Solution to Exercise 2: Create a basic data entry form

Key Point(s):

- The identifier is the most important variable in a record
- EpiData is not case-sensitive, but some other software is. It is therefore advisable to use a simple rule such as consistently using lower-case for field names.

Tasks:

- **Finalize the data entry form for the remaining results variables.** Note that the fields for scanty results cannot be *Must Enter*. Note further the options in the Drop down menu for what is the default “Skip Next Field” to pick the best option for the last result.

- **Align the field correctly using the Alignment icon.** Note that correct vertical alignment is critical if two variables are on the same horizontal pane (EpiData Manager gives nice blue and red guiding lines). If two variables on the same horizontal pane are vertically mismatched, the sequence of data entry will go wrong!

- **Tell EpiData Manager to create the Codebook and save the output file as a text file “a_ex02_codebook.txt”**.

Solution:

The data entry form may look as follows:

```
Tuberculosis Microscopy Laboratory

Laboratory serial number
Registration date
Examinee's sex
Examinee's age in years
Reason for examination

Result of specimen 1
Result of specimen 2
Result of specimen 3

label_result
label_result
label_result

label_scanty
label_scanty
label_scanty
```

Once a data entry form has been prepared, it is best to test it right away in the EntryClient with some fake data (without saving) to identify quickly problems.

You can leave the data entry form open in EpiData Manager and access the EpiData EntryClient via the menu and after prompting the Manager will close.

Opening in the EntryClient:
we see that all fields which should be Must Enter actually are (orange-brownish color) and that the fields which can be bypassed (for quantified scanty results) are not.

Entering fake data, we get:

It all looks as it should, neat and nicely. Do not save the record and exit without saving.

We saved the CodeBook as text file and can look at it in a text editor. It must reflect what we defined in the Data documentation sheet but is now much more detailed and a superb document that can be shared with others who later collaborate in the analysis:

```
 Report:  CodeBook
 Created: 28-04-2015 18:33:16

-------------------------------------------------
File 1: C:\EpiData_course\a_ex02.epx
-------------------------------------------------
```

course_a_ex02_solution
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## Dataform: Microscopy lab

### List Overview

<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Length</th>
<th>Missing</th>
<th>Value[es]</th>
<th>Value Label</th>
<th>Question / Caption</th>
</tr>
</thead>
<tbody>
<tr>
<td>H1</td>
<td>Heading</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Tuberculosis Microscopy Laboratory</td>
</tr>
<tr>
<td>serno</td>
<td>Integer</td>
<td>4</td>
<td></td>
<td></td>
<td></td>
<td>Laboratory serial number</td>
</tr>
<tr>
<td>regdate</td>
<td>Date (DMY)</td>
<td>10</td>
<td></td>
<td></td>
<td></td>
<td>Registration date</td>
</tr>
<tr>
<td>sex</td>
<td>Integer</td>
<td>1</td>
<td></td>
<td></td>
<td></td>
<td>Examinee's sex</td>
</tr>
<tr>
<td>age</td>
<td>Integer</td>
<td>3</td>
<td></td>
<td></td>
<td></td>
<td>Examinee's age in years</td>
</tr>
<tr>
<td>reason</td>
<td>Integer</td>
<td>1</td>
<td></td>
<td></td>
<td></td>
<td>Reason for examination</td>
</tr>
<tr>
<td>res1</td>
<td>Integer</td>
<td>1</td>
<td></td>
<td></td>
<td></td>
<td>Result of specimen 1</td>
</tr>
<tr>
<td>res2sc</td>
<td>Integer</td>
<td>1</td>
<td></td>
<td></td>
<td></td>
<td>Result of specimen 1 scanty</td>
</tr>
<tr>
<td>res2</td>
<td>Integer</td>
<td>1</td>
<td></td>
<td></td>
<td></td>
<td>Result of specimen 2</td>
</tr>
<tr>
<td>res2sc</td>
<td>Integer</td>
<td>1</td>
<td></td>
<td></td>
<td></td>
<td>Result of specimen 2 scanty</td>
</tr>
<tr>
<td>res3</td>
<td>Integer</td>
<td>1</td>
<td></td>
<td></td>
<td></td>
<td>Result of specimen 3</td>
</tr>
<tr>
<td>res3sc</td>
<td>Integer</td>
<td>1</td>
<td></td>
<td></td>
<td></td>
<td>Result of specimen 3 scanty</td>
</tr>
</tbody>
</table>

### Field: serno: Laboratory serial number

Type: Integer  
Length: 4  
Show Value Label: true

### Field: regdate: Registration date

Type: Date (DMY)  
Length: 10  
Entry Mode: Must Enter  
Range: 01-01-2000-31-12-2005  
Show Value Label: true

### Field: sex: Examinee's sex

Type: Integer  
Length: 1  
Entry Mode: Must Enter  
Show Value Label: true  
Show Picklist: true

Value label: label_sex [I]: (Integer)

