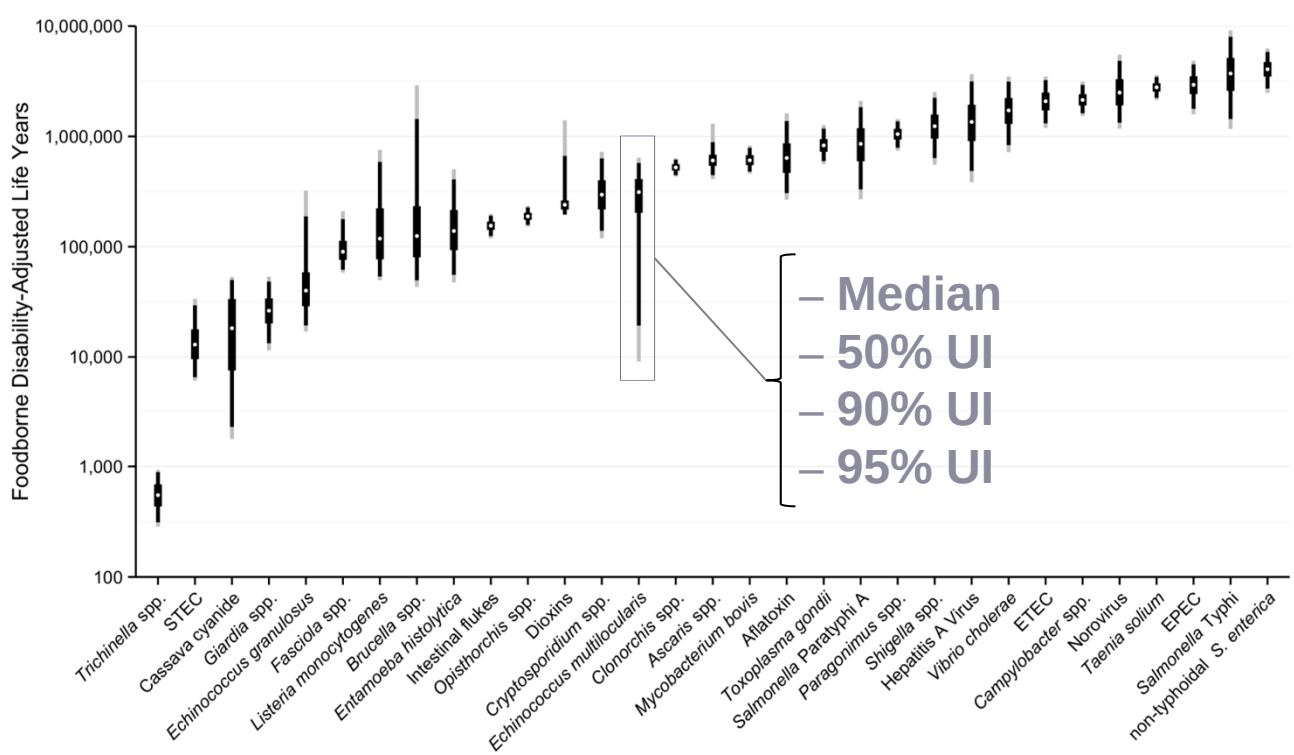


Probabilistic burden assessment

- Incidence, mortality, YLD, YLL, DALY rate
  - Per hazard, outcome, country, age, sex
- Absolute numbers: 2010 population sizes
- Standard life expectancy for YLLs
  - highest projected LE for 2050
  - LE at birth of 92, males and females
- No age weighting, no time discounting
- No correction for comorbidity, except
  - HIV infected invasive salmonellosis cases and deaths
  - HIV infected *M. bovis* deaths

Probabilistic burden assessment

- *Probabilistic*: parameter + imputation uncertainty
  - 10,000 Monte Carlo simulations
  - Uncertainty distribution instead of single estimate
    - Median, 95% uncertainty interval



Probabilistic burden assessment

- *Probabilistic*: parameter uncertainty
  - 10,000 Monte Carlo simulations
  - Uncertainty distribution instead of single estimate
    - Median, 95% uncertainty interval
- Implemented in R and JAGS
  - All code available as 'FERG' package
  - https://github.com/brechtdv/FERG

