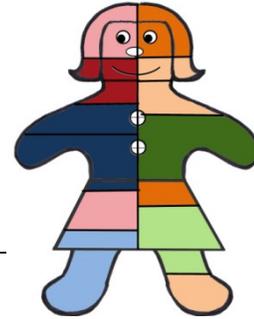


DNA Painter—Part 2: What Are the Odds? Tool

Debbie Parker Wayne, CG®



INTRODUCTION TO DNA PAINTER

In the last issue we introduced the DNA Painter website created by Jonny Perl of London, England, providing tools to help with autosomal DNA analysis.¹ The site also offers access to tools created by others, with permission of the creator, and sometimes modifies or automates the tool using rights granted through a Creative Commons license.² These additional tools include the Shared cM Project³ by Blaine T. Bettinger and What Are the Odds? (WATO)⁴ by Leah LaPerle Larkin. Access is free for the basic tools. Some useful features require a subscription.

There is an ongoing discussion in the genealogical community about whether genealogical databases should be available to law enforcement investigators and researchers working with law enforcement when no warrant or subpoena compels a company to allow access. At this time, this is not an issue with DNA Painter. Data imported to an account is only available to the account holder unless explicitly shared with another person. Additionally, raw DNA data is not uploaded to DNA Painter; only the

1All URLs accessed on 21 July 2019.

Jonny Perl, *DNA Painter* (<https://dnapainter.com/>) and *Facebook* (<https://www.facebook.com/dnapainter/>).

2 For an explanation of Creative Commons licenses, see “About The Licenses,” Creative Commons (<https://creativecommons.org/licenses/>).

3 Blaine T. Bettinger, Leah LaPerle Larkin, and Jonny Perl, “The Shared cM Project 4.0 tool v4,” *DNA Painter* (<https://dnapainter.com/tools/sharedcmv4>). Bettinger provided the Shared cM data. Larkin provided the underlying data for the probability indications. Perl developed the website where these tools are housed along with others, some written by Perl, such as the “cM Estimator.” Images were from the v3 version of the tool which has been updated. Search Bettinger’s blog posts for the most recent update to the project such as the August 2017 update at <https://thegeneticgenealogist.com/2017/08/26/august-2017-update-to-the-shared-cm-project/>. The project charts are periodically updated.

4 Jonny Perl, “What Are the Odds?,” *DNA Painter* (<https://dnapainter.com/tools/probability>) based on Leah LaPerle Larkin, “Science the Heck Out of Your DNA - Part 7,” *The DNA Geek* (<https://thednageek.com/science-the-heck-out-of-your-dna-part-7/>) with links to parts 1 through 6.

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information about shared matches is needed and aliases can be used in place of real test-taker names when privacy is a consideration.

This article focuses on using the WATO tool offered by DNA Painter. The WATO tool can be used without creating an account on the DNA Painter website. Please refer to the article in the June 2019 issue of *Stirpes* for an introduction to using DNA Painter.

ACCESSING “WHAT ARE THE ODDS?” (WATO)

Access the website (<https://dnapainter.com/>), click on “Tools” in the top navbar, then click on “What Are the Odds?” on the tools screen. The page displayed contains detailed instructions on how to use the WATO tool. Please read the instructions carefully and consider printing or saving a copy of the instructions for future reference. The tool description on the website is

Instructions

This tool is designed to help you work out how one person, the "target", [*sic*] is related to a family group of people who have taken DNA tests. In particular, the tool is designed for when you have limited or no tree information about the target. The target may, for example, be an adoptee trying to work out how they fit into the family tree of a group of DNA matches. Or the target might be a new and unidentified DNA match who appears in your list.

Requirements

To use the tool you will need to have the following on hand:

- A set of DNA matches who are all descended from the same ancestor (or couple) and from whom you suspect the target is also descended.
- The amount of DNA in centimorgans shared between the target person and each other person in the family group.
- Enough information about how members of the group are related to one another to build a basic family tree, including the common ancestor (or couple) from whom everyone in the family group is descended.
- Educated guesses (called "hypotheses") for where the target person might fit into the family tree.

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GETTING STARTED WITH WATO

While following the rest of this article please keep in mind that the “target person” is the test taker whose place in the family tree is under analysis. Shared ancestors in the trees of DNA matches and shared DNA amounts to the target person help determine the most likely place where the target person fits. Best results will likely be seen by finding multiple DNA matches who have the same ancestor(s) in their tree. Create a tree that merges the lines from each shared ancestor of each DNA match to the target person.

