Gedmatch Utilities
by Barton Lewis and Kitty Cooper)
March 3, 2015

Table of Contents
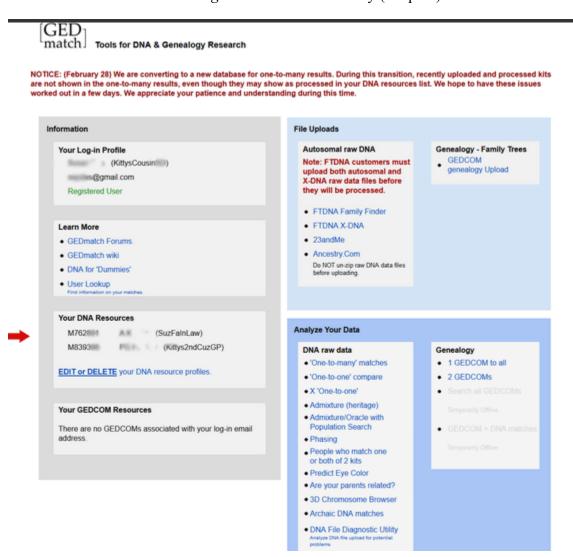
INTRODUCTION

Gedmatch (found at www.gedmatch.com) is a third party website that permits people who have tested at any of the three major DNA testing companies (Ancestry, 23andme and Family Tree DNA) to compare their DNA with others who have tested at any of those companies.

To use the site, you first need to register (create a username and password). The site is free but additional utilities are available called Tier1 with a $10 donation; you get a month for every $10.

Once you are registered and logged in, upload your data by clicking on the company link applicable to you in the top right box labeled *File Uploads*. Follow the instructions carefully. Once your data has been uploaded, it may be used for all tools except *One to Many* and *Triangulation*. It takes about 2-6 weeks for the kit to fully process, so that you can then access these two additional tools. *Triangulation* is a Tier 1 utility (i.e. paid).

Your home page will list the ids of all DNA kits you have uploaded, as well as all GEDcoms you have uploaded in the left hand column boxes. The right hand column boxes have functions you can use. Above is a sample non paid home page with the names blurred out.

The headings listed in this document are all functions found on the Home page, under the caption *Analyze Your Data*.

Analyze Your Data: DNA Raw Data

ONE TO MANY MATCHES

This is the utility that you will probably want to use first once your kit has processed. It will show you a list of all your matches on the site. Enter your kit number (preceded by a letter depending on which company you tested with -- "F" if you have tested at FTDNA, "A" if you have tested at Ancestry and "M" if you have tested at 23andme). The default number of cMs is the minimum largest segment of both autosomal and X-DNA which can be considered a "true" match. You may want to raise the minimum to 10cM the first time so as to have fewer and more significant matches. Once you are more familiar with the utilities, you can adjust the cM threshold settings.

Click Display Results to get your matches.

One-to-many DNA comparison

Enter your kit number: [_____]

Select the threshold of the largest segment to be included in the list :
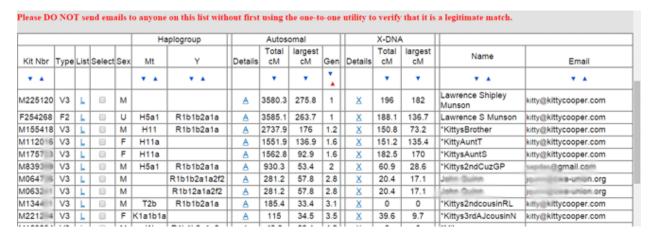and whether it is based on Autosomal or X
Selecting 5 or 6 cM may result in much slower response.

⦿ Autosomal
◯ X

[7 ▾]

Click here to display your results: [Display Results]

Wait until all your matches are listed – and be patient, it can take up to several minutes. When the site is very busy this will not run so try late at night (west coast) or very early in the morning (east coast)

The matches are listed in the order of those with whom you share the most DNA ("Total cM") down to the smallest amount of shared DNA. Columns can be sorted, click on the blue arrows to do this. For example, sorting by *largest cM* segment can be useful.

