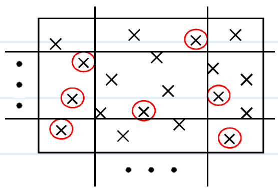
Two-way Contingency Table

- Two *cross-classified* categorical variables X_1 and X_2
  - ➢ X_1 has I categories, denoted by $i = 1, 2, \ldots, I$
  - ➢ X_2 has J categories, denoted by $j = 1, 2, \ldots, J$

population



- Classifications of subjects in some *population* on X_1 and X_2 have IJ possible combinations. Define the population parameters:
  - ➢ π_{ij} = the proportion of the subjects in the population with $X_1=i$ and $X_2=j$
    - ▪ arrange π_{ij}'s in the *cells* of a rectangular table having I rows for categories of X_1 and J columns for categories of X_2 to display the population distribution

X_1 \ X_2	1	$\cdots$	J	
1	π_{11}	$\cdots$	π_{1J}	π_{1+}
$\cdots$	$\cdots$	$\cdots$	$\cdots$	$\cdots$
I	π_{I1}	$\cdots$	π_{IJ}	π_{I+}
	π_{+1}	$\cdots$	π_{+J}	$\pi_{++}=1$

  - ➢ $\pi_{i+} \equiv \sum_{j=1}^{J} \pi_{ij}$ and $\pi_{+j} \equiv \sum_{i=1}^{I} \pi_{ij} \Rightarrow$ *marginal proportion*
  - ➢ $\pi_{++} \equiv \sum_{i=1}^{I}\sum_{j=1}^{J} \pi_{ij} = \sum_{i=1}^{I} \pi_{i+} = \sum_{j=1}^{J} \pi_{+j} = 1$

  - ➢ $\pi_{i|j} \equiv \pi_{ij}/\pi_{+j}$ and $\pi_{j|i} \equiv \pi_{ij}/\pi_{i+} \Rightarrow$ *conditional proportion*

    $\Rightarrow \sum_{i=1}^{I} \pi_{i|j} = 1, \forall j$ and $\sum_{j=1}^{J} \pi_{j|i} = 1, \forall i$

- **Q**: For the population, what questions might be of interest?
  - ➢ $\pi_{1+} = \cdots = \pi_{I+}$? or $\pi_{+1} = \cdots = \pi_{+J}$?
  - ➢ Are X_1 and X_2 observed from a randomly sampled subject independent, i.e., does X_1 affect X_2 and vice versa? If X_1 and X_2 are independent, then
    - ▪ $\pi_{ij} = P(X_1 = i, X_2 = j) = P(X_1 = i)P(X_2 = j) = \pi_{i+}\pi_{+j}$
    - ▪ $\pi_{i|j} = P(X_1 = i | X_2 = j) = P(X_1 = i) = \pi_{i+}, \forall j$

      $\pi_{j|i} = P(X_2 = j | X_1 = i) = P(X_2 = j) = \pi_{+j}, \forall i$
    - ▪ $\pi_{11} : \cdots : \pi_{1J} = \pi_{21} : \cdots : \pi_{2J} = \cdots = \pi_{I1} : \cdots : \pi_{IJ}$

      $\pi_{11} : \cdots : \pi_{I1} = \pi_{12} : \cdots : \pi_{I2} = \cdots = \pi_{1J} : \cdots : \pi_{IJ}$
    - ▪ For 2×2 table, odd ratio

$$\Delta = \frac{\pi_{11}/\pi_{12}}{\pi_{21}/\pi_{22}} = \frac{\pi_{11}/\pi_{21}}{\pi_{12}/\pi_{22}} = \frac{\pi_{11}\times\pi_{22}}{\pi_{12}\times\pi_{21}} = 1$$

π_{11}	π_{12}
π_{21}	π_{22}

For $I \times J$ table and any $1 \le i < I$ and $1 \le j < J$,

π_{ij}	π_{iJ}
π_{Ij}	π_{IJ}

$$\Delta_{ij} = \frac{\pi_{ij} \times \pi_{IJ}}{\pi_{iJ} \times \pi_{Ij}} = 1$$

- For a *sample* drawn from the population, let
  - y_{ij} = total number of subjects in the sample with $X_1 = i$ and $X_2 = j$
  - marginal totals (row totals or column totals) $y_{i+} \equiv \sum_{j=1}^{J} y_{ij}$ and $y_{+j} \equiv \sum_{i=1}^{I} y_{ij}$
  - grand total $y_{++} \equiv \sum_{i=1}^{I} \sum_{j=1}^{J} y_{ij} = \sum_{i=1}^{I} y_{i+} = \sum_{j=1}^{J} y_{+j}$

X_1 \ X_2	1	…	J	
1	y_{11}	…	y_{1J}	y_{1+}
…	…	…	…	…
I	y_{I1}	…	y_{IJ}	y_{I+}
	y_{+1}	…	y_{+J}	y_{++}

- When the cells of the rectangular table contain y_{ij}'s, it is called a $I \times J$ *contingency table*
- The above treatments for π's and y's can be generalized to more than two categorical variables
- **Q**: how to model the data (i.e., what's the joint distribution of y_{ij}'s)?
  - The statistical modeling of the data depends on the *sampling schemes*.

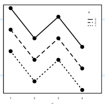
- consider an example of wafer data:
- Consider the sampling schemes
  1. Observe the manufacturing process for a certain period of time
  2. Decide to sample 450 wafers
  3. Decide to sample 400 wafers without particles and 50 wafers with particles
  4. Scheme 3 and the 450 wafers must also include, by design, 334 good wafers and 116 bad ones
  - Note 1: the first three schemes are all plausible
  - Note 2: scheme 4 seems less likely in this example; such a scheme is more attractive when one level of each variable is relatively rare and we choose to over-sample both levels to ensure some representation

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

- Scheme 1
  - Model: $\boxed{y\text{: fixed; } Y\text{: random; red square: free}}$

X_1 \ X_2	1	2	
1	Y_{11}	Y_{12}	Y_{1+}
2	Y_{21}	Y_{22}	Y_{2+}
	Y_{+1}	Y_{+2}	Y_{++}

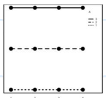
- Response: $Y_{ij} \sim$ Poisson(μ_{ij}), i=1, 2; j=1, 2
- For a *random sample*, can assume $\mu_{ij} = t \times \pi_{ij}$, where t is an unknown value of a size variable
- X_1 (=i) and X_2 (=j) are covariates

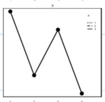


➢ Suppose the data (from an $I \times J$ table) is fitted with a Poisson GLM with log link

- When $\pi_{ij}=\pi_{i+}\pi_{+j}$ (X_1 and X_2 independent),

$$\eta_{ij} = \log(\mu_{ij}) \;=\; \log(t\,\pi_{ij}) = \log(t\,\pi_{i+}\,\pi_{+j}) \;=\; \log(t) + \log(\pi_{i+}) + \log(\pi_{+j})$$