After closing the instruction page the user is presented with a way to begin entering people in a pedigree chart as shown in figure 1.

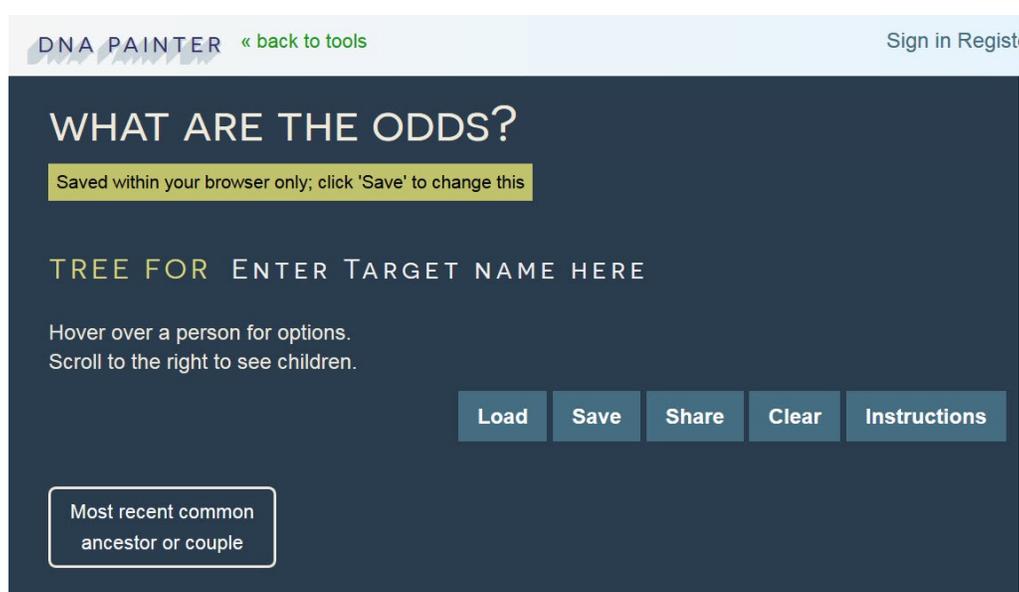


Figure 1. WATO Start Screen

Hovering the mouse over any rectangular ancestor-entry-block pops up a list of possible actions. Figure 2 shows that hovering the mouse over the initial person block labelled “Most recent common ancestor or couple” allows editing the text to enter a name or names of the ancestral person or couple, adding a child for this person, or adding a parent for this person. These three basic actions allow for quick tree creation. The user can enter as many or as few details on each person as desired. Short names can be entered to get a quick idea of where a target person best fits in a tree or to

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create a tree using aliases that protect the privacy of DNA test takers. More details on each test taker can be entered for personal use.

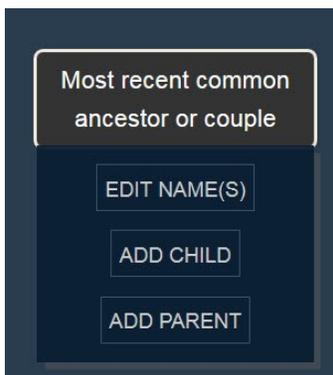


Figure 2. Edit options for first person or couple in a tree

Once a tree has been started additional data entry options for each person are displayed as shown in figure 3. These allow a person to be deleted, the shared amount of DNA to be entered (Enter Match cM), half relationships to be defined (half siblings as opposed to full siblings, for example), and hypothetical relationships to be entered for analysis of the likely odds of the relationship.

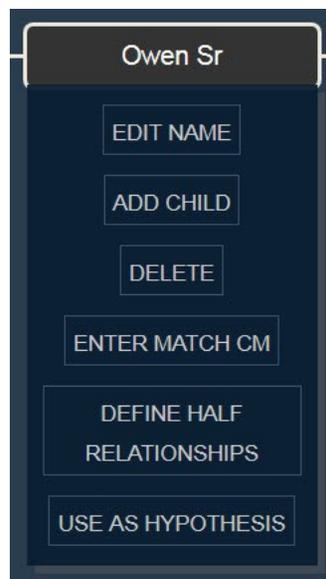


Figure 3. Edit options for subsequent person or couple in a tree

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Enter shared ancestors of DNA matches along with the amount of DNA each match shares with the target person (white and tan rectangles in figure 4). Then enter the target person as an hypothesis (blue rectangles). Each hypothesis will be assigned a score as to the odds of the target person fitting that place in the tree. Scores are shown in red boxes if the relationship is unlikely and green boxes if the relationship is possible based on the shared amounts of DNA entered.

