

## *SMD Utility Quick Guide*

### **You'll need:**

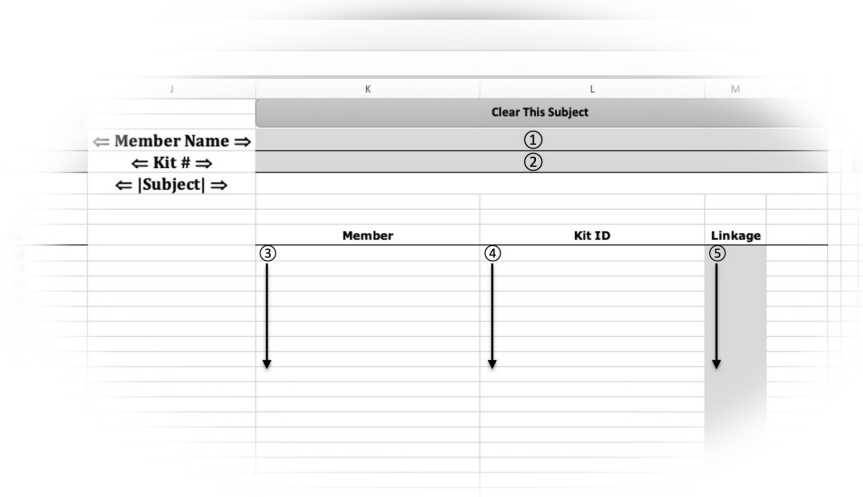
- the *SMD Utility*, available from:  
<http://www.discoveringnewancestors.com/smd/>
- a full set of downloaded DNA matches for:
  - Yourself
  - one of your DNA Matches
  - Shared Matches common to Yourself and your Match

### **To begin:**

- open the *SMD Utility*
- click [Enable Macros] when asked.
- [OK] the informational dialog

### **Process:**

- open the downloaded DNA matches file for Yourself in Excel.
- enter your DNA match data into the leftmost columns of the *SMD Utility* as follows:



### **SMD Utility Data Entry**

For each of three Trio Subjects:

- ① Enter *Subject Name*
- ② Paste value of Subject's *Test Kit ID*
- ③ Paste *Names* of DNA matches
- ④ Paste *Kit IDs* of DNA matches
- ⑤ Paste *shared linkage* of DNA matches

- repeat this data entry process for your Match and your Shared Match using the open subject columns of the *SMD Utility*.

- read the status of your Shared Match Trio from the right side of the *SMD Utility*. You may need to recalculate the sheet if manual recalculation is selected in your Excel preferences.

Full sets of DNA matches for (3) Subjects

Clear Subject data

Read NON-TRIO/FAVORABLE/UNFAVORABLE status of Subjects *here*

Scripted buttons transfer Trio status and metrics to the *application log*, which can be sorted/exported/printed and cleared.

- use the scripted buttons in the upper right corner of the *SMD Utility* to copy your shared match details into the application log and to sort, print and clear the log.
- to evaluate another Shared Match, clear any individual (1, 2, or 3) and repeat the data entry process from the previous page.
- the *SMD Utility* can evaluate larger sets of shared matches by breaking *n*-element collections into overlapping shared match trios.

Shared Match Differentiation (SMD) and the *SMD Utility* are patent-pending processes of:



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