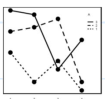


$\Rightarrow$ corresponds to a main-effect model, i.e., $Y_{ij} \sim X_1 + X_2 \equiv S$

- When $\pi_{ij}=\pi_{i+}\pi_{+j}$ and $\pi_{1+} = \cdots = \pi_{I+}$ (or $\pi_{+1} = \cdots = \pi_{+J}$)

$$\eta_{ij} = \log(t) + \log(\pi_{+j}) \quad (\text{or} \;\; \eta_{ij} = \log(t) + \log(\pi_{i+}))$$

$\Rightarrow$ corresponds to the model $Y_{ij} \sim X_2$ (or $Y_{ij} \sim X_1$)



- When $\pi_{ij} \neq \pi_{i+}\pi_{+j}$ (X_1 and X_2 not independent)

$\Rightarrow$ add interaction $X_1{:}X_2$

$\Rightarrow$ may consider $Y_{ij} \sim X_1 + X_2 + X_1{:}X_2 \equiv L$ (saturated model)

- **Q**: what type of π's corresponds to the following models?

$$Y_{ij} \sim 1 \qquad Y_{ij} \sim X_1 + X_1{:}X_2 \qquad Y_{ij} \sim X_2 + X_1{:}X_2$$

➢ Recall. For a Poisson GLM with log link, $X^T Y = X^T \hat{\mu}$

For models without interactions,

$\Rightarrow$ $X^T Y$ is only related to marginal totals

$\Rightarrow$ the fitted values $\hat{\mu}$ is a function of marginal totals

$\Rightarrow$ for example, for main-effect model $Y_{ij} \sim X_1 + X_2$

$$\hat{\mu}_{ij} = Y_{++}\,\hat{\pi}_{i+}\,\hat{\pi}_{+j} = Y_{i+}\,Y_{+j}/Y_{++}$$

➢ To test whether $\pi_{ij}=\pi_{i+}\pi_{+j}$ (H_0) $\Rightarrow$ H_0: S vs. H_1: $L \backslash S$

- Deviance based: $D_S - D_L \overset{a}{\sim} \chi^2_{(I-1)(J-1)}$

- Pearson's X^2 (goodness-of-fit measure) under S:

$$X_S^2 = \sum_{ij} \frac{(Y_{ij} - \hat{\mu}_{ij})^2}{\hat{\mu}_{ij}} = \sum_{ij} \frac{(O_{ij} - E_{ij})^2}{E_{ij}} \overset{a}{\sim} \chi^2_{(I-1)(J-1)}$$

  - *Yate's continuity correction*:
    - Subtracts 0.5 from $Y_{ij} - \hat{\mu}_{ij}$ when it is positive
    - Add 0.5 to $Y_{ij} - \hat{\mu}_{ij}$ when it is negative

    this give superior results for small samples

➢ To test H_0: $\pi_{1+} = \cdots = \pi_{I+}$ (or $\pi_{+1} = \cdots = \pi_{+J}$),

compare models S^* and L^* (H_0: S^* vs. H_1: $L^* \backslash S^*$), where

S^*: $Y_{ij} \sim X_2 + X_1{:}X_2$ and L^*: $Y_{ij} \sim X_1 + X_2 + X_1{:}X_2$

S^*: $Y_{ij} \sim X_1{:}X_2$ and L^*: $Y_{ij} \sim X_1 + X_1{:}X_2$

S^*: $Y_{ij} \sim X_2$ and L^*: $Y_{ij} \sim X_1 + X_2$

S^*: $Y_{ij} \sim 1$ and L^*: $Y_{ij} \sim X_1$

- Deviance-based test: $D_{S^*} - D_{L^*} \overset{a}{\sim} \chi^2_{df_{S^*} - df_{L^*}}$

➢ Can be generalized to X_1 with I levels and X_2 with J levels

- Scheme 2:

➢ Model: for a random sample, we can assume

$(Y_{11}, Y_{12}, Y_{21}, Y_{22})$

$\sim$ multinomial$(y_{++}, \pi_{11}, \pi_{12}, \pi_{21}, \pi_{22})$

X_1 \ X_2	1	2	
1	Y_{11}	Y_{12}	Y_{1+}
2	Y_{21}	Y_{22}	Y_{2+}
	Y_{+1}	Y_{+2}	y_{++}

where π_{ij} (i=1, 2; j=1, 2) is linked to X_1 and X_2 according to the model we choose

➢ Connection between Poisson and multinomial:

Let $Y_i \sim$ Poisson(λ_i), i=1,…,k, and independent,

$(Y_1,\ldots,Y_k | \Sigma_i Y_i = n) \sim$ multinomial$(n, \lambda_1/\Sigma_i\lambda_i, \ldots, \lambda_k/\Sigma_i\lambda_i)$

$\Rightarrow$ the parameter t (value of size variable) in Poisson is removed, but π_{ij}'s are not affected

$\Rightarrow$ would expect there is a lot of similarity between the inferences for Poisson and multinomial models

➢ Log-likelihood of the multinomial:

$$\log(\mathcal{L}) \propto \sum_{ij} Y_{ij} \log(\pi_{ij})$$

(cf., log-likelihood for Poisson $\propto \sum_{ij} Y_{ij} \log(\mu_{ij}) - \mu_{ij}$)

➢ The inferences in the multinomial model would coincide with that in Poisson model, i.e.,
- same estimates (MLE)
- same test statistics and p-values

The Poisson model is easier to execute in R, so we can fit a Poisson GLM for data from a multinomial sampling scheme

➢ Can be generalized to $I \times J$ table in the same manner

- Scheme 3:

➢ Model: for a random sample, can assume

$Y_{1j} \sim$ binomial$(y_{+j}, \pi_{i=1|j}=\pi_{1j}/\pi_{+j})$, j=1, 2

	X_2: 1	2	
X_1	1	2	
1	$\boxed{Y_{11}}$	$\boxed{Y_{12}}$	Y_{1+}
2	Y_{21}	Y_{22}	Y_{2+}
	y_{+1}	y_{+2}	y_{++}

where $\pi_{i=1|j}$ is linked to the covariate X_2 (=j) only according to the model we choose

➢ **Q**: compared to schemes 1 and 2, what information has been gone/questionable in this scheme?

