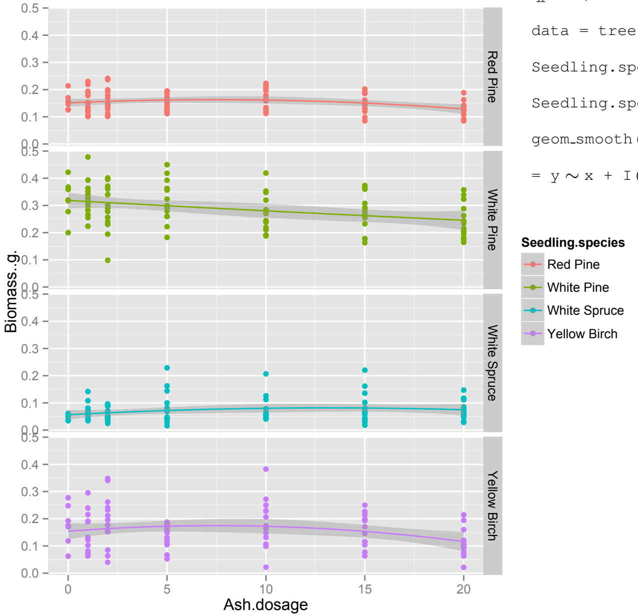
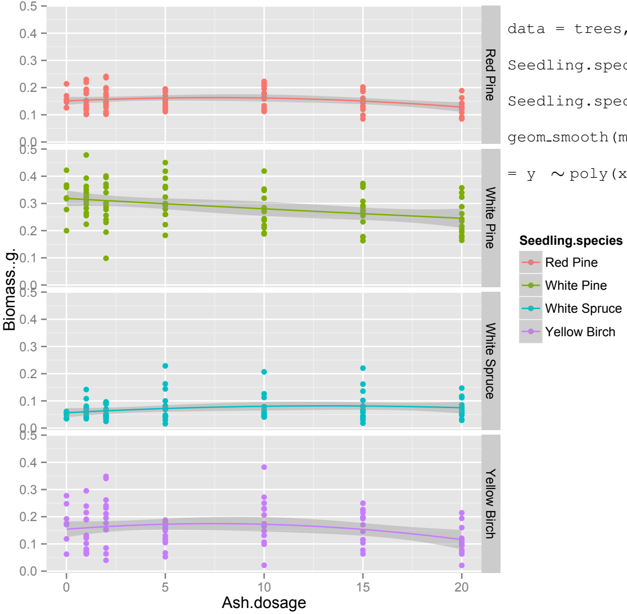
Today

- HW 1: due *today*, 11.59 pm.
- HW 2: due March 4, posted soon
- Backback to Briefcase, Feb 10 6 - 8 pm (Career Centre)
- Recap on trees analysis
- Contingency tables
- Next week: Generalized Linear Models Chs. 6 and 7
- after mid-term break: random effects, mixed linear and non-linear models, nonparametric regression methods
- Young Statisticians writing Competition



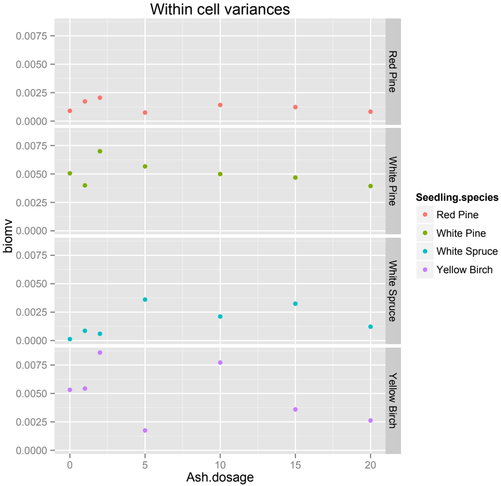

```
qplot(Ash.dosage, Biomass..g.,
data = trees, facets =
Seedling.species ~ ., color =
Seedling.species) +
geom_smooth(method = "lm", formula
= y ~ x + I(x^2), se = T)
```




```
qplot(Ash.dosage, Biomass..g.,
data = trees, facets =
Seedling.species ∼ ., color =
Seedling.species) +
geom_smooth(method = "lm", formula
= y  ∼ poly(x,2), se = T)
```