Most of the column headings, like *Kit Nbr* are self explanatory but a few need more explanation (*Type* refers to the chip, thus the selection of SNPs used to generate your results).

Please DO NOT send emails to anyone on this list without first using the one-to-one utility to verify that it is a legitimate match.

					Haplogroup			Autosomal				X-DNA			
Kit Nbr	Type	List	Select	Sex	Mt	Y	Details	Total cM	largest cM	Gen	Details	Total cM	largest cM	Name	Email
M225120	V3	L	☐	M			A	3580.3	275.8	1	X	196	182	Lawrence Shipley Munson	kitty@kittycooper.com
F254268	F2	L	☐	U	H5a1	R1b1b2a1a	A	3585.1	263.7	1	X	188.1	136.7	Lawrence S Munson	kitty@kittycooper.com
M155418	V3	L	☐	M	H11	R1b1b2a1a	A	2737.9	176	1.2	X	150.8	73.2	*KittysBrother	kitty@kittycooper.com
M11206	V3	L	☐	F	H11a		A	1551.9	136.9	1.6	X	151.2	135.4	*KittyAuntT	kitty@kittycooper.com
M17573	V3	L	☐	F	H11a		A	1562.8	92.9	1.6	X	182.5	170	*KittysAuntS	kitty@kittycooper.com
M8393	V3	L	☐	M	H5a1	R1b1b2a1a	A	930.3	53.4	2	X	60.9	28.6	*Kittys2ndCuzGP	septies@gmail.com
M06476	V3	L	☐	M		R1b1b2a1a2f2	A	281.2	57.8	2.8	X	20.4	17.1	John Quinn	jq...@wa-union.org
M0632	V3	L	☐	M		R1b12a1a2f2	A	281.2	57.8	2.8	X	20.4	17.1	John Quinn	jq...@wa-union.org
M1344	V3	L	☐	M	T2b	R1b1b2a1a	A	185.4	33.4	3.1	X	0	0	*Kittys2ndcousinRL	kitty@kittycooper.com
M22124	V3	L	☐	F	K1a1b1a		A	115	34.5	3.5	X	39.6	9.7	*Kittys3rdAJcousinN	kitty@kittycooper.com

Sample partial output from one to many

4

The column labeled *Total cM* displays the total amount of cM across all chromosomes shared with each match (cM stands for "centiMorgan" and is the fundamental unit for estimating relationships—the higher the better). The column labeled *largest cM* displays the single longest segment of DNA shared with each match. The column labeled *Gen* is the number of likely generations between you and your match. A parent and child should see a 1, a first cousin a 2 and a second cousin a 3. These numbers get less accurate the further away the relationship is.

The column labeled "Select" allows you to run various functions listed at the top of the "one to many page" after clicking that box for the profiles you wish to look at; these functions are discussed below, after the following instructions on how to use the various "letter" functions contained in each row of your matches.

In each row of your table of matches are utilities which you can invoke by clicking on the underlined letters: L, A and X.
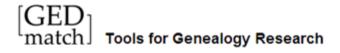
Clicking on "L" will generate a list of a person's matches, and in most cases will not be useful unless you want to check to see if a specific match of yours matches that person.

Click on "A" for details on Autosomal comparison. This utility is very useful as it generates a table which lists the chromosome(s) where you share DNA with someone; the start and stop location of each segment; the amount of cMs in the segments and the number of SNPs. You can request the graph display or just the segment table.

Below is the form on your screen that you get when you click on the A. It will fill in the two boxes with the kit numbers for you (marked with red arrows in the picture). This is the same utility you get when you click the "one to one" comparison command on the logged in Home page but when used from the Home page you have to fill in the kit numbers yourself.

Normally you would leave the boxes alone to get the defaults. When comparing to a known relative you may prefer to lower the cM size to 5 and the SNPs to 400 or some other combination.

Another option is whether to get the pretty pictures of the chromosomes or not. The output page without the pictures can be cut and pasted into a spreadsheet very easily.

GEDmatch.Com DNA one-to-one
Comparison Entry Form

This utility allows you to make detailed comparisons of 2 DNA kits. Results may be based on either default thresholds, or thresholds that you provide. Estimates of 'generations' are provided as a relative means of comparison, and should not be taken too literally, especially for more than a couple of generations back.