➢ Suppose fit the data with a Binomial GLM with logit link:

- When $\pi_{ij}=\pi_{i+}\pi_{+j}$ (X_1 and X_2 independent),

$$\text{logit}(\pi_{i=1|j}) = \log\left[(\pi_{1j}/\pi_{+j})/(\pi_{2j}/\pi_{+j})\right]$$

$$= \log\left[(\pi_{1+}\pi_{+j})/(\pi_{2+}\pi_{+j})\right] = \log(\pi_{1+}/\pi_{2+})$$

$\Rightarrow$ corresponds to a constant-effect model, i.e., $Y_{1j} \sim 1 \equiv S$

- When $\pi_{ij}\neq\pi_{i+}\pi_{+j}$ (X_1 and X_2 not independent)

$\Rightarrow Y_{1j} \sim X_2 \equiv L$ (saturated model)

➢ To test whether $\pi_{ij}=\pi_{i+}\pi_{+j}$ (H_0) $\Rightarrow H_0$: S vs. H_1: $L\backslash S$
- Deviance based: $D_S - D_L = D_S$
- Perason X^2 under S

➢ Can be generalized to X_2 with J (>2) levels in the same manner

➢ For the case that X_1 has I (>2) levels

$(Y_{1j}, \ldots, Y_{Ij})\sim$multinomial$(y_{+j}, \pi_{i=1|j}, \ldots, \pi_{i=I|j})$, j=1,…,J

$\Rightarrow$ called product multinomial model (cf., unrestricted multinomial model in scheme 2)

	X_2: 1	2	
X_1: 1	$\boxed{Y_{11}}$	Y_{12}	y_{1+}
2	Y_{21}	Y_{22}	y_{2+}
	y_{+1}	y_{+2}	y_{++}

- Scheme 4:
  - Model: if $\pi_{ij}=\pi_{i+}\pi_{+j}$ (H_0), for a random sample, Y_{11} ~ hypergeometric(y_{1+}, y_{+1}, y_{+2}), i.e.,

$$P(Y_{11}=y_{11}) = \binom{y_{+1}}{y_{11}}\binom{y_{+2}}{y_{12}}\Big/\binom{y_{++}}{y_{1+}}$$

$$\boxed{y_{11} \le \min\{y_{+1}, y_{1+}\}} \quad = \frac{y_{1+}!\,y_{2+}!\,y_{+1}!\,y_{+2}!}{y_{11}!\,y_{12}!\,y_{21}!\,y_{22}!\,y_{++}!}$$

  - Under Scheme 3 and H_0, the joint pmf of $(Y_{11}, Y_{12}, Y_{21}, Y_{22})$ is:

$$\binom{y_{+1}}{y_{11}}\pi_{1|1}^{y_{11}}\pi_{2|1}^{y_{21}} \times \binom{y_{+2}}{y_{12}}\pi_{1|2}^{y_{12}}\pi_{2|2}^{y_{22}} = \frac{y_{+1}!\,y_{+2}!}{y_{11}!\,y_{21}!\,y_{12}!\,y_{22}!}\pi_{1+}^{y_{11}+y_{12}}\pi_{2+}^{y_{21}+y_{22}}$$

  - Under Scheme 3 and H_0, the sufficient statistics of π_{1+} and π_{2+} are Y_{1+} and Y_{2+}, respectively, and their joint pmf is:

$$\frac{y_{++}!}{y_{1+}!\,y_{2+}!}\pi_{1+}^{y_{1+}}\pi_{2+}^{y_{2+}}$$

  - When $\pi_{ij}\neq\pi_{i+}\pi_{+j}$ (H_1), the probability a black ball is drawn is different from the probability a white ball is drawn

- To test whether $\pi_{ij}=\pi_{i+}\pi_{+j}$ (*Fisher's exact test*)
  - Because Y_{11} can only take a limited number of values, can compute the probability of all these outcomes under H_0
    $\Rightarrow$ can compute the total probability (p-value) of all outcomes that are *more extreme* than the one observed
  - **Q**: what outcomes are more extreme? Some options:
    - The outcomes with probability $\le P(Y_{11}=y_{11})$
    - Outcomes y_{11}' s.t. $|y_{11}'-E(Y_{11})| \ge |y_{11}-E(Y_{11})|$
    - Others (see Agresti, 2013, 3.5)
- Generalization to $I\times J$ table for testing H_0: $\pi_{ij}=\pi_{i+}\pi_{+j}$
  $\Rightarrow$ use multiple hypergeometric as null distribution, whose probability mass function is:

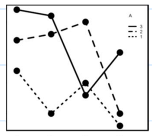
$$\left(\prod_i y_{i+}!\right)\left(\prod_j y_{+j}!\right)\Big/\left(y_{++}!\times\prod_{ij} y_{ij}!\right)$$

- Some notes:
  - The situation that both marginal totals are fixed is rather less common in practical sampling applications

- It can arise when classifying objects into one of 2 types when the true proportions of each type are known
  - Example: the lady tasting tea
- It suggests a more accurate test for independence
  - Fisher's exact test is attractive because the null distribution for deviance-based and Pearson's X^2 test statistics is only *approximately* χ^2 distributed.
  - For tables with small counts, this χ^2 approximation is suspicious, which makes the exact method valuable.
  - Fisher's exact test becomes more difficult to compute for larger tables. However, the χ^2 approximation will tend to be accurate for larger tables.

❖ **Reading**: Faraway (2006, 1st ed.), 4.1, 4.2

Correspondence Analysis (CA)



- **Q**: when independence of a 2-way contingency table is rejected, how to know where the dependence is coming from?
  - ➢ Interaction terms in a Poisson GLM contain dependence information; however, interpretation of them could be difficult.

  - ➢ CA: a visual residual analysis for contingency table
- Singular value decomposition
  - ➢ R=[R_{ij}]: an $r\times c$ matrix. W.l.o.g, assume $r\geq c$ and rank(R)=c, then

$$R = U_{r\times c} D_{c\times c} V_{c\times c}^T = \Sigma_k\, d_k U_k V_k^T \text{ , i.e.,}$$

$$R_{ij} = \sum_{k=1}^{c} U_{i\,k}\, d_k\, V_{j\,k} \text{ , where}$$

    - U=[U_{ij}]=[U_1, …, U_c]: an $r\times c$ column orthonormal matrix, i.e., U^TU=$I_{c\times c}$; its columns are called *left singular vectors*
    - V=[V_{ij}]=[V_1, …, V_c]: a $c\times c$ column orthonormal matrix, i.e., V^TV=$I_{c\times c}$; its columns called *right singular vectors*
    - D=diag(d_1, …, d_c), $d_1 \geq \ldots \geq d_c > 0$, called *singular values*
  - ➢ Some properties
    - Columns of $U_{r\times c}$ are eigenvectors of $(RR^T)_{r\times r}$
    - Columns of $V_{c\times c}$ are eigenvectors of $(R^TR)_{c\times c}$
    - $\{d_1^2, \ldots, d_c^2\}$ are eigenvalues of RR^T and R^TR
- Procedure of correspondence analysis on Pearson residuals

a) Fit a GLM corresponding to independence on the contingency table and compute its Pearson residuals, r_P's (**Q**: what information contained in the r_P's?)

b) Write r_P's in the matrix form $[R_{ij}] \equiv R_{r\times c}$ as in contingency table

c) Perform the singular value decomposition on $R = UDV^T$

d) It is common for the first few singular values of R to be much larger than the rest. *Suppose that the first 2 dominate*. Then,

