Alaska Birth Defect Registry
Data Analysis Methods

Contents

Surveillance Notes

Calculation of Report and Prevalence Estimates

Analyses are based on each occurrence of a unique combination of child and condition. An infant can have multiple defects and is counted as a separate case for each defect. For example an infant with Trisomy 21 and Cleft Lip would be counted as a unique case for Trisomy 21 and a unique case for Cleft Lip. Thus the number of different cases cannot be added together to reach the total number of infants with a defect.

When an infant has two or more conditions within the same category in an analysis it is only counted once.

Ideally, for measure of disease occurrence, the incidence rate would be used. However, the population at risk (denominator) is difficult to quantify for birth defects research. Since the number of conceptions is unknown as are the number of cases lost through spontaneous or other abortion and some fetal deaths we cannot determine incidence. For this reason the prevalence at birth is used to represent the disease occurrence.

Birth defects are rare events and Alaska's population is small. To account for year-to-year variation all prevalence estimates are based on 5-year moving averages (Note: estimates contained in specific reports if available may display 3-year moving average trend lines). To be included, a reported individual must link to an Alaskan birth certificate. Prevalence Estimates are always cited as per 10,000 live births.

Report Prevalence

The report prevalence is the prevalence at birth of a specific defect based on the count of unique children identified through a reported ICD code representing a specified condition regardless of case confirmation status.

$$Report\ Prevalence =$$

$$\frac{Number\ of\ Uniqe\ Children\ with\ ICD\ code(s) for\ condition}{Number\ of\ live\ births} x\ 10{,}000$$

Note: both the numerator and denominator are restricted to the same timeframe (3-year or 5-year window) and are based on birth year of the child.

Defect Prevalence

The defect prevalence is the estimated prevalence at birth of a specific defect. This estimate uses a Bayesian approach to incorporate the historical sampled confirmation probability and the estimated missed cases probability by restricting the analysis to children diagnosed and seen by a medical provider before age 3 years.

$$Bayes's\ theorem: p(A|B) = \frac{p(B|A) * p(A)}{p(B)}$$

We use the informative known prior obtained through sampled case confirmation of reported cases (Positive Predictive Value) and (1-Negative Predictive Value) to calculate the estimated probability of defect. Thus:

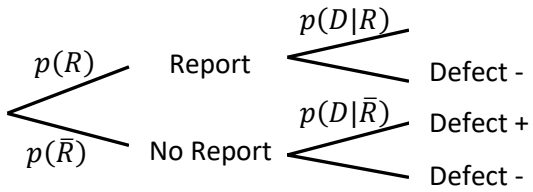
$$\text{Positive Predictive Value (PPV)} = \text{p(D|R)}$$

$$\text{Negative Predictive Value (NPV)} = \text{p}(\overline{\text{D}}|\overline{\text{R}})]$$

$$p(D) \approx [p(R) * p(D|R)] + [p(\bar{R}) * p(D|\bar{R})]$$

$$Where, P = probability, R = report, \bar{R} = \ no\ report\ D = defect, and\ \overline{D} = \ no\ defect$$

Under a visual tree diagram representation this is:



The $p(D|\bar{R})$ is generated by enumerating the "missed" case probability from reports of children ages 3-6 years of age among historical data. This estimate is calculated for each condition and considered a constant over time, under the assumption that children reported for the first time for condition "x" between the ages of 3 and 6 years will follow a constant distribution over time. These estimates will be refined with additional sample draws, confirmations, and assessments.

The Confidence interval for both the estimate based on reports without confirmation and defect estimate are based on the Poisson distribution. The exact method for estimation:

$$Confidence\ Interval:$$

$$(1-\alpha)\ \%\ CI = \left(\frac{x^2_{2N,\frac{\alpha}{2}}}{2T}, \frac{x^2_{2(N+1),1-\frac{\alpha}{2}}}{2T}\right)$$

$$Where\ N = the\ number\ of\ cases\ and\ T = the\ person-time\ or\ population\ at\ risk$$

Note: Confidence Intervals are calculated using an 'exact' method. This method is based on the exact distribution opposed to an approximation. Exact methods are a conservative approach and useful with small cell counts.

Interpreting Prevalence Estimates

The Registry's focus is to:

- Improve the consistency of reporting among core agencies.
- Stabilize and improve the confidence in calculated prevalence estimates.

The Registry has attempted to produce prevalence estimates with improved accuracy by incorporating informative prior information and by utilizing specific condition defect estimates (DE) from medical record reviews.

Differences in defect and reported prevalence estimates over time or between regions may reflect variance in reporting, leading to differential detection bias, true differences influenced by genetic, environmental or other causes, or even chance differences.

These estimates are limited to live births occurring in Alaska, as such estimates for certain defects that result in spontaneous abortion, high fetal mortality, or frequently delivered out-of-state are likely under-represented.

Defect classification in the Alaska Birth Defect Registry is made by collecting and aggregating ICD codes representing birth defects from multiple agencies across the state. As such, variation in clinical and diagnosis practices, expertise, electronic health records, and miscoding by coders/providers all may influence case detection and classification. ICD codes used in passive surveillance system can potentially misrepresent the actual prevalence, and caution should be used when interpreting the reported prevalence in the absence of estimated defect prevalence.

The estimates provided are believed to be the most accurate, but are subject to large variation resulting from surveillance methodology.

As additional samples are drawn and medical records abstraction and confirmation occurs, the defect estimates will be updated and expanded.