Kit Number 1:	M225120
Kit Number 2:	
Show graphic bar for each Chromosome?	○ Yes ◉ No
For compressed graphic, enter width in pixels (zero or blank for expanded graphic)	1000
SNP count minimum threshold to be considered a matching segment (Leave blank for default value)	
Minimum segment cM size to be included in total: (Leave blank for default value)	
Threshold for noise reduction: (Leave blank for default value)	
Size (in SNPs) of Mismatch Evaluation window. (Leave blank for default value)	
Size (in SNPs) of Mismatch-Bunching limit. (Leave blank for default value)	

Submit

Here is a sample output without the chromosome map

GEDmatch.Com Autosomal Comparison

Comparing Kit M225120 (Lawrence Shipley Munson) and ....

Minimum threshold size to be included in total = 700 SNPs
Mismatch-bunching Limit = 350 SNPs
Noise Reduction Threshold = 0.85
Minimum segment cM to be included in total = 5.0 cM

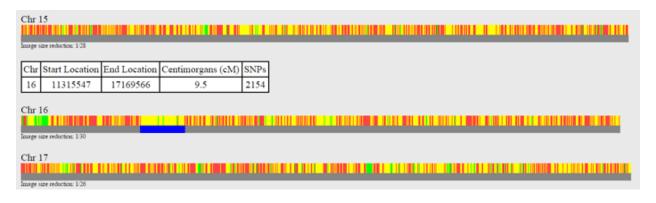| Chr	Start Location	End Location	Centimorgans (cM)	SNPs
8	70,406,494	90,677,362	16.3	3,394
9	38,762,575	78,095,970	10.4	1,666

Largest segment = 16.3 cM
Total of segments > 5 cM = 26.7 cM
Estimated number of generations to MRCA = 4.5

Comparison took 0.25206 seconds.

Sample Output of One to Many

And here is an extract from a different one to one compare that included the picture. The blue line at the is the place where the two kits are matching. The line above shows yellow for half identical, green for fully identical, and red for not matching.

Chr 15

Image size reduction: 1/28

Chr	Start Location	End Location	Centimorgans (cM)	SNPs
16	11315547	17169566	9.5	2154

Chr 16

Image size reduction: 1/30

Chr 17

Image size reduction: 1/26

Functions Available Using the Select Button on the One to Many Page

The following functions are accessed by clicking the "Select" column for any number of desired matches and then clicking the four buttons for these functions which are located at the top of the "One to Many" page.

DNA matches to Kit M83▓

These matches are calculated from DNA raw data files submitted by users.
Results are based on the default parameters for the GEDmatch Autosomal comparison software.
These results are for comparison only and will likely be somewhat different than those shown by your testing company.

Default parameters (and results) may change periodically based on feedback from users, and from new research results.

Click on 'L' for list of matches for that person
Click on 'A' for details on Autosomal comparison (Detail data may take up to a minute to process).
Click on 'X' for details on X-DNA comparison.

Select 2 or more from 'Select' column, and click this button for a Chromosome Browser comparison.
> Chr-Browse

Select 2 or more from 'Select' column, and click this button for an Autosomal Matrix comparison.
> A-Matrix

Select 2 or more from 'Select' column, and click this button for a Generations Matrix comparison.
> Generations

Select 2 or more from 'Select' column, and click this button for an X-DNA Matrix comparison.
> X-Matrix

* 'Adj cM' column has an adjustment applied to compensate for sex differences in X-Chromosome

Intensity of **GREEN background** indicates how recent (within last 30 days) a match is.

Chromosome Browser comparison

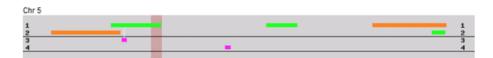**Select 2 or more from 'Select' column, and click this button for a Chromosome Browser comparison**

This utility will generate graphs which show where on each chromosome you are sharing DNA with others; you will be able to see overlapping segments where the people you have selected are sharing DNA with you and each other, if applicable. Plus it will show if they overlap with each other on the same spot as an "old branch" by drawing a little white vertical line as in the example below (hard to see but there is a line between 1 and 3 at the beginning). Note that the color coding indicates the size in cMs since the graph is in terms of base pairs.