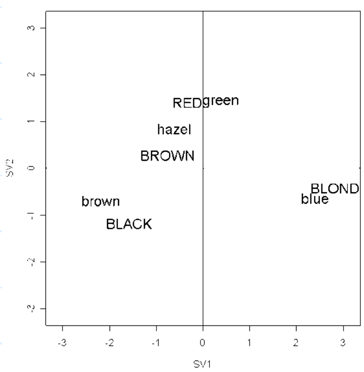
- $$\begin{aligned} R_{ij} &\approx U_{i1} d_1 V_{j1} + U_{i2} d_2 V_{j2} \\ &= (U_{i1}\sqrt{d_1})(V_{j1}\sqrt{d_1}) + (U_{i2}\sqrt{d_2})(V_{j2}\sqrt{d_2}) \\ &\equiv U'_{i1} V'_{j1} + U'_{i2} V'_{j2} \end{aligned}$$

- $$R \approx \begin{array}{cc|ccccc} & & V'_{11} & \cdots & V'_{j1} & \cdots & V'_{c1} \\ & & 1 & \cdots & j & \cdots & c \\ \hline U'_{11} & 1 & U'_{11}V'_{11} & \cdots & U'_{11}V'_{j1} & \cdots & U'_{11}V'_{c1} \\ \cdots & \cdots & \cdots & \cdots & \cdots & \cdots & \cdots \\ U'_{i1} & i & U'_{i1}V'_{11} & \cdots & U'_{i1}V'_{j1} & \cdots & U'_{i1}V'_{c1} \\ \cdots & \cdots & \cdots & \cdots & \cdots & \cdots & \cdots \\ U'_{r1} & r & U'_{r1}V'_{11} & \cdots & U'_{r1}V'_{j1} & \cdots & U'_{r1}V'_{c1} \end{array} + \begin{array}{cc|ccccc} & & V'_{12} & \cdots & V'_{j2} & \cdots & V'_{c2} \\ & & 1 & \cdots & j & \cdots & c \\ \hline U'_{12} & 1 & U'_{12}V'_{12} & \cdots & U'_{12}V'_{j2} & \cdots & U'_{12}V'_{c2} \\ \cdots & \cdots & \cdots & \cdots & \cdots & \cdots & \cdots \\ U'_{i2} & i & U'_{i2}V'_{12} & \cdots & U'_{i2}V'_{j2} & \cdots & U'_{i2}V'_{c2} \\ \cdots & \cdots & \cdots & \cdots & \cdots & \cdots & \cdots \\ U'_{r2} & r & U'_{r2}V'_{12} & \cdots & U'_{r2}V'_{j2} & \cdots & U'_{r2}V'_{c2} \end{array}$$

- $R \approx U'_1 V'^T_1 + U'_2 V'^T_2$, where for $k = 1, 2$,
  $U'_k = (U'_{1k}, \ldots, U'_{rk})^T$ and $V'_k = (V'_{1k}, \ldots, V'_{ck})^T$.

e) The 2-dimensional correspondence plot displays U'_{i2} vs. U'_{i1} and V'_{j2} vs. V'_{j1} on *same* graph (Note: because the distance between points will be of interest, it is important that the plot is scaled so that the visual distance is proportionately correct)

- Some notes:
  - **Q**: what does a large positive R_{ij} mean? a large negative R_{ij}?
  - $\Sigma_k d_k^2$ = Pearson's X^2, because $\Sigma_{ij}\, r_P^2 = \text{trace}(R^T R) = \Sigma_k d_k^2$ (**Q**: What does a large $\Sigma_k d_k^2$ indicate?)
- **Q**: what should we look for in a correspondence plot?
  - Large values in $|U'_k|$ (and $|V'_k|$)
    - the profiles of the rows (or the columns) corresp. to the large values are different from the marginal dist.



- e.g.: BLOND *hair* ⇒ the distribution of *eye colors* within this group is not typical
- e.g.: BROWN *hair* ⇒ the distribution of *eye colors* within this group close to the marginal distribution of columns

➢ Row and column levels close together and far from the origin

- a large positive R_{ij} would be associated with the combination
- e.g.: BLOND *hair* ↔ blue *eye* ⇒ strong association

➢ Row and column levels situate apart on either side of the origin

- a large negative R_{ij} would be associated with the combination
- e.g.: BLOND *hair* ↔ brown *eye* ⇒ relatively fewer people

➢ Points of two row (or two column) levels are close together

- The two rows/columns have a similar pattern of association ⇒ might consider to combine the two categories
- e.g.: hazel *eye* ↔ green *eye* ⇒ similar *hair color* distribution

- Other versions of CA: see Venables and Ripley (2002, `corresp` in the MASS package of R), or Blasius and Greenacre (1998)

❖ **Reading**: Faraway (2006, 1st ed.), 4.2

Matched Pairs Design (MPD)

- Design

➢ A block factor: y_{++} levels, each level represents a block, each block of size 2, i.e., 2 experimental units (EUs) in one block

➢ A treatment factor: 2 levels A and B, randomly assigned to the 2 EUs in each blocks

➢ A response variable: categorical

➢ 2 formats of representing data

➢ Comparison 1: MPD ↔ MCCD

➢ Comparison 2: MPD ↔ Paired sample t-test

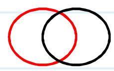
- Data for contingency table: observe *one* type of categorical measure on *two matched* objects (EUs)

➢ In contrast, in the typical 2-way contingency table, observe *two* (different) types of categorical measures (X_1 and X_2) on *one* object

X_1 \ X_2	1	…	I	
1	π_{11}	…	π_{1I}	π_{1+}
…	…	…	…	…
I	π_{I1}	…	π_{II}	π_{I+}
	π_{+1}	…	π_{+I}	1

➢ e.g., left (X_1) and right (X_2) eye performance of a person

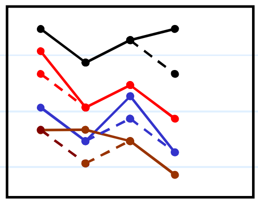
- Contingency table for matched pair data is a square matrix and
  - ➢ no marginal totals are fixed in advance
  - ➢ grand total Y_{++} could be random or fixed
- **Q**: what questions are of interest for matched pair data?
  - ➢ row and column marginals are *homogeneous*, i.e., $\pi_{i+}=\pi_{+i}$?
  - ➢ $[\pi_{ij}]_{I\times I}$ is a *symmetric* matrix, i.e., $\pi_{ij}=\pi_{ji}$?
    - symmetry implies marginal homogeneity (MH), but, the reverse statement not necessarily true (except for 2×2 table)
    - **Q**: how to interpret symmetry?
  - ➢ When row and column marginal totals are quite different, might be interested in whether



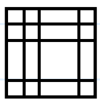
$$\pi_{ij}=\pi_{i+}\pi_{+j}\gamma_{ij}, \quad \text{where} \quad \gamma_{ij}=\gamma_{ji}?$$

    - It is called *quasi-symmetry* (QS)
    - MH + QS ⇔ symmetry
  - ➢ X_1 and X_2 are *independent*, i.e., $\pi_{ij}=\pi_{i+}\pi_{+j}$ for all i and j?