linear models

```
# straight lines for each species, all with same slope:

trees.lm <- lm(formula = Biomass..g. ~ Ash.dosage + Seedling.species, data = trees) #

# orthogonal polynomials as in class

trees.lm2 <- lm(formula = Biomass..g. ~ as.ordered(Ash.dosage) + Seedling.species,
    data = trees)

# ordinary quadratics (no indication that any higher orders are needed

trees.lm3 <- lm(formula = Biomass..g. ~ Ash.dosage + I(Ash.dosage^2) + Seedling.species,
    data = trees)

# this allows a different slope for each species

trees.lm4 <- lm(formula = Biomass..g. ~ Ash.dosage * Seedling.species, data = trees)

# and a different quadratic for each species

trees.lm5 <- lm(formula = Biomass..g. ~ poly(Ash.dosage, 2) * Seedling.species,
    data = trees)
```




```
vartrees <-
ddply(trees,.(Seedling.species,
Ash.boiler.type,
Ash.dosage),summarize, biomv =
var(Biomass..g.))
qplot(Ash.dosage, biomv, data =
vartrees, facets =
Seedling.species   .,
color=Seedling.species, main =
"Within cell variances")
```

Contingency tables

ELM Ch. 4

Quality	No Particles	Particles	Total
Good	320	14	334
Bad	80	36	116
Total	400	50	450

- see p.70 for data.frame `wafer` and use of `xtabs`

- Poisson regression:

```
modl <- glm(y   particle + quality, data = wafer, family = poisson)
```

```
glm(formula = y ~ particle + quality, family = poisson, data = wafer)
...
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   5.6934     0.0572  99.535   <2e-16 ***
particleyes  -2.0794     0.1500 -13.863   <2e-16 ***
qualitybad   -1.0575     0.1078  -9.813   <2e-16 ***
---
...
       Null deviance: 474.10  on 3  degrees of freedom
Residual deviance:  54.03  on 1  degrees of freedom
```

... contingency tables

Quality	No Particles	Particles	Total
Good	320	14	334
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```
modl <- glm(y   particle + quality, data = wafer, family = poisson)
```

Model:

$$\log \mu_{ij} = \gamma + \alpha_i + \beta_j$$

```
---
...
      Null deviance: 474.10  on 3  degrees of freedom
Residual deviance:  54.03  on 1  degrees of freedom
```

Test of no interaction between particle and quality

... contingency tables

Quality	No Particles	Particles	Total
Good	320	14	334
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Total	400	50	450

Multinomial model: fix total sample size (450):

$$y \sim \text{Mult}(n; p); p_{ij} = \Pr\{\text{single observation is in cell}(i, j)\}$$

$$L(p; y) = \frac{n!}{y_{11}!y_{12}!y_{21}!y_{22}!} p_{11}^{y_{12}} p_{12}^{y_{21}} p_{21}^{y_{21}} p_{22}^{y_{11}}$$

Independence: $p_{ij} = p_i \times p_j$

Maximum likelihood estimates:

– under independence $\hat{p}_{ij} = \hat{p}_i \hat{p}_j =$

– unrestricted $\tilde{p}_{ij} =$

... contingency tables

Quality	No Particles	Particles	Total
Good	320 296.89	14 37.11	334
Bad	80 103.11	36 12.89	116
Total	400	50	450

```
2*sum(sum(ov*log(ov/fv))
[1] 54.03045
```

see ELM for construction of `ov` and `fv`

```
sum((ov-fv)^ 2/fv)
[1] 62.81231
```

```
 modb <- glm (matrix(wafer$y, nrow=2) ~ 1, family = binomial)


    Null deviance: 54.03  on 1  degrees of freedom
Residual deviance: 54.03  on 1  degrees of freedom

modb2 <- glm(matrix(wafer$y, nrow = 2) ~ c("nop","p"), family = binomial)

     Null deviance: 54.03  on 1  degrees of freedom
Residual deviance:  0.00  on 0  degrees of freedom
```

... contingency tables

Quality	No Particles	Particles	Total
Good	320	14	334
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Fisher's exact test of independence: condition on all marginal totals

only y_{11} free to vary   or any other single element

$$\Pr(Y_{11} = y_{11} \mid y_{1+}, y_{+1}, n) = \frac{\binom{y_{1+}}{y_{11}}\binom{n-y_{1+}}{y_{1+}-y_{11}}}{\binom{n}{y_{1+}}}$$

```
> fisher.test(ov)

