

## Solution to Exercise 3: Incremental yield from serial smears

### Key Learning Points

When you have a hypothesis to test, remember that it may be logical to:

- Create and use a subset of the working dataset
- Create new variable(s)

### Tasks:

Exercise hypothesis:

H<sub>0</sub>: Not more than 125 third smear examinations have to be made to find one additional case of tuberculosis in each of the four study countries

- Determine with a program C\_EX03.PGM the number of suspects with the patterns listed above*
- Create a table in spreadsheet by country*
- Interpret the findings*

### Solution:

The following output was created in EpiData Analysis:

	country	nnp	npX	px	nnn	nn9	tot	sm95low	smpoint	sm95high	hypothesis
1	Moldova	34	84	1013	8424	1579	12713	186.3	248.8	374.3	Refute
2	Mongolia	12	42	1663	12264	708	15397	653.5	1023.0	2354.0	Refute
3	Uganda	107	487	6686	14736	3325	28666	116.7	138.7	171.0	Accept
4	Zimbabwe	155	325	2969	17740	2706	26601	99.8	115.5	136.9	Accept

### Interpretation:

The recorded results show that the number of smears that need to be examined to find one additional case on a third serial smear examination that had not been found already on the first two exceeded 125 (one week's work) in Moldova and Mongolia, indicating the inefficiency of the requirement for three smears before declaring a patient smear-negative at least in these two countries.

We used the following program C\_EX03.PGM to get these outputs:

```
* Part C, Exercise 3
* This is b_ex03 EpiData Analysis program
* to determine the incremental yield from serial smears

* Data courtesy:
* Moldova: Dumitru Laticeschi, OR Paris 2003
* Mongolia: Nymadawa Naranbat, OR Paris 2004
* Uganda: Achilles Katamba, OR Paris 2003
* Zimbabwe: Biggie Mabaera, OR Paris 2004
```

```
* Written by: Hans L Rieder
* First version: 12 Feb 2009
* Last revision: 28 Apr 2013
```

```
cls
close
logclose
```

```
*****
```

```
* Prepare data set
```

```
cls
close
logclose
```

```
read "c_ex01.rec"
```

```
* Definition positive: any AFB in any of three results
* Values: "P" (positive) or "N" (negative)
* or "9" (unknown)
```

```
* Define essential patterns from
* all possible patterns
```

```
cls
gen s(3) pattern="NNN"
if result3=9 then pattern="NN9"
if result2=9 then pattern="N99"
if result3>0 and result3<9 then pattern="NNP"
if result2>0 and result2<9 then pattern="NPx"
if result1>0 and result1<9 then pattern="Px"
label pattern "Essential patterns"
```

```
select reason=0
```

```
keep pattern country
savedata "temp_01.rec" /replace
```

```
*****
```

```
* Analysis
```

```
cls
close
logclose
```

```
read "temp_01.rec"
```

```
aggregate pattern country /save="yield.rec" /replace /close
```

```
* Note: a more efficient way to do the following will be shown in Part D
```

```
cls
close
read "yield.rec"
select pattern="NNP"
gen i nnp=n
savedata "nnp.rec" /replace
```

```
cls
close
read "yield.rec"
select pattern="NPx"
gen i npx=n
savedata "npx.rec" /replace
```

```
cls
close
read "yield.rec"
select pattern="Px"
gen i px=n
savedata "px.rec" /replace
```

```
cls
close
read "yield.rec"
select pattern="NNN"
```

```

gen i nnn=n
savedata "nnn.rec" /replace

cls
close
read "yield.rec"
select pattern="NN9"
gen i nn9=n
savedata "nn9.rec" /replace

cls
close
read "yield.rec"
select pattern="NN9"
gen i n99=n
savedata "n99.rec" /replace

cls
close
read "nnp.rec"
merge country /file="npx.rec"
merge country /file="px.rec"
merge country /file="nnn.rec"
merge country /file="nn9.rec"
merge country /file="n99.rec"

define tot #####
tot=nnp+npx+px+nnn+nn9+n99

define totpos #####
totpos=nnp+npx+px

drop n pattern mergevar
savedata "pattern.rec" /replace

cls
close
read "pattern.rec"

define p #.#####
p=nnp/(nnp+nnn)

define sep #.#####
sep=sqrt(p*(1-p)/(nnp+nnn))

define cilow #.#####
cilow=p-1.96*sep

define cihigh #.#####
cihigh=p+1.96*sep

define smpoint ###.#
smpoint=1/p

define sm95low ###.#
sm95low=1/cihigh

define sm95high ###.#
sm95high=1/cilow

define hypothesis _____
hypothesis="Accept"
if sm95low>125 then hypothesis="Refute"

set display databrowser=on
browse country nnp npx px nnn nn9 tot sm95low smpoint sm95high hypothesis
set display databrowser=off

```