  - ➢ If not independent, whether $\pi_{ij}=a_i\times b_j$ for $i\neq j$? It is called *quasi-independent* (QI).



    - **Q**: how to interpret QI?



- Tests for these hypotheses based on log-linear model, e.g.,

X_1 \ X_2	1	2	3	
1	y_{11}	y_{12}	y_{13}	y_{1+}
2	y_{21}	y_{22}	y_{23}	y_{2+}
3	y_{31}	y_{32}	y_{33}	y_{3+}
	y_{+1}	y_{+2}	y_{+3}	y_{++}

$$Y=(y_{11}, y_{21}, y_{31}, y_{12}, y_{22}, y_{32}, y_{13}, y_{23}, y_{33},)^T$$

  - ➢ Test for symmetry (H_0) hypothesis:
    - Generate a vector with I^2 components for an $(I(I+1)/2)$-level nominal factor with the structure:

l_1	l_2	l_3
l_2	l_4	l_5
l_3	l_5	l_6

$$\text{sym-factor} = (l_1, l_2, l_3, l_2, l_4, l_5, l_3, l_5, l_6)^T$$

    - $Y \sim$ sym-factor $\equiv S_{\text{sym}}$
    - Deviance-based/Pearson X^2 goodness-of-fit test for S_{sym}
  - ➢ Test for QS (H_0) hypothesis
    - $\log(\pi_{ij}) = \log(\pi_{i+}\,\pi_{+j}\,\gamma_{ij}) = \log(\pi_{i+}) + \log(\pi_{+j}) + \log(\gamma_{ij})$

- $Y \sim X_1 + X_2 +$ sym-factor $\equiv S_{\text{qsym}}$
- Deviance-based/Pearson X^2 goodness-of-fit test for S_{qsym}

➢ Test for MH (H_0) hypothesis

- No log-linear models that directly corresponds to MH
- An indirect test using log-linear models **when** S_{qsym} **already holds**
  - ▫ Deviance-based test for H_0: S_{sym} vs. H_1:$S_{\text{qsym}} \backslash S_{\text{sym}}$
- Other approaches, see Agresti (2013), 11.3

➢ Test for QI (H_0) hypothesis

- Approach 1
  - ▫ Omit the diagonal data, i.e., let

$$Y' = (y_{21}, y_{31}, y_{12}, y_{32}, y_{13}, y_{23})^T$$

  - ▫ $Y' \sim X_1 + X_2 \equiv S_{\text{qindep1}}$
  - ▫ Deviance-based/Pearson X^2 goodness-of-fit test for S_{qindep1}
- Approach 2

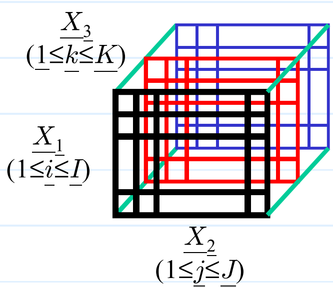
  - ▫ Generate a vector with I^2 components for an (I+1)-level nominal factor with the structure:

l_1	l_0	l_0
l_0	l_2	l_0
l_0	l_0	l_3

$$\text{QI-factor} = (l_1, l_0, l_0, l_0, l_2, l_0, l_0, l_0, l_3)^T$$

  - ▫ $Y \sim X_1 + X_2 +$ QI-factor $\equiv S_{\text{qindep2}}$
  - ▫ Deviance-based/Pearson X^2 goodness-of-fit test for S_{qindep2}

❖ **Reading**: Faraway (2006, 1st ed.), 4.3

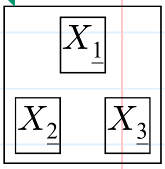


Three-Way Contingency Table

- The π's and Y's are defined in the same manner as in the 2-way table
- Poisson GLM approach to investigate how X_1, X_2, X_3 interact

➢ Mutual independence (X_1, X_2, X_3 are independent)

- $\pi_{ijk} = \pi_{i++}\pi_{+j+}\pi_{++k}$
- $\log(\pi_{ijk}) = \log(\pi_{i++}\pi_{+j+}\pi_{++k}) = \log(\pi_{i++}) + \log(\pi_{+j+}) + \log(\pi_{++k})$



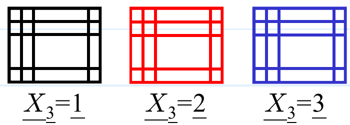
- $Y \sim X_1 + X_2 + X_3 \equiv S_1$
  - The estimates of parameters in this model correspond only to the marginal totals y_{i++}, y_{+j+}, and y_{++k}
  - The coding we use will determine exactly how the parameters relate to the margin totals, e.g., let β be an main effect of X_1 that codes i_1 and i_2 categories as **0** (reference) and 1

$$\Rightarrow e^{\hat{\beta}}/(1+e^{\hat{\beta}}) = \hat{\pi}_{i_2++}/(\hat{\pi}_{i_1++} + \hat{\pi}_{i_2++})$$
$$= y_{i_2++}/(y_{i_1++} + y_{i_2++})$$

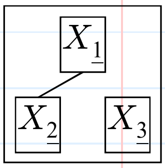
  - Insignificant factor, say $X_1 \Rightarrow \pi_{1++} = \pi_{2++} = \ldots = \pi_{I++}$

➢ Joint independence ($\{X_1, X_2\}$ and X_3 are independent)

- $\pi_{ijk} = \pi_{ij+} \times \pi_{++k} \Leftrightarrow \pi_{ij|k} = \pi_{ij+}$

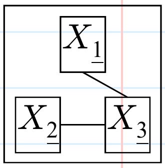


- $\log(\pi_{ijk}) = \log(\pi_{ij+}\pi_{++k})$
$$= \log(\pi_{ij+}) + \log(\pi_{++k})$$

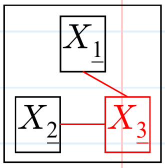


- $Y \sim X_1 + X_2 + X_1{:}X_2 + X_3 \equiv S_2$ ($\supseteq S_1$)

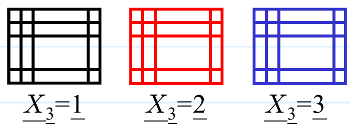
➢ Conditional independence (X_1, X_2 are independent given X_3)

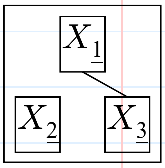


- $\pi_{ij|k} = \pi_{i+|k}\pi_{+j|k} \Leftrightarrow \pi_{ijk} = \pi_{i+k}\pi_{+jk}/\pi_{++k}$
- $\log(\pi_{ijk}) = \log(\pi_{i+k}\pi_{+jk}/\pi_{++k})$
$$= \log(\pi_{i+k}) + \log(\pi_{+jk}) - \log(\pi_{++k})$$