Fisher's Exact Test for Count Data

data:  ov
p-value = 2.955e-13
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
  5.090628 21.544071
sample estimates:  odds ratio   10.21331  {\rf ?where is 10.213 in previous analyses}
```

Fisher's exact test

Agresti, CDA 2nd ed., p.92

- test of independence in 2×2 table
- based on hypergeometric distribution
- conditions on all marginal totals
- this eliminates all nuisance parameters (parameters governing marginal distribution)
-

	Guess poured first		
Poured First	Milk	Tea	Total
Milk	3	1	4
Tea	1	3	4
Total	4	4	8

$$\Pr(y_{11} \geq 3) = \frac{\binom{4}{3}\binom{4}{1}}{\binom{8}{4}} + \frac{\binom{4}{4}\binom{4}{0}}{\binom{8}{4}} = 0.229 + 0.014 = 0.243$$

```
Fisher's Exact Test for Count Data
data: tea p-value = 0.4857 alternative hypothesis: true odds ratio is not equal to 1 95
percent confidence interval: 0.2117329 621.9337505 sample estimates: odds ratio 6.408309
```

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... Fisher's exact test

- achievable p-values: 0.014, 0.243, 0.757, 0.986, 1.0
- null distribution concentrated on only 5 sample points
- Agresti recommends mid p-value:

$$\frac{1}{2}\Pr(Y_{11} = 3) + \Pr(Y_{11} = 4) = 0.129$$

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Several 2 $\times$ 2 Tables

ELM, §4.4; SM, Example 10.19

Age (years)	Smokers	Non-smokers
Overall	139/582 (24)	230/732 (31)
18–24	2/55 (4)	1/62 (2)
25–34	3/124 (2)	5/157 (3)
35–44	14/109 (13)	7/121 (6)
45–54	27/130 (21)	12/78 (15)
55–64	51/115 (44)	40/121 (33)
65–74	29/36 (81)	101/129 (78)
75+	13/13 (100)	64/64 (100)

Table 6.8 Twenty-year survival and smoking status for 1314 women (Appleton *et al.*, 1996). The smoker and non-smoker columns contain number dead/total (% dead).

	Smoker	Non-smoker	
dead	139 (24%)	230 (31%)	
alive	443	502	
total	582	732	1314

... 2 × 2 tables

```
>  summary(glm(cbind(alive,dead) ~ smoker, data = smoking, family = binomial))
Call:
glm(formula = cbind(alive, dead) ~ smoker, family = binomial,
    data = smoking)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-12.173   -5.776    1.869    5.674    9.052

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.78052    0.07962   9.803  < 2e-16 ***
smoker       0.37858    0.12566   3.013  0.00259 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 641.5  on 13  degrees of freedom
Residual deviance: 632.3  on 12  degrees of freedom
AIC: 683.29

Number of Fisher Scoring iterations: 4
```

... 2 × 2 tables

	Smoker	Non-smoker	
dead	139 (24%)	230 (31%)	
alive	443	502	
total	582	732	1314

```
> anova(glm(cbind(alive,dead) ~ smoker, data = smoking, family = binomial))
Analysis of Deviance Table

Model: binomial, link: logit

Response: cbind(alive, dead)

Terms added sequentially (first to last)


       Df Deviance Resid. Df Resid. Dev
NULL                      13      641.5
smoker  1   9.2003        12      632.3
> with(smoking, xtabs(cbind(dead,alive) ~ smoker))

smoker dead alive
     0  230   502
     1  139   443
> summary(.Last.value)
Call: xtabs(formula = cbind(dead, alive) ~ smoker)
Number of cases in table: 1314
Number of factors: 2
Test for independence of all factors:
Chisq = 9.121, df = 1, p-value = 0.002527
```

... 2 × 2 tables

	sm	non-sm	sm	non-sm	sm	non-sm	
d	2	1	3	5	14	7	
a	53	61	121	152	95	114	...
	55	62	124	157	109	121	
Age	18-24		25-34		35-44		...

```
> summary(glm(cbind(alive,dead) ~ smoker + factor(age), data = smoking, family = binomial))
...
Coefficients:
                  Estimate Std. Error z value Pr(>|z|)
(Intercept)         3.8601     0.5939   6.500 8.05e-11 ***
smoker             -0.4274     0.1770  -2.414 0.015762 *
factor(age)25-34   -0.1201     0.6865  -0.175 0.861178
factor(age)35-44   -1.3411     0.6286  -2.134 0.032874 *
factor(age)45-54   -2.1134     0.6121  -3.453 0.000555 ***
factor(age)55-64   -3.1808     0.6006  -5.296 1.18e-07 ***
factor(age)65-74   -5.0880     0.6195  -8.213  < 2e-16 ***
factor(age)75+    -27.8073 11293.1437  -0.002 0.998035
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 641.4963  on 13  degrees of freedom
Residual deviance:   2.3809  on  6  degrees of freedom
AIC: 65.377