Value Label: Missing (M), set: label_sex

1: Female  
2: Male  
9: Not recorded

### Field: age: Examinee's age in years

Type: Integer  
Length: 3  
Entry Mode: Must Enter  
Range: 0-125

Value label: label_age [I]: (Integer)
**Value Label**

**Missing (M), set: label_age**

999 Age not recorded

---

Field: reason: Reason for examination

**Type** Integer

**Length** 1

**Entry Mode** Must Enter

**Show Value Label** true

**Show Picklist** true

---

**Value label: label_reason [I]: (Integer)**

---

**Value Label**

**Missing (M), set: label_reason**

---

0 Diagnosis
1 Follow-up at 1 month
2 Follow-up at 2 months
3 Follow-up at 3 months
4 Follow-up at 4 months
5 Follow-up at 5 months
6 Follow-up at 6 months
7 Follow-up at 7 months or later
8 Follow-up, month not stated
9 Reason not recorded

---

Field: res1: Result of specimen 1

**Type** Integer

**Length** 1

**Entry Mode** Must Enter

**Jumps**
0 > Skip Next Field
1 > Skip Next Field
2 > Skip Next Field
3 > Skip Next Field
4 > Skip Next Field
5 > Skip Next Field
9 > Skip Next Field

**Show Value Label** true

**Show Picklist** true

---

**Value label: label_result [I]: (Integer)**

---

**Value Label**

**Missing (M), set: label_result**

---

0 Negative
1 1+ positive
2 2+ positive
3 3+ positive
4 Positive, not quantified
5 Scanty, not quantified
6 Scanty, quantified
9 Result not recorded

---

Field: res1sc: Result of specimen 1 scanty

**Type** Integer

**Length** 1

**Show Value Label** true

**Show Picklist** true

---

**Value label: label_scanty [I]: (Integer)**

---

**Value Label**

**Missing (M), set: label_scanty**

---

1 1 AFB per 100 OIF
2 2 AFB per 100 OIF
3 3 AFB per 100 OIF
4 4 AFB per 100 OIF
5 5 AFB per 100 OIF
6 6 AFB per 100 OIF
7 7 AFB per 100 OIF
8 8 AFB per 100 OIF
9 9 AFB per 100 OIF

---
Field: res2: Result of specimen 2
------------------------------------
Type                         Integer
Length                             1
Entry Mode                Must Enter
Jumps            0 > Skip Next Field
                 1 > Skip Next Field
                 2 > Skip Next Field
                 3 > Skip Next Field
                 4 > Skip Next Field
                 5 > Skip Next Field
                 9 > Skip Next Field
Show Value Label   true
Show Picklist       true
---------------------
Value label: label_result [I]: (Integer)
------------------------------------
Value Label                    Missing (M), set: label_result
----------------------------------------------------------------------------------
0     Negative
1     1+ positive
2     2+ positive
3     3+ positive
4     Positive, not quantified
5     Scanty, not quantified
6     Scanty, quantified
9     Result not recorded
----------------------------------------------------------------------------------
Field: res2sc: Result of specimen 2 scanty
------------------------
Type             Integer
Length                 1
Show Value Label    true
Show Picklist       true
------------------------
Value label: label_scanty [I]: (Integer)
----------------------------------------------------------------------------------
Value Label             Missing (M), set: label_scanty
----------------------------------------------------------------------------------
1     1 AFB per 100 OIF
2     2 AFB per 100 OIF
3     3 AFB per 100 OIF
4     4 AFB per 100 OIF
5     5 AFB per 100 OIF
6     6 AFB per 100 OIF
7     7 AFB per 100 OIF
8     8 AFB per 100 OIF
9     9 AFB per 100 OIF
----------------------------------------------------------------------------------
Field: res3: Result of specimen 3
--------------------------------
Type                     Integer
Length                         1
Entry Mode            Must Enter
Jumps            0 > Save Record
                 1 > Save Record
                 2 > Save Record
                 3 > Save Record
                 4 > Save Record
                 5 > Save Record
                 9 > Save Record
Show Value Label   true
Show Picklist       true
--------------------------------
Value label: label_result [I]: (Integer)
----------------------------------------------------------------------------------
Value Label                    Missing (M), set: label_result
----------------------------------------------------------------------------------
0     Negative
1     1+ positive
2     2+ positive
3     3+ positive
4     Positive, not quantified
5     Scanty, not quantified
6     Scanty, quantified
9     Result not recorded
Field: res3c: Result of specimen 3 scanty
------------------------
Type             Integer
Length                 1
Show Value Label    true
Show Picklist       true
------------------------

Value label: label_scanty [I]: (Integer)

Value Label             Missing (M), set: label_scanty
------------------------------------------------------
1     1 AFB per 100 OIF
2     2 AFB per 100 OIF
3     3 AFB per 100 OIF
4     4 AFB per 100 OIF
5     5 AFB per 100 OIF
6     6 AFB per 100 OIF
7     7 AFB per 100 OIF
8     8 AFB per 100 OIF
9     9 AFB per 100 OIF