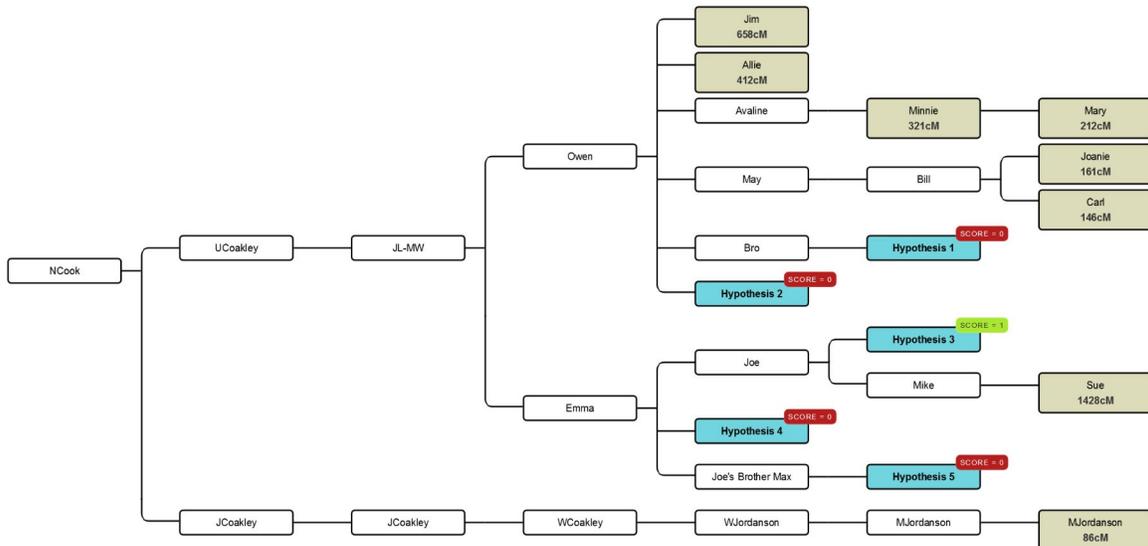


Figure 4. Tree and hypotheses entered using WATO tool

The enlargement of the tree in figure 5 shows five hypothetical placements for the target person. Four hypotheses have a score of 0 (in red) indicating these relationships are not statistically probable. One hypothesis has a score of 1 (in green) indicating the relationship is possible, but higher score numbers indicate more likelihood. In this case, we probably need more test takers to be able to make any determination.

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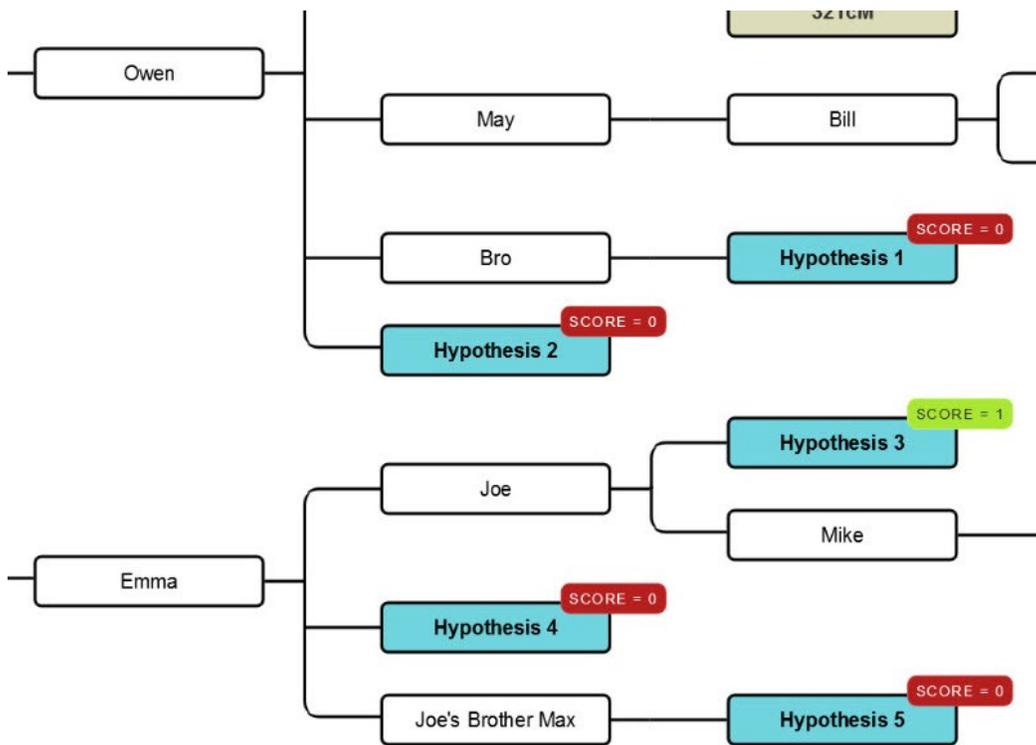