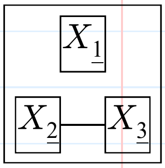


- $Y \sim X_1 + X_1{:}X_3 + X_3 + X_2 + X_2{:}X_3 \equiv S_3$

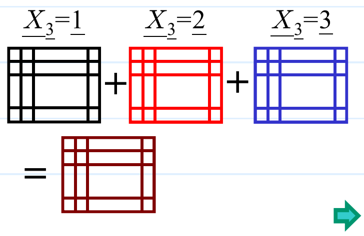




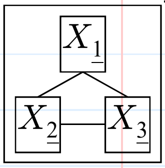
- Note that $S_3 \not\supseteq S_2$, but X_2 is jointly independent of $\{X_1, X_3\}$ implies that X_1, X_2 are independent given X_3



- **Q**: can this conditional independence imply independence between X_1 and X_2, i.e., $\pi_{ij+} = \pi_{i++}\pi_{+j+}$? (Ans: No. Check singular value decomposition in LNp.5-15)



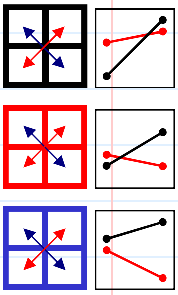
➢ Uniform association (UA)



- Consider a model with *all* two-factor interactions
  $$Y \sim X_1 + X_2 + X_3 + X_1{:}X_2 + X_1{:}X_3 + X_2{:}X_3 \equiv S_4\ (\supset S_3)$$
- S_4 has **no simple** interpretation **in terms** of independence
- S_4 asserts that for every level of one variable, say X_3, we have the same association between X_1 and X_2

$$Y \sim X_1 + X_2 + X_3 + X_1{:}X_2 + X_1{:}X_3 + X_2{:}X_3$$

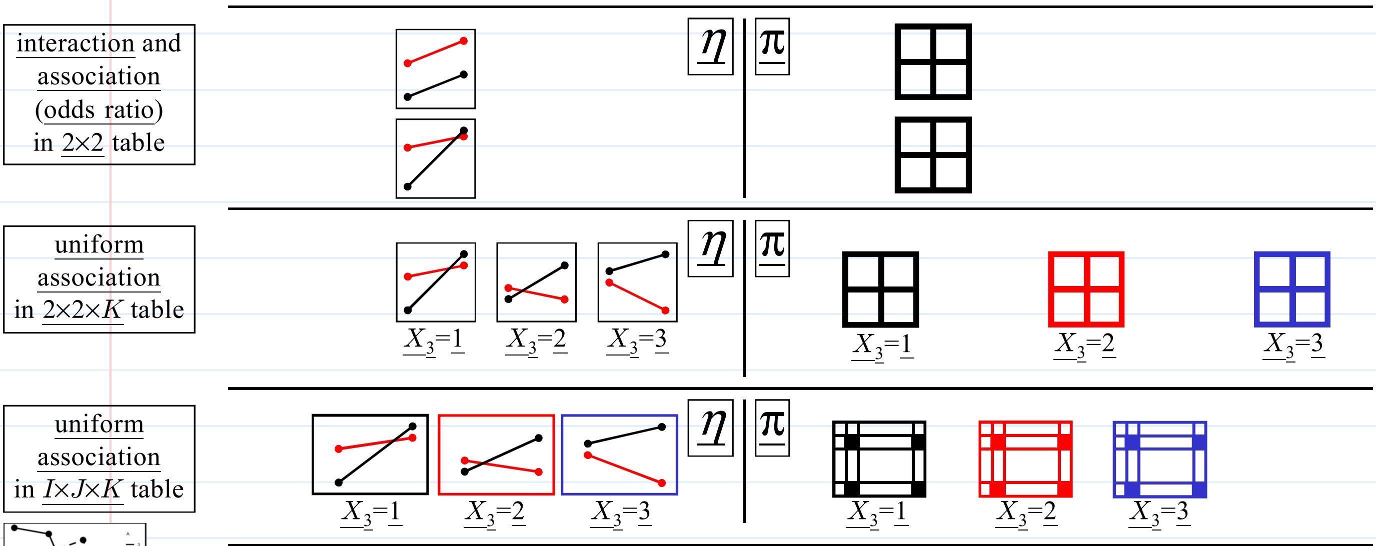
  - For each levels of X_3, the *reduced models* of S_4 have *different* coefficients for the main effects of X_1 and X_2, but have the *same* coefficients for the interaction $X_1{:}X_2$
  - e.g., $I=J=2$, same fitted odds-ratio between X_1 and X_2 for each category of X_3. Note that

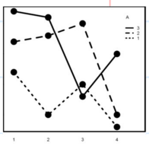


$$\text{fitted odd-ratio} = \frac{\hat{y}_{11k}\hat{y}_{22k}}{\hat{y}_{12k}\hat{y}_{21k}} = \frac{\hat{\pi}_{11k}\hat{\pi}_{22k}}{\hat{\pi}_{12k}\hat{\pi}_{21k}} = e^{\hat{\beta}_{12k}}$$

where β_{12k} is the coefficient of the $X_1{:}X_2$ term (under a coding $\propto$ {+1, −1}) in the reduced model of $X_3=k$.

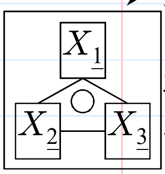
- **Q**: What does uniform association mean? How to interpret the association? How does it connect with interaction terms?



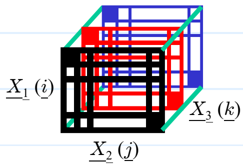


- S_4 is not saturated ⇒ some degrees of freedoms left for goodness-of-fit test

➢ A saturated model corresponds to a 3-way table with *different association* between, say X_1 and X_2, across K levels of X_3 whereas $Y \sim 1$ corresponds to a 3-way table with constant π



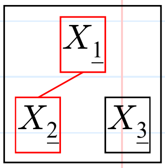
- **Q**: how to examine whether X_1, X_2, X_3 in a 3-way table are mutually independent (S_1), jointly independent (S_2), conditionally independent (S_3), or uniformly associated (S_4), individually?
  - **Ans**: Perform deviance-based/Pearson's X^2 goodness-of-fit (GoF) tests for S_1, S_2, S_3, S_4 (as H_0), respectively.
  - However, be careful of zero or small y_{ijk} (rule of thumb: 20% of cells less than 5) in the table $\Rightarrow$ there will be some doubt about the accuracy of chi-square approximation in GoF test
  - The chi-square approximation is better in comparing models than assessing GoF
- Analysis strategy: start with complex Poisson GLM (e.g., saturated one) and see how far the model can be reduced (e.g., using model selection or sequential deviance-based tests as in ANOVA to compare models).