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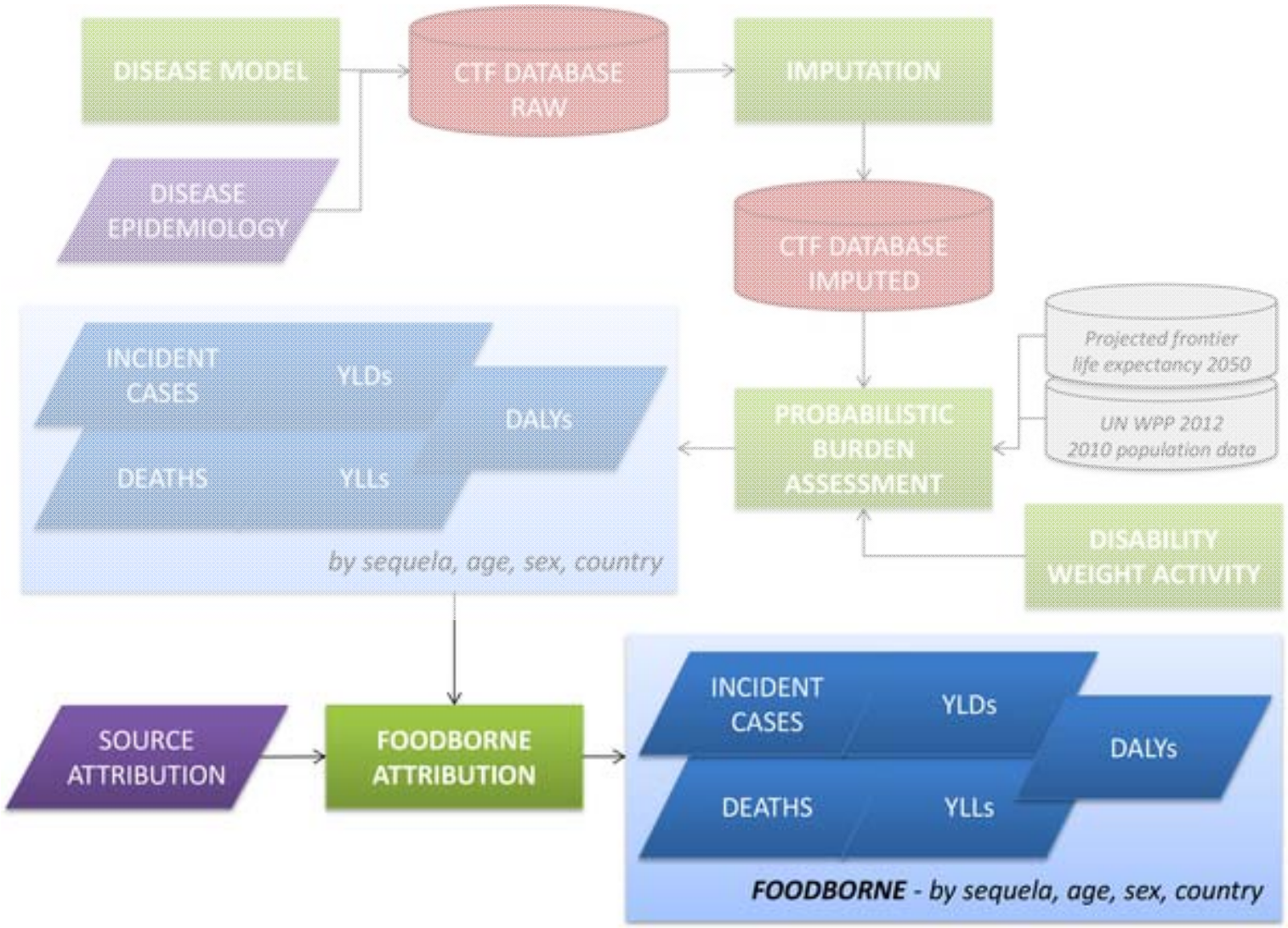
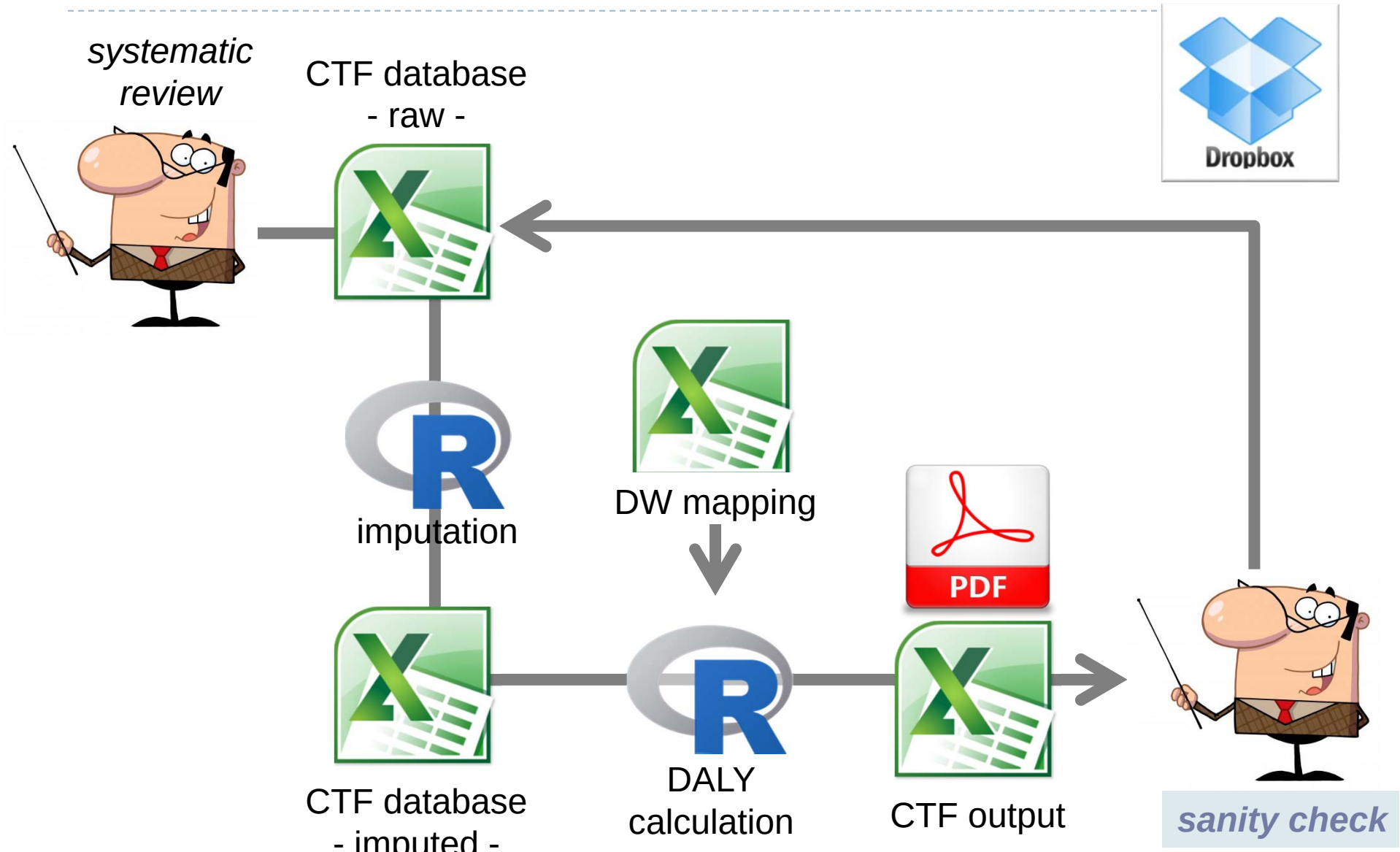


Foodborne attribution

- Some hazards considered 100% foodborne
  - *L. monocytogenes*, *M. bovis*, foodborne trematodes, *T. solium*, *Trichinella* spp., aflatoxin, cyanide in cassava, dioxin, peanut allergens
- Remaining hazards: structured expert elicitation
  - See next presentation
  - FB disease burden

    = overall disease burden × proportion FB

Traceability & transparency



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