Kitty did a detailed blog post about the chromosome browser at:

http://blog.kittycooper.com/2014/09/using-gedmatch-with-an-ancestry-kit-the-gedmatch-chromosome-browser/

Chr 5

Match ID	Type	Name	Matching segments on Chromosome 5	Overlap with previous match
1	V3	*Kittys2ndc 431)	27561817 - 50093800 (19.3519 cM),
98414385 - 112346827 (10.362 cM),
146845403 - 180623543 (55.433 cM)	New Root
2	V3	John 726)	91139 - 31688243 (52.2141 cM), 173984643 -
180000281 (11.898 cM)	27561817 - 31688243, 173984643 -
180000281
3	F2	Mar 21859)	32463775 - 34577069 (3.6762 cM)	Old Branch (1) , 32463775 - 34577069
4	F2	Dona' 735)	79578880 - 81889003 (3.6277 cM)	New Root

Chr 5

Autosomal Matrix comparison

Select 2 or more from 'Select' column, and click this button for an Autosomal Matrix comparison.

Autosomal DNA comparison matrix

Value shown is cM total of matching segments over minimum threshold.

Kit	name	F1	M1	F	N	AS
F19	s		798.2	114.5	37.7	43.8
M1		798.2		25.9	17.4	79.6
F19	s	114.5	25.9		5.3	
M		37.7	17.4	5.3		
N		43.8	79.6			

This utility will generate a table which shows how much DNA each of the people selected share with each other.

This feature allows you to enter a kit number and generate all of the matches with that kit. Then you can select any number of people (at least three) to see whether they share DNA with each other. In the table below, Barton's father is James Edward Lewis, and he's the person whose kit is entered. Barton then selected four people from his list of matches. Their kit numbers are listed next to their names and across the x axis. The gray boxes indicate that a person doesn't match with themselves.

Autosomal DNA comparison matrix

Value shown is cM total of matching segments over minimum threshold.

Kit	name	F1947.	M1802	F1936.	M1445.	M8144.
F19475	James		798.2	114.5	37.7	43.8
M1802.	Linda	798.2		25.9	17.4	79.6
F1936( )	Gerald	114.5	25.9		5.3	
M1445.	*dc.	37.7	17.4	5.3		
M8144	*jp	43.8	79.6			

The numbers in the first column of decimal numbers show how much DNA Barton's dad James shares with each of the people listed beneath him. This same amount appears on the X axis in the first row for each applicable kit. The second column of decimal numbers displays the amount of DNA Linda shares with the others, the third column of numbers the amount of DNA that Gerald shares with the others, and so on.

Since Linda is Barton's dad's paternal first cousin, she shares DNA with his dad's fourth cousin, Gerald, as well as dc, who is related to his dad through his other paternal grandparent (Barton's dad's and Linda's grandmother). But Gerald and dc also share DNA. They shouldn't, since Gerald is related to his dad through his paternal grandfather and dc is related to his dad through his paternal grandmother. But Gerald and dc only share 5cM of DNA. This is below the threshold amount that is generally considered IBD (identical by descent, or reflective of a true relationship, as opposed to IBC, or identical by coincidence).

This tool is useful for checking if your matches are related to each other. It doesn't tell you how, but it can eliminate a connection if no DNA is being shared between two people you think are related to each other through a specific line.

X-DNA Matrix comparison

Select 2 or more from 'Select' column, and click this button for an X-DNA Matrix comparison.

This utility shows how much DNA (if any) on the X chromosome is shared between selected matches. The output looks similar to the Autosomal Matrix.

Other Options for Analyzing your Data on the Home Page

ONE TO ONE COMPARE

This utility tells you exactly where you are matching with a match (chromosome and segment start and stop points, SNPs, cM). Just enter the kit numbers (and don't forget to put an A, F or M before the number!). See the A command above for the sample entry screen and output.