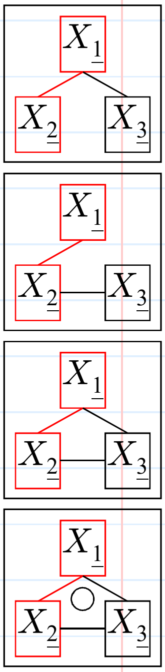
• Binomial (or multinomial) GLM approach for 3-way table

- If y_{ij+}'s regarded as fixed, can treat Y_{X_3} as response and X_1, X_2 as covariates

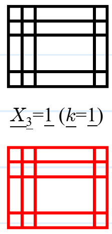
- **Q**$_1$: what information been gone? **Q**$_2$: what still attainable?
  - **Ans** for **Q**$_1$: information about π_{ij+}
  - **Ans** for **Q**$_2$: information about $\pi_{k|ij}$
- Statistical Modeling
  - $Y_{X_3} = Y_{ij1} \sim$ binomial(y_{ij+}, $\pi_{k=1|ij}$) when K=2
  - $Y_{X_3} = (Y_{ij1}, \ldots, Y_{ijK})$
    $\sim$ multinomial(y_{ij+}, $\pi_{k=1|ij}$, …, $\pi_{k=K|ij}$) when $K > 2$
- **Q**: how is a binomial GLM connected to a Poisson GLM in 3-way tables?



  - $Y_{X_3} \sim 1 \Leftrightarrow S_2$ (joint independence)
    - $\pi_{ijk} = \pi_{ij+} \times \pi_{++k} \Leftrightarrow \pi_{k|ij} = \pi_{++k}$
    - The binomial GLM implicitly assumes an association between X_1 and X_2 (**Q**: why?)
    - Poisson GLM allows us to drop the X_1:X_2 term, but binomial GLM does not



- $Y_{X_3} \sim 1 + X_1 \Leftrightarrow X_2, X_3$ are independent given X_1
  - $\pi_{ijk} = \pi_{ij+}\pi_{i+k}/\pi_{i++} \Leftrightarrow \pi_{k|ij} = \pi_{k|i+}$
  - **Q**: how about $Y_{X_3} \sim 1 + X_2$?
  - **Q**: Can we exam whether X_1, X_2 are independent given X_3?
- $Y_{X_3} \sim 1 + X_1 + X_2 \Leftrightarrow$ S_4 (uniform association)
- The saturated binomial GLM, $Y_{X_3} \sim 1 + X_1 + X_2 + X_1{:}X_2$, corresponds to a Poisson GLM for *different association*
- Using binomial GLM loses little when we are interested in the relationship between the response X_3 and the two covariates X_1, X_2, and not interested in the association between X_1 and X_2



X_3=1 (k=1)

X_3=2 (k=2)

⋮

- **Q**: Poisson or binomial GLM approach? Which to use?
  - ➢ Binomial if one variable is clearly identified as the response
  - ➢ Poisson if relationship between 3 variables is more symmetric

- Correspondence analysis
  - ➢ Cannot directly apply to 3-way table
  - ➢ Can combine two of the factors, say X_1 and X_2, into a factor with $I\times J$ levels and apply correspondence analysis on the 2-way table formed by the new factor and X_3
  - ➢ **Q**: which two factors should be chosen to merge?
    Ans: pick up the two whose association is least interesting to us
- Simpson's paradox
  - ➢ example:

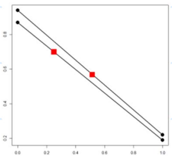
- X_1 (i): age
- X_2 (j): smoker
- X_3 (k): dead or alive

	smoker	dead	alive			smoker	dead	alive	
age=35-44	yes	14	95	109 (.47)	⇒	yes	.13	.87	1
	no	7	114	121 (.53)		no	.06	.94	1
age=65-74	yes	29	7	36 (.22)	⇒	yes	.81	.19	1
	no	101	28	129 (.78)		no	.78	.22	1
marginal total over age	yes	43	102	145 (.37)	⇒	yes	.30	.70	1
	no	108	142	250 (.63)		no	.43	.57	1

- 109/145 =.75
- 121/250 =.48

- *marginal association* added over X_1 is different from the *conditional association* observed within each category of X_1

➤ **Q**: Why it occurs? Why the table of y_{+jk} gives a contradictory result to the tables of $y_{jk|i}$?



- If $\frac{y_{112}}{y_{11+}} = \frac{y_{112}}{y_{111}+y_{112}} < \frac{y_{122}}{y_{121}+y_{122}} = \frac{y_{122}}{y_{12+}}$

  and $\frac{y_{212}}{y_{21+}} = \frac{y_{212}}{y_{211}+y_{212}} < \frac{y_{222}}{y_{221}+y_{222}} = \frac{y_{222}}{y_{22+}}$

  $\Rightarrow \frac{y_{112}+y_{212}}{y_{111}+y_{112}+y_{211}+y_{212}} \overset{?}{<} \frac{y_{122}+y_{222}}{y_{121}+y_{122}+y_{221}+y_{222}}$

- Note. $\frac{y_{1j2}+y_{2j2}}{y_{1j+}+y_{2j+}} = \frac{y_{1j2}}{y_{1j+}} \frac{y_{1j+}}{y_{1j+}+y_{2j+}} + \frac{y_{2j2}}{y_{2j+}} \left(1 - \frac{y_{1j+}}{y_{1j+}+y_{2j+}}\right)$

- Note that smoker are more concentrated in the younger age group and younger people are more likely to live longer

• Mantel-Haenszel (MH) test for $2\times2\times K$ table

➤ Designed to test *independence* in 2×2 tables across K categories

➤ Recall. association of a 2×2 table can be completely characterized/measured by its odds-ratio Δ

- $\Delta = 1 \Leftrightarrow$ independence
- $\Delta > 1 \Leftrightarrow$ positive association
- $\Delta < 1 \Leftrightarrow$ negative association

➤ Null and alternative hypotheses of MH test

- H_0: $\Delta_1 = \Delta_2 = \ldots = \Delta_K = 1$ (conditional independence)
- H_1^*: at least one $\Delta_k \neq 1$ (different association) or
  H_1: $\Delta_1 = \Delta_2 = \ldots = \Delta_K \neq 1$ (uniform association)
- The test works better when the odds ratios of the K 2×2 tables do not vary greatly, e.g., the null of the GoF test for uniform association, $\Delta_1=\Delta_2=\ldots=\Delta_K$, does not rejected

➤ Procedure of the MH test

- Suppose the marginal totals of each 2×2 table carry no information (e.g., fixed in advance) or are conditioned.
  - under H_0, can assume a hyper-geometric distribution for y_{11k} in each 2×2 table
    $\Rightarrow y_{11k}$ is sufficient for testing independence of kth table

- MH statistic combine information of y_{11k}'s from K tables:

$$\frac{\left(\left|\sum_k [y_{11k} - E(y_{11k})]\right| - 1/2\right)^2}{\sum_k Var(y_{11k})} \overset{a}{\sim} \chi_1^2$$

where $E(y_{11k})$ and $Var(y_{11k})$ are calculated under the H_0

- can calculate an exact p-value for smaller dataset using hypergeometric distribution
  - ⇒ useful when data is sparse, under which the χ^2 approximations based on asymptotic thm is questionable

- MH test is sometimes called Cochran-Mantel-Haenszel test because a version without the 1/2 is published earlier by Cochran (1954).

