

A meta regression analysis

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METHODS

Data sources and extraction

- **PubMed** and **Embase** were searched for studies reported prevalence of *H. pylori* infection among Japanese population (until 30 June, 2016).
- 43 papers

 JPHC Cohort II
 JPHC-NEXT Cohort Study
 included for meta-regression analysis
 (Table 1).
- Prevalence of H. pylori infection reported by birth year group of participants^[1~7].

- 38 studies reported prevalence with age groups.
 - 34 studies reported data collection period:
 - Example:
 60-70 years old group;
 data collection done in 1990;
 birth year should be 1920~1930.
 - 4 studies reported age groups with data collection year unavailable, year of publication was used instead of data collection period.
- [1] Ueda J. Helicobacter. 2014; [2] Watanabe M. Cancer Sci. 2015;
- [3] Reploge M.L. Int J Epidemiol. 1996; [4] Shimoyama T. Gastric Cancer. 2012;
- [5] Shimatani T. *J Gastroenterol Hepatol.* 2005; [6] JPHC Cohort II; [7] JPHC-NEXT

STATISTICAL ANALYSIS

273 Data Points from 45 Studies were available for meta-regression

Show 100 - entries			Search:		
No	Author	adultdults.or.childhildren 🖣	Source.population *	Specimen.type 🖣	kit.
1	Kikuchi, 1998	adult	General	serum	fc
1	Kikuchi, 1998	adult	General	serum	fc
1	Kikuchi, 1998	adult	General	serum	fc
1	Kikuchi, 1998	adult	General	serum	fc
2	Fujisawa, 1999	adult	General	serum	fc
	Fiiicara				5 / 15

Step 1: Weight Calculation

```
library(meta)
library(metafor)
library(mgcv)
meta <- metaprop( event = Number_of_Positive,</pre>
                        = Number_of_Subjects_in_the_corresponding_group,
                  byvar = Birth_Year,
                  sm = "PLOGIT", # Logit transformation
             method.tau = "REML") # Restricted Maximum-likelihood
                                       # estimator to estimate the
                                       # between-study variance
weight<-meta$w.random # Weight of each data point extracted</pre>
```

Step 2: Meta-regression (Generalized Additive Mixed Model, GAMM)

```
res1 <- gam(cbind(event,n) ~ s(Birth_Year, bs="cr") +
                                  # Cubic Spline Regression 三次スプライン曲級
            s(Study_ID, bs="re") + # Study ID as random effect
            Source_of_population + # Community OR Clinical based
            Specimen_type + # Serum OR Others (urinary, salivary, st
            Kit.from + # Antigen derived from demostic or forei
                                  # Data collection period, cutoff = 2000
            early,
            data = data, weights=weight,
            family="binomial"(link=logit), method="REML")
#########################
res2 <- gam(cbind(event,n) ~ s(Birth_Year, bs="cr") +
            s(Study_ID, bs="re") +
            Specimen_type,
            data = data, weights=weight,
            family="binomial"(link=logit), method="REML")
########################
res3 <- gam(cbind(event,n) ~ s(Birth_Year, bs="cr") +
            s(Study_ID, bs="re"),
            data = data, weights=weight,
            family="binomial"(link=logit), method="REML")
                                                                   7 / 15
```

TABLE 2. Informations for tested models.

	AIC	BIC	LogLik
Model 1: Logit(P) = s(birth year) + r(study ID) + f(source of population) + f(diagnostic test) + f(ELIZA kits) + f(research year)	1716.444	1895.216	-808.6935 (df=49.53)
Model 2: Logit(P) = s(birth year) + r(study ID) + f(diagnostic test)	1730.349	1904.178	-817.0157 (df=48.16)
Model 3: Logit(P) = s(birth year) + r(study ID)	1731.451	1906.366	-817.2658 (df=48.46)
Abbreviations and definitions: AIC: Akaike's information criterion; BIC: Bayesian information criterion; LogLik: Log-likelihood; P: prevalence; s: penalized cubic spline; r: random effect; f: fixed effect; df: degree of freedom.			