Analyze Your Data

DNA raw data
- 'One-to-many' matches
- 'One-to-one' compare
- X 'One-to-one'
- Admixture (heritage)
- Admixture/Oracle with Population Search
- Phasing
- People who match one or both of 2 kits
- Predict Eye Color
- Are your parents related?
- 3D Chromosome Browser
- Archaic DNA matches
- DNA File Diagnostic Utility
  Analyze DNA file upload for potential problems.

Genealogy
- 1 GEDCOM to all
- 2 GEDCOMs
- Search all GEDCOMs

  Temporarily Offline.

- GEDCOM + DNA matches

  Temporarily Offline.

PHASING

This utility is used to determine the alleles (reported values) in a two-parent, child trio. It can also be used for one parent and one child although with less accuracy. This allows you to create a pair of kits for yourself which is just the DNA received from each parent.
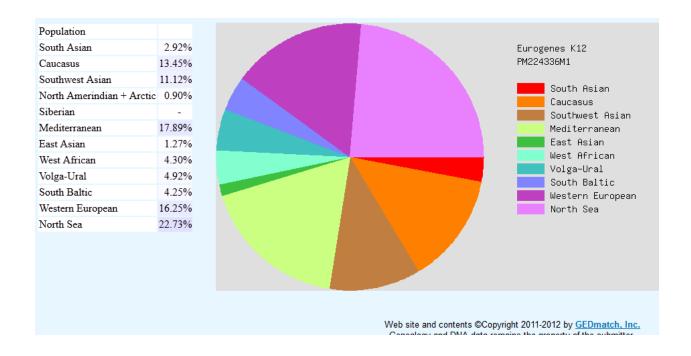
Through phasing, you can tell which parent passed to you the allele on any given marker. You can use that information, if needed, to compare you (or your parent's) phased data with someone else, should that become necessary. In almost all instances, it will not be, but if there is uncertainty as to which side you are matching on with your match on a given chromosome and segment (your mother's or father's), or whether a run of HIRs is as reported, as long as you can obtain the phased data for the match, you can resolve these ambiguities.

ADMIXTURE

The admixture tools on this site are the best available. Different calculators are better for different population sets. K12 is quite good for Europeans. A number of these are explained in the slides from Kitty's presentation:

http://slides.com/kittycooper/gedmatch#/12

Also see Kitty's blog post about these at: http://blog.kittycooper.com/2012/11/gedmatch-a-wonderful-tool/

Population	
South Asian	2.92%
Caucasus	13.45%
Southwest Asian	11.12%
North Amerindian + Arctic	0.90%
Siberian	-
Mediterranean	17.89%
East Asian	1.27%
West African	4.30%
Volga-Ural	4.92%
South Baltic	4.25%
Western European	16.25%
North Sea	22.73%

Eurogenes K12
PM224336M1

- South Asian
- Caucasus
- Southwest Asian
- Mediterranean
- East Asian
- West African
- Volga-Ural
- South Baltic
- Western European
- North Sea

FIND PEOPLE WHO MATCH WITH YOU ON A SPECIFIED SEGMENT

If you match someone and are interested to see what others match you and this person on the segment, you can input the segment start and stop points to see that list.

It's useful when you know how you are related to someone and are researching that line for other matches through the same ancestor. You can obtain the start and stop points by going to the Chromosome Browser if you tested at FTDNA and downloading your data into an Excel spreadsheet. This will list all your matches and where on each chromosome you are matching with them (start and stop points).

It can also help track down a specific segment match by seeing who else might match you there.

PEOPLE WHO MATCH ONE OR BOTH OF 2 KITS

This utility allows you to enter in two kit numbers and see who else is matching one or both of those kits. It can be used as a "triangulation" tool to see what other people are matching you and a known cousin. If you use yourself and a known third cousin as the kits to compare, for example, it would tell you what other matches are related to you through the same pair of second great grandparents.

DNA FILE DIAGNOSTIC UTILITY

Use this tool to check and see if your kit downloaded properly. In most cases, it always does. You can also check to see when your kit was downloaded in case you forgot when that was, so you can estimate when it will be fully processed.

Tier I Utilities

 … More will be written here in the future

See Kitty's blog post

http://blog.kittycooper.com/2014/10/new-utilities-at-gedmatch-tier-1-for-paid-members/