

What's new at DNA Painter?

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DNA Painter is a popular website for genealogists working with DNA. You can find it at dnapainter.com.

In this webinar I'll describe some new features in existing tools – ancestral trees, probability tools and chromosome mapping – before walking you through some new standalone tools.

Ancestral trees

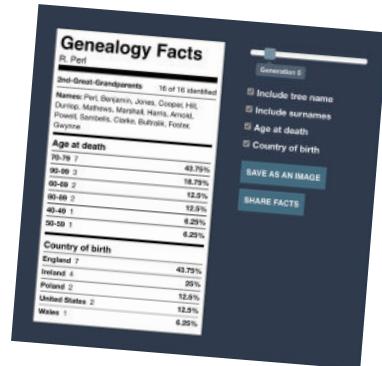
At DNA Painter you can import your tree on a “no-commitment” basis. By that I mean the site is only ever extracting your direct line, so this isn't attempting to replace your chosen family tree software or web platform. However, it does provide an easy way to share information with DNA matches on a single, searchable page.

Dimensions

The big new feature in ancestral trees is called **Dimensions**. A dimension is simply a new categorization that you can add to your direct line to create new visualizations

There are automated dimensions that the site can generate for you from your GEDCOM file or the information you enter. These include Country of Birth, Age at Death and Birth Century.

But you can also create your own custom dimensions according to your research needs. For example, users have created dimensions to show which relatives they've managed to find in the recently released 1950 US



Census. Once you've added dimensions, they are also summarized for you in a sharable 'Genealogy Facts' table.

Pedigree with haplogroups

A useful DNA-related feature of ancestral trees is the ability to overlay inheritance paths for X, Y and mtDNA onto your own tree. You can also add Y and mt haplogroups to individual ancestors in the tree, which provides an additional 'scorecard' for your DNA research.



You can also add kit numbers from mitoYDNA.org, a free online database for comparing mitochondrial and Y-DNA.

Probability tools

There's a new feature hiding in the popular Shared cM tool at <https://dnapainter.com/tools/sharedcmv4> that allows you to generate a tree based on the number of centimorgans entered. The tree is created in the What are the Odds? (WATO) tool (for example, <https://dnapainter.com/tools/probability/cm/432> is the tree for 432cM shared). You can then edit and save this tree to your account if you'd like to.

By default, the tree will be very broad, but if you add approximated birth years to the match person and the target, you can click 'Regenerate hypotheses.' This will narrow down the possibilities, and you can remove any other hypotheses you feel are unlikely in order to make it still more manageable.

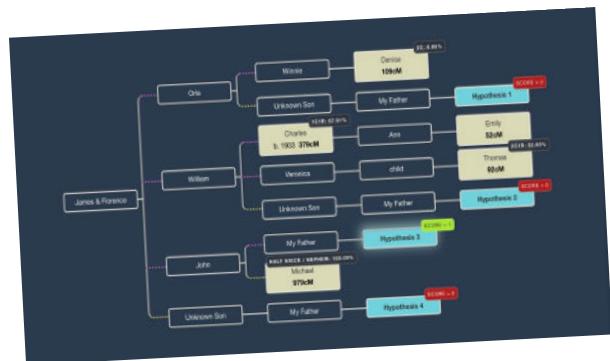
WATO's probability-based features are covered in depth in the webinar at <https://familytreewebinars.com/webinar/what-are-the-odds-an-online-tool-that-can-help-solve-dna-puzzles/>

It can also be used as a tool to identify potential testers who inherited X,

Y or mtDNA from a particular person in your tree. When you import a GEDCOM, there is now an option that allows you to narrow down your import based on these descendant types.

Other new features in WATO include:

- **Focus mode** allows you to see the calculated relationships and probabilities for a hypothesis by clicking on its score
- **Drag and drop mode** allows you to move nodes around within the tree
- **Colour coding** now allows you to add a custom colour to any person in the tree who is not a match or hypothesis.



Chromosome mapping

Within chromosome maps there are some minor new features

- You can change all groups to be ‘maternal’, ‘paternal’ or ‘both’ all at once. This will be particularly helpful to those using the Cluster Auto Painter tool at Gedmatch using a phased kit.
- You can now choose to import only selected chromosomes during a bulk import.
- You can now bulk-import segments from Geneanet.org and import ‘chromosome painting’ population segments from FamilyTreeDNA.

New standalone tools

Bucketing

This new tool allows you to filter a list of segments using another list of segments. For example:

- I can choose my father’s segments file as the main file

- I can add files from his maternal half-brother and maternal first cousin as other files
- The bucketing tool will return a file containing just segments from matches who appear in one of the files from his maternal relatives.



Shared cM Investigator



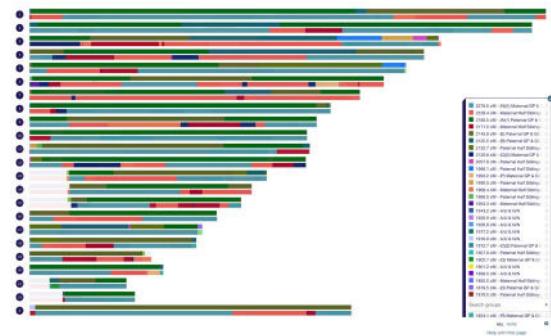
This tool takes multiple sets of segments that siblings share with a match and uses a mathematical formula to estimate the cMs of DNA the parent is likely to have shared with this match.

Distinct segment generator

Similar to the Shared cM Investigator, this tool omits the mathematical formula, so is useful in cases where you don't have a set of siblings. For example, if first cousins both share DNA with a match, you can use it to establish quickly how the number of cMs of distinct DNA that this represents.

Library of matches

A special chromosome map created by DNA Painter user and genealogist Cody Ely, the Library of Matches is a collection of real example matches and shared segments from a wide variety of relationships, to be used for relationship prediction and reference.



Useful links

Ancestral trees

Dimensions

<https://dnapainter.com/blog/dna-painter-dimensions-a-new-way-to-showcase-your-ancestral-line/>

Haplogroups and mitoYDNA integration

<https://dnapainter.com/blog/bringing-y-mt-and-mitoydna-into-dna-painter-trees/>

Probability tools

Generate a tree from the shared cM tool

<https://dnapainter.com/blog/generate-a-tree-from-the-shared-cm-tool/>

Focus mode in WATO

<https://dnapainter.com/blog/focus-mode-in-what-are-the-odds-wato/>

Color coding and dragging and dropping in WATO

<https://dnapainter.com/blog/new-features-for-maps-trees-and-wato-at-dna-painter/>

Previous WATO webinar

https://familytreewebinars.com/download.php?webinar_id=1288

New standalone tools

Bucketing

<https://dnapainter.com/blog/bucketing-tool-at-dna-painter/>

Shared cM Investigator

<https://dnapainter.com/blog/put-your-sibling-tests-to-work-with-the-shared-cm-investigator/>

Distinct Segment Generator

<https://dnapainter.com/blog/distinct-segment-generator/>

Library of matches

<https://dnapainter.com/blog/introducing-the-library-of-matches/>