Summary from Model 1 comparable to Table 3

```
##
## Family: binomial
## Link function: logit
##
## Formula:
## cbind(mp, n_total - mp) ~ s(birth.year_high, bs = "cr") + s(No,
      bs = "re") + Source.population + Specimen.type + kit.from +
##
##
      early
##
## Parametric coefficients:
                          Estimate Std. Error z value Pr(>|z|)
##
## (Intercept)
                                     0.14022 - 1.217
                          -0.17064
                                                      0.2236
## Source.populationPatient 0.28630 0.20234 1.415
                                                      0.1571
## Specimen.typeother -0.41271 0.19256 -2.143
                                                      0.0321 *
## kit.fromforeign 0.01836 0.16847 0.109
                                                      0.9132
## kit.fromunknown -0.11517 0.25923 -0.444
                                                      0.6569
## earlylate
                                     0.15813 - 1.611
                        -0.25471
                                                      0.1072
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
                       edf Ref.df Chi.sq p-value
##
## s(birth.year_high) 7.372 8.158 4255 <2e-16 ***
## s(No)
                                  1910 <2e-16 ***
                    34.754 38.000
```

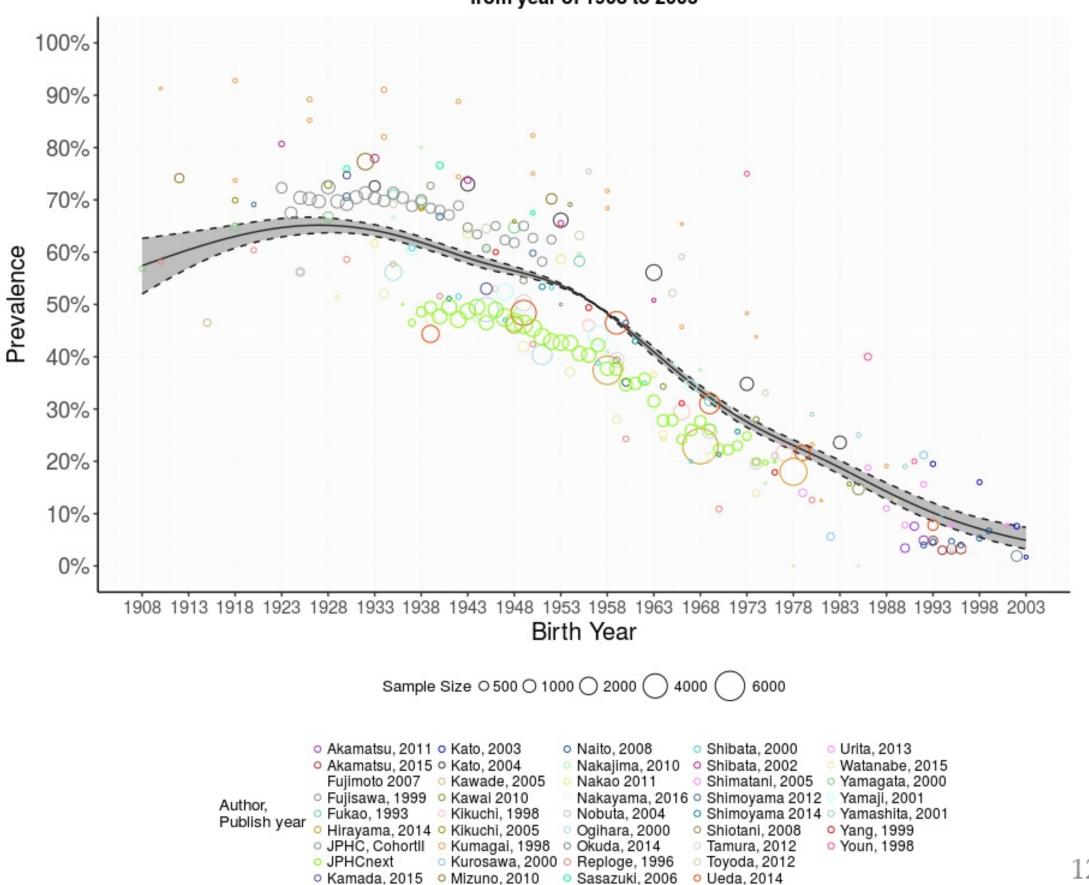
9 / 15

Table 4 Predicted Prevalence of *H. pylori* infection from 1908 to 2003

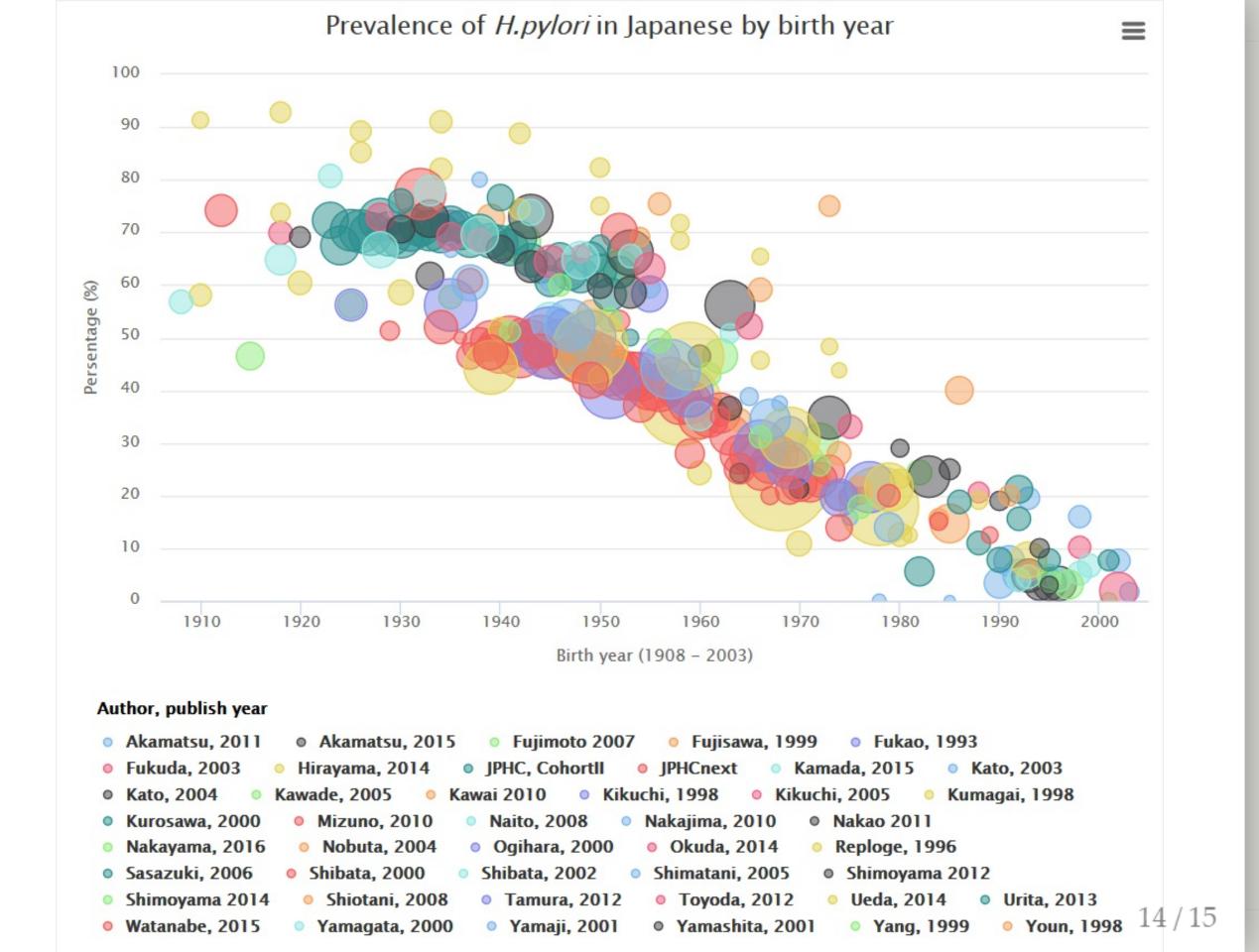
Show 100 → entries		Search	Search:		
Birthyear	Pres	valence • 95%CI_low	95%CI_high •		
1908	0.574	0.520	0.626		
1909	0.580	0.530	0.628		
1910	0.586	0.540	0.631		
1911	0.592	0.549	0.633		
1912	0.597	0.559	0.635		
1913	0.603	0.567	0.638		
1914	0.609	0.576	0.640		
1915	0.614	0.584	0.643		
1916	0.619	0.591	0.645		

PLOT

Figure 2. Multivariable adjusted prevalence of *H. pylori* infection in Japanese by birth year from year of 1908 to 2003



Interactive PLOT



Thanks!

Slides made by using xaringan package

Slides address:

https://winterwang.github.io/For_Inoue_pylori/#1