Number of Fisher Scoring iterations: 20
```

Log-linear models

ELM 4.4

- suppose we have 3 factors, each with several levels
- observe a response at each combination of factors
- linear model might be

$$y_{ijk} = \mu + \alpha_i + \beta_j + \gamma_k + \epsilon_{ijk}, \quad k = 1, \ldots, K; j = 1, \ldots, J; i = 1, \ldots I$$

- or

$$y_{ijk} = \mu + \alpha_i + \beta_j + \gamma_k + (\alpha\beta)_{ij} + (\alpha\gamma)_{ik} + (\beta\gamma)_{jk} + \epsilon_{ijk}$$

- if the y_{ijk} are positive counts, rather than continuous, then Poisson model could have

$$y_{ijk} \sim Po(\mu_{ijk}), \quad \log(\mu_{ijk}) = \mu + \alpha_i + \beta_j + \gamma_k$$

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... §4.4

- several log-linear models for smoking data are fit
- and compared to binomial model above
- joint independence, conditional independence, marginal independence, uniform association
- all related to sub-models of general log-linear Poisson model

- binomial model above estimates parameters that control marginal probabilities
- Mantel-Haenszel test is a $2 \times 2 \times k$ version of Fisher's exact test

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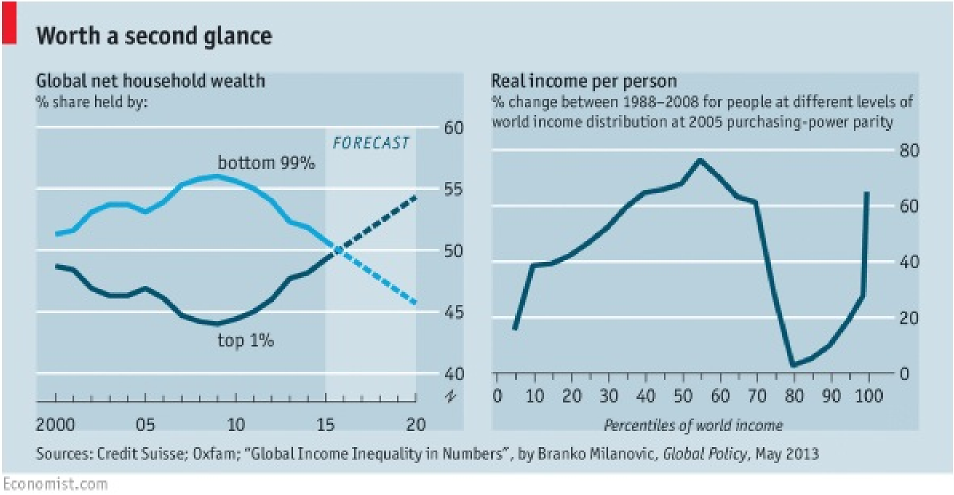
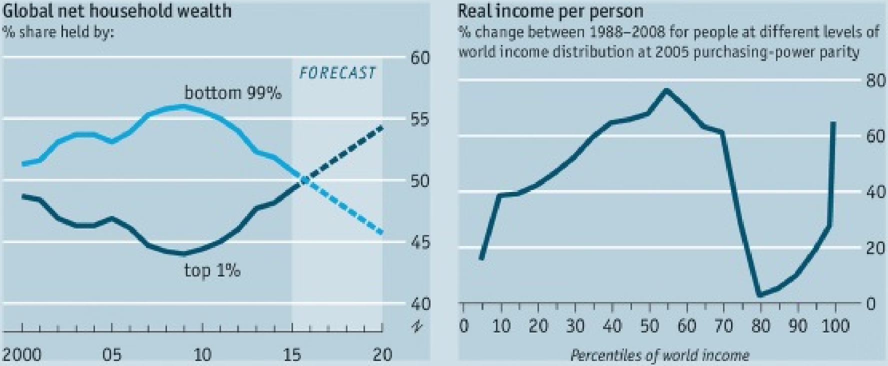
... §4.4