Figure 5. Enlarged portion of tree and hypotheses entered using WATO tool

WATO ANALYSIS OF THE TREE HYPOTHESES

Each hypothesis entered is analyzed and assigned a score. Scores are assigned relative to the hypothesis with a score of 1. A score of 0 should rule out the associated hypothesis. The highest score is the most likely of the hypotheses entered. Ideally, enough test takers and hypotheses should be entered so that one hypothesis has a score many times higher than the others. For example, say three non-zero hypotheses remain with scores of 1,000 for hypothesis 1, 50 for hypothesis 2, and 1 for hypothesis 3. Then hypothesis 1 is 1,000 times more likely to be true than hypothesis 3. Hypothesis 2 is 50 times more likely to be true than hypothesis 1. The best result is when all hypotheses except one have a score of zero.

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If all of the scores are low, then better prediction numbers may be seen by adding test takers who are closely related to the hypothetical parents or grandparents of the target person. After honing in on a likely parent for a target person it would help if several children or grandchildren of that potential parent will consent to testing.

In addition to the scores displayed in the tree, more detailed analysis is seen by scrolling down the page to the sections labeled "Hypothesis" and "Collated match data." "The name "PAUL" represents our target person in the tables below. The most likely hypothesis and those not statistically possible are marked.

Notes indicate things that seem to be incorrect or should be confirmed as shown for hypothesis 1 in the "Hypothesis table." The "Collated match data" table shows the hypothesized relationships between other test takers and the target person. The likelihood of the hypothetical relationship to be true, based on the shared DNA amounts, is shown; zero or no likelihood is highlighted in red. Then each relationship probability is combined with the others to calculate the combined odds ratio.

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Hypotheses

Here are the calculated probabilities, with the most likely hypothesis first. A higher score means a higher likelihood that this hypothesis is correct:

Hypothesis 3 PAUL is the child of Joe and grandchild of Emma	Score = 1	Possible This is the most likely (or equal most likely) hypothesis but is not significantly more likely than other hypotheses
Hypothesis 1 PAUL is the child of Bro and grandchild of Owen	Score = 0	Not statistically possible with the amounts and tree as entered Note: Is the tree definitely correct, or could there be a misattributed paternity event somewhere that is invalidating this hypothesis? It might be worth looking at the collated match data below to check.
Hypothesis 2 PAUL is the child of Owen and grandchild of JL-MW	Score = 0	Not statistically possible with the amounts and tree as entered
Hypothesis 4 PAUL is the child of Emma and grandchild of JL-MW	Score = 0	Not statistically possible with the amounts and tree as entered
Hypothesis 5 PAUL is the child of Joe's Brother Max and grandchild of Emma	Score = 0	Not statistically possible with the amounts and tree as entered

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Collated match data

Match name	Shared cM	Hyp. 1	Hyp. 2	Hyp. 3	Hyp. 4	Hyp. 5
Jim	658	Aunt / Uncle 0.00%	Sibling 0.00%	1C1R 47.57%	1C 52.15%	1C1R 47.57%
Allie	412	Aunt / Uncle 0.00%	Sibling 0.00%	1C1R 77.71%	1C 0.00%	1C1R 77.71%
Minnie	321	1C 0.00%	Niece / Nephew 0.00%	2C 50.18%	1C1R 42.18%	2C 50.18%
Joanie	161	1C1R 0.68%	Great-Niece / Nephew 0.00%	2C1R 52.78%	1C2R 28.14%	2C1R 52.78%
Carl	146	1C1R 0.00%	Great-Niece / Nephew 0.00%	2C1R 53.78%	1C2R 21.67%	2C1R 53.78%
Sue	1428	2C1R 0.00%	1C2R 0.00%	Niece / Nephew 92.81%	Great-Niece / Nephew 7.19%	1C1R 0.00%
MJordanson	86	4C1R 1.93%	3C2R 10.54%	4C1R 1.93%	3C2R 10.54%	4C1R 1.93%
Combined odds ratio		0.00	0.00	1.00	0.00	0.00