❖ **Reading**: Faraway (2006, 1st ed.), 4.4

Ordinal Variables

- Some variables have a nature ordering between categories
  - e.g., education: HS, BA, MA; political ideology: VL, SL, M, SC, VC

- The ordinal structure not matter when # of categories = 2
- For ordinal variables, can use the methods for nominal variable
  - But, more information can be extracted by taking advantage of the ordinal structure
- Treatments for ordinal response (future lecture) and ordinal covariates are different

- Treatment for ordinal predictors: assign each category a *score*
  - It kind of turns an ordinal variable into a continuous variable
  - The choice of scores requires some judgment
    - If no particular preference, even spacing allows for the simplest interpretation
    - For interval scales, midpoints of the intervals are often used
  - Should check whether the inference is robust to different assignments of scores
    - If *qualitative* conclusions are changed, this is an indication that you cannot make any strong finding based on scores
- Poisson GLM with linear-by-linear association for 2-way tables:
  - Consider table with ordinal row (X_1) and column (X_2) variables

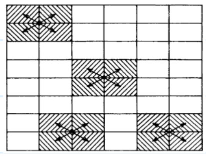
- assign scores $u_1 \leq u_2 \leq \ldots \leq u_I$ to rows, denoted by $u(X_1)$
- assign scores $v_1 \leq v_2 \leq \ldots \leq v_J$ to columns, denoted by $v(X_2)$

➢ Linear-by-linear association model:

$$\eta_{ij} = \log(\mu_{ij}) = \log(t\,\pi_{ij}) = \log(t) + \log(\pi_{i+}) + \log(\pi_{+j}) + \gamma \times u_i \times v_j$$

where u_i's, v_j's are known scores, and γ is an unknown parameter

- $Y \sim X_1 + X_2 + u(X_1)v(X_2) \equiv S_{O\times O}$



➢ Some notes about γ:

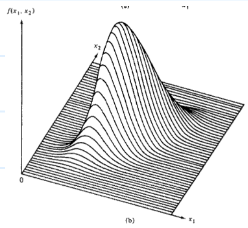
- values of γ represents the amount of association
- γ=0 $\Leftrightarrow$ independence
- positive and negative γ
- Interpretation of γ by log-odds-ratio:

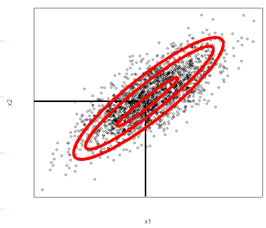
$$\log\left(\frac{\pi_{i,j}\,\pi_{i+1,j+1}}{\pi_{i,j+1}\,\pi_{i+1,j}}\right) = \log\left(\frac{\mu_{i,j}\,\mu_{i+1,j+1}}{\mu_{i,j+1}\,\mu_{i+1,j}}\right)$$

$$= (\eta_{i,j} + \eta_{i+1,j+1}) - (\eta_{i,j+1} + \eta_{i+1,j}) = \gamma(u_{i+1} - u_i)(v_{j+1} - v_j)$$

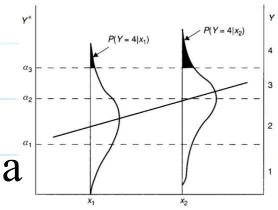
  - for evenly spaced scores, these log-odds-ratios are equal $\Rightarrow$ called uniform association in Goodman (1979)

- Latent (continuous) variable Z motivation for γ:
  - Assume π_{ij}'s are obtained by putting a grid on an approximately bi-variate Normal (Z_1, Z_2) for latent variables and u_i's and v_j's are cutpoints
  - γ can then be identified with the correlation coefficient ρ of the latent variables (cf., positive and negative ρ)



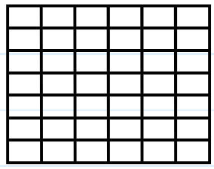


➢ **Q**: for the tests of independence or goodness-of-fit, what is the benefit of using $S_{O\times O}$ over the nominal approach, i.e., fitting a nominal-by-nominal model $S_{N\times N}$: $Y \sim X_1 + X_2 + X_1{:}X_2$? As shown in a lab example,



- in the $N\times N$ approach, interaction effects reduce a deviance of 40.743 on 36 degrees of freedom, but
- the $O\times O$ interaction effect reduces a deviance of 10.175 on *one* degrees of freedom, i.e., the other 35 interaction effects only reduce a deviance of 30.568

- Ordinal-by-nominal model (or nominal-by-ordinal model)
  - Rows (or columns) assigned scores, but column (or row) variable treated as a nominal variable
  - called *column* (or *row*) *effects model* because the columns (or rows) are not assigned scores; instead, their effects are estimated
    - alternative viewpoint: the scores of the ordinal columns (or rows) regarded as parameters
  - Column effects model:



$$\eta_{ij} = \log(\mu_{ij}) = \log(t\,\pi_{ij})$$
$$= \log(t) + \log(\pi_{i+}) + \log(\pi_{+j}) + u_i \times \gamma_j$$

where u_i's, i=1,…, I, are known scores, and

γ_j's, j=1,…, J, are unknown parameters (over-parameterized; only requires J–1 parameters),

- $Y \sim X_1 + X_2 + u(X_1){:}X_2 \equiv S_{O\times N}$ ($\supset S_{O\times O}$)

  - Some notes about γ_j's, called the *column effects*:

- Equality of the γ_j's (then, $u_i\times\gamma_j = u_i\times\gamma$) corresponds to the hypothesis of independence between X_1 and X_2
- For ordinal column variable, if the model $S_{O\times O}$ were a good fit, we would expect the estimates of the γ_j's in $S_{O\times N}$ to be roughly proportional to v_j's (e.g., for evenly spaced v_j's, estimates of γ_j's should follow a linear trend)
- We can use the estimates of γ_j's in $S_{O\times N}$ (1) to examine whether the chosen scores for columns in $S_{O\times O}$ (i.e., v_j's) are appropriate, or (2) to possibly suggest better scores (see an example in lab)

- Some advantages of using scores for ordinal variables
  - helpful in reducing the complexity of models for categorical data with ordinal variables
  - especially useful in higher dimensional table where a reduction in the # of parameters is particularly welcome
  - can also sharpen our ability to detect associations

❖ **Reading**: Faraway (2006, 1st ed.), 4.5