```
> data(femsmoke)
> ct3 <- xtabs(y ~ smoker + dead + age, data = femsmoke)
> apply(ct3, 3, function(x)(x[1,1]*x[2,2])/(x[1,2]*x[2,1]))
   18-24     25-34     35-44     45-54     55-64     65-74       75+
2.301887 0.753719 2.400000 1.441748 1.613672 1.148515       NaN
> mantelhaen.test(ct3,exact=T)

Exact conditional test of independence in 2 x 2 x k tables

data:  ct3
S = 139, p-value = 0.01591
alternative hypothesis: true common odds ratio is not equal to
95 percent confidence interval:
 1.068889 2.203415
sample estimates:
common odds ratio
         1.530256
```



Economist, January 24 2015

Worth a second glance



Sources: Credit Suisse; Oxfam; "Global Income Inequality in Numbers", by Branko Milanovic, *Global Policy*, May 2013

Economist.com

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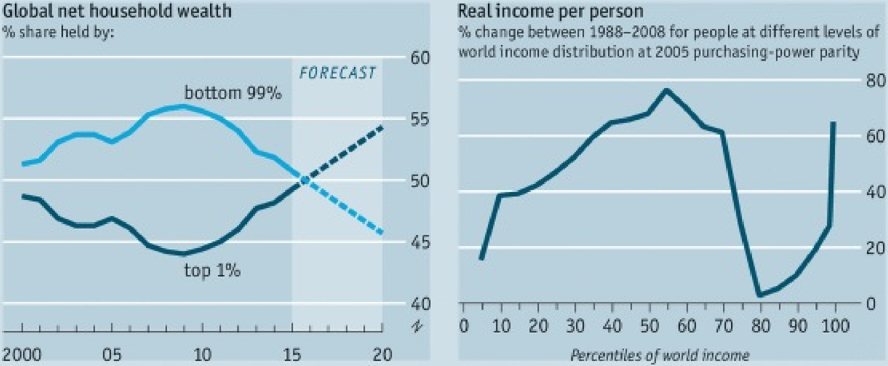

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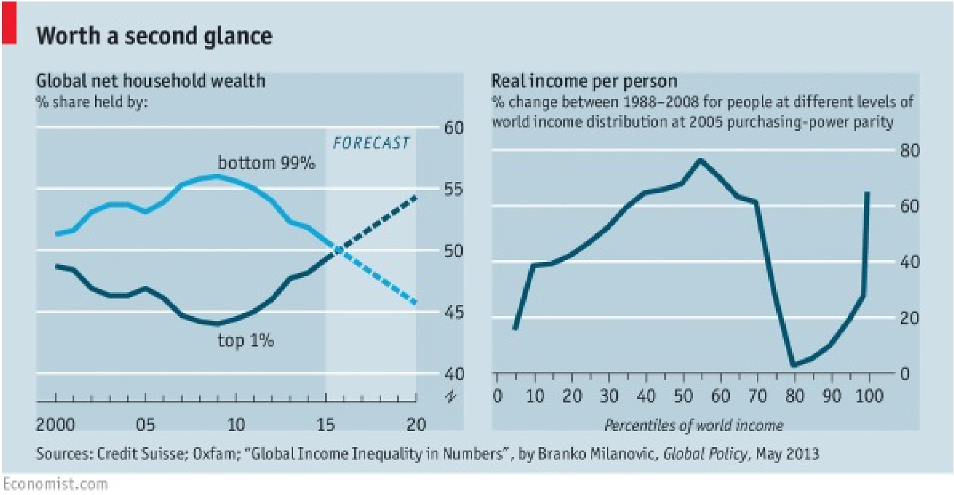

Worth a second glance
Global net household wealth
% share held by:
FORECAST
bottom 99%
top 1%
60
55
50
45
40
2000
05
10
15
20
Real income per person
% change between 1988–2008 for people at different levels of world income distribution at 2005 purchasing-power parity
80
60
40
20
0
0
10
20
30
40
50
60
70
80
90
100
Percentiles of world income
Sources: Credit Suisse; Oxfam; "Global Income Inequality in Numbers", by Branko Milanovic, *Global Policy*, May 2013
Economist.com

Worth a second glance
Global net household wealth
% share held by:
FORECAST
bottom 99%
top 1%
60
55
50
45
40
2000
05
10
15
20
Real income per person
% change between 1988–2008 for people at different levels of world income distribution at 2005 purchasing-power parity
80
60
40
20
0
0
10
20
30
40
50
60
70
80
90
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Percentiles of world income
Sources: Credit Suisse; Oxfam; "Global Income Inequality in Numbers", by Branko Milanovic, Global Policy, May 2013
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