In the hypothetical example in this article we obviously need more test takers who are more closely-related to get a higher probability score than 1. A sample case provided on the DNA Painter website illustrates hypotheses with scores of 63879, 383, 3, and 1.⁵

SAVING AND RELOADING SAVED TREES

After a tree is entered it can be saved for later access using the “Save” button shown in figure 1. This is helpful to add new DNA matches as they appear in a match list for the target person.

⁵ Jonny Perl, “What Are the Odds?,” Example 1, *DNA Painter* (<https://dnapainter.com/tools/probability/examples/e1>).

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Users must have an account and be logged into the DNA Painter website to save trees on the site. Even with no DNA Painter account trees can be saved on a user's own device as a text file (file suffix .txt) using a name assigned by the user. Open a previously saved tree using the "Load" button shown in figure 1. Click "Load," click "Browse," navigate to the folder on your device where the file was saved, then select the file. Figure 6 shows a previously saved WATO tree in the file named PCxyz_WATO_Tool_Data.txt (where xyz is a name blurred here for privacy purposes). After selecting the file name and clicking "Open," then click on "Import data" on the web page. The saved tree is now reloaded and can be modified and updated.



Figure 6. Loading a saved tree into WATO tool

A message is displayed indicating whether the file was imported successfully. After a successful import the user can scroll down and view the tree. After importing a tree all of the editing functions described above are available.

Be sure to save any changes and additions or the modifications will be lost once the browser window is closed.

CONCLUSION AND CAUTIONS

WATO is an easy-to-use yet powerful tool for determining the likely places where a target person fits into a family tree. The more and closer the DNA matches are to the target person the easier it will be to find the most likely relationships. The tool works better for more recent matches and is less useful for matches with a shared ancestor many generations back. This is because the amount of shared DNA between two test takers varies more as the shared ancestors are further back in time; random recombination has

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more generations to cause variance the further back in our tree we go to locate the common ancestor.

The DNA Painter website lists some caveats to be aware of and credits:

ABOUT THIS TOOL

This tool has been built to help solve DNA puzzles (including unknown parentage cases) by undertaking the calculations described by Leah Larkin in her series Science the heck out of your DNA...⁶

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CAVEATS

Due to the lack of statistical data available, this tool has limited applications to the following scenarios:

- Double-cousin relationships
- 3/4 sibling relationships
- Matches with endogamous ancestry

CREDITS

The underlying calculations that convert the compounded probabilities into the odds ratio used for the score were developed by Dr. Andrew Millard.

Valuable advice on the user interface and functionality was provided by Mike Mulligan. Many thanks also to the early beta testers from the GG&T group on Facebook.

The static tree layout is derived from an example by Peiwen Lu.⁷

6 Leah LaPerle Larkin, "Science the Heck out of Your DNA," *The DNA Geek*, 2 January to 9 July 2018 (<http://thednageek.com/science-the-heck-out-of-your-dna-part-1/>) with links to all seven parts of the series.

7 Jonny Perl, "What Are the Odds?," Example 1, *DNA Painter* (<https://dnapainter.com/tools/probability/examples/e1>).

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Debbie Parker Wayne, CG, is a board-certified genealogist experienced using DNA analysis and traditional techniques for family history research. Debbie edited the book and authored one chapter of *Advanced Genetic Genealogy: Techniques and Case Studies*; coauthored the award-winning DNA workbook, *Genetic Genealogy in Practice*; and developed the online, self-paced course *Continuing Genealogical Studies: Autosomal DNA*, offered by National Genealogical Society. She is the DNA Project Chair for the Texas State Genealogical Society and the Early Texans DNA Project. Her publications include columns on DNA analysis for several genealogical journals and magazines including the *Stirpes* journal of Texas. Debbie was the course coordinator for the first beginner and intermediate DNA courses offered at four major US genealogy institutes. See <http://debbiewayne.com/> for more information and for archived versions of many of her articles.

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