

Appendix 1: Analytical methods

As a general outline, trends in the number of hospitalizations were estimated by birth cohort, and then these trends were used to predict the future burden in the younger birth cohorts as they aged. Next, rates and rate ratios were calculated by three different measures of the cohort effect: by year of hospitalization; at the same age; and future lifetime. Current year and near-term predictions focus on the visible burden. The same age comparison is a proxy measure of the relative prevalence. The future lifetime comparison is similar to the comparison used in cost-effectiveness analysis.

The first step was to estimate the trend in the number of hepatitis C and liver disease-associated hospitalizations for each 5-year birth cohort from 1915-19 to 1980-84. A generalized linear model (GLM) with a log link, Poisson distribution and dispersion parameter specified[1] was fit to the annual number of hospitalizations stratified by birth cohort with year of discharge (fiscal year) and a constant term as the model covariates. The quasi-Poisson regression model equation to predict the annual number of hospitalizations ($Hosp_{i,j}$) for birth cohort j ($j=1915-19$ to 1980-84) in batch year i ($i=2004/05$ to 2010/11) is given by:

(1)

The estimated trend parameter value ($\beta_{2,j}$) and its standard error were converted to an average annual percentage change ($e^{\beta_{2,j}} - 1$) for each birth cohort. The same model was used to estimate the overall trend for all birth cohorts combined.

The second step was to use a parametric bootstrap approach, which involves generating simulated values of the parameters, to facilitate the calculation of confidence intervals (CI) for the projected rate ratios. The bootstrap is a computationally intensive statistical technique that allows the researcher to make inferences from data with complex distributions (in this case, the ratios of projected rates)[1-3]. Random values were generated using the normal distribution with the mean and standard deviation given by the

trend ($\beta_{2,j}$) and standard error estimated in the quasi-Poisson regression model in the first step. The number of hospitalizations for each birth cohort in the last year of available data ($Hosp_{2010,j}$) was also simulated from the distribution of uncertainty (standard error) associated with model predicted value for 2010/11. In the third step, the average age at hospitalization over the study period was calculated for each birth cohort and the simulated values for the cohort-specific trends ($\beta_{2,j}$) were interpolated linearly to obtain trend estimates for each single year of age [1]. The fourth step was to project the number of hospitalizations until age 90 for each 5-year birth cohort and then sum the predicted number of hospitalizations for the time period of interest (for example, next 10 years, at age 75, or future lifetime) and calculate hospitalization rates. Future lifetime hospitalizations were calculated by summing the projected values from 2011/12 until age 90 and rates were calculated by dividing by the population in 2010. The 1970-74 birth cohort was selected as the reference for the rate ratios, as a comparison with this birth cohort is an important consideration for screening recommendations and for comparability of the same-age ratios with prevalence ratios used in the development of the CDC guidelines. Same-age rate ratios were reported for age 75. (The simulated projections by birth cohort are proportional as illustrated in Figure 3b.) The final step was to calculate the mean and standard deviation of the rate ratios from the previous step. Results from steps 1 (trends), 4 (projections) and 5 (rate ratios) are reported. SAS Enterprise Guide 5.1 [1] was used for the analysis.

References

1. SAS Institute Inc. *SAS Enterprise Guide 5.1*, Cary, NC: SAS Institute Inc.; 2006.
2. Haukoos JS, Lewis RJ. Advanced Statistics: Bootstrapping Confidence Intervals for Statistics with Difficult Distributions. *Acad Emerg Med* 2008;12:360-5.

3. Henderson AR. The bootstrap: A technique for data-driven statistics. Using computer-intensive analyses to explore experimental data. *Clin Chim Acta* 2005;359:1-26.