1. Run *meta.emperorPenguin* on each experiment immediately after you finish clustering.

(Note: It is possible to do multiple experiments at once. In that case, name the resulting sheet *master* and move to Step 4.)

1. Move all emperor Excel spreadsheets that have been run with identical settings into a new empty folder.
2. Run *meta.excelStitch* on this folder to combine all sheets into a *master* sheet.
3. Run *meta.addCellNums* on the resulting sheet, calling the new output masterCellNums.
4. Add any extra columns you like to *masterCellNums* (e.g. genotype, region, dose, etc.). Unique experiment numbers and will be added automatically in the next step, and mouse IDs can be too if they are in the folder name.
5. Run *meta.kingPenguin* on *masterCellNums* to add rate maps, experiment numbers, and possibly mouse IDs. The resulting *masterMat.mat* file will be used for all further analysis.
6. Optional: copy all columns except for maps into new sheet in Excel (*masterMATLAB*).