## Advancements in Relationship Predictions

Brit Nicholson

## Advancements in relationship predictions

A person is asking for help with a surprise DNA match. They share 1,763 centiMorgans over 49 segments and can see that the match is on their paternal side. What's the relationship?

## Traditional Relationship Predictions

Enter the total number of cM for your match here:

## Enter the total cMs shared <br> 1111

cMs = centiMorgans
renter \%
Then any relationships that fit will stand out below
You will need to scroll the page to the right to see all relationships
Click here for a shareable link to the cM amount above

Most distant common ancestors
Assuming no pedigree collapse or endogamy, and that you're related in just one way, the furthest back you might need to go to find common ancestors for match of 1111 cM is Great-Grandparent level or generation 4 on your pedigree chart.

The connection may be closer. Also, depending on your family, this match could be a close younger generation relative, such as the descendant of your sibling.

Relationship probabilities (based on stats from The DNA Geek) New: View these relationships in a tree

## See the probability for the most likely group of relationships



98\% Great-Grandparent Great-Aunt/Uncle Half Aunt / Uncle Half Niece / Nephew Great-Niece / Nephew Great-Grandchild

2\% Half Sibling $\dagger$ Aunt / Uncle $\dagger$
Niece / Nephew $\dagger$ Grandparent Grandchild
https://dnapainter.com/tools/sharedcmv4

## Why not just look at the ranges of shared DNA?

| Relationship | Lower (cMs) | Average (cMs) | Upper (cMs) |
| :--- | :--- | :--- | :--- |
| Full Sibling | 2,191 | 2,592 | 2,952 |
| Paternal Half Sibling | 1,190 | 1,719 | 2,250 |
| Maternal Half Sibling | 1,314 | 1,719 | 2,122 |
| Patrilineal 1st Cousin | 462 | 837 | 1,260 |
| Matrilineal 1st Cousin | 503 | 827 | 1,188 |
| Half 1st Cousin | 145 | 415 | 760 |
| 2nd Cousin | 39 | 198 | 428 |

Data simulated from Ped-sim. Averages and ranges are similar to what you would see at AncestryDNA, MyHeritage, or FTDNA, but are based on the total cMs and low cM cutoff ( 8 cMs ) at Ancestry.

## Relationships with wider ranges of shared DNA are more probable at cM values far away from the mean



IBD Autosomal CentiMorgans (CMs) at 23andMe

## Relationships with wider ranges of shared DNA are more probable at cM values far away from the mean



IBD Autosomal CentiMorgans (CMs) at 23andMe

## Relationships with wider ranges of shared DNA are more probable at cM values far away from the mean



IBD Autosomal CentiMorgans (CMs) at 23andMe

## Paternal relationships are more probable at cM values far away from the mean



Aunt/uncle/niece/nephew probabilities were included in the calculations, but are not shown

## Differences between maternal and paternal relationships

e dna-sci.com

- $38.2 \%$ shared between a woman and her paternal grandmother
- This relationship always shares a full $X$ Chromosome copy
- Her father has tested and shares $50 \%$ with both women


Submit

| Relationship Type | Probability | Group |
| :--- | :---: | :---: |
| *Full-Sibling |  | $79.4 \%$ |
| Grandparent/Grandchild |  | $\mathbf{1 9 . 8 \%}$ |
| $\quad$ Paternal | $19.7 \%$ |  |
| $\quad$ Maternal | $0.1 \%$ |  |
| Half-Sibling |  | $\mathbf{0 . 9 \%}$ |
| $\quad$ Paternal | $0.9 \%$ |  |

## Orogen predictions at dna-sci.com

- Released in February of 2022
- Based only on total shared DNA-percentage or cMs
- The only predictions to use a peer-reviewed data source: Ped-sim developed at Cornell University
- All other relationship predictions have been developed at testing sites where methodologies are proprietary
- The Orogen methodology has been submitted to and published in a science journal: Forensic Science International, https://doi.org/10.1016/j.fsigss.2022.09.011

The new relationship predictor


SegcM - Predictions that take the number of segments into account

The tool is available at dna-sci.com/tools/SegcM


## How to use SegcM

Enter the total
CMs shared


Close family predictions from SegcM


## What's a good close family prediction?



Paternal and maternal designations

| Paternal Maternal 1st Cousin | Father's Sister's Child |
| :--- | :--- |
| Paternal Maternal Half Aunt | Father's Mother's Child |
| Paternal Maternal Great Aunt | Father's Mother's Sibling |

$1,398 \mathrm{cMs}$ and 27 segments

| Relationship Type Prob | Probability | Group |
| :---: | :---: | :---: |
| Grandparent/Grandchild |  | 46.2\% |
| Maternal | 42.8\% |  |
| Paternal | 3.4\% |  |
| Half-Sibling |  | 44.1\% |
| Paternal | 44.1\% |  |
| G-Grandparent/G-Grandchild |  | 5.4\% |
| Pat. Mat. or Mat. Pat. (x2) | 2.1\% |  |
| Maternal Maternal | 1.0\% |  |
| Paternal Paternal | 0.2\% |  |
| Half- Aunt/Uncle/Niece/Nephew | phew | 2.1\% |
| Paternal Paternal | 1.4\% |  |
| Pat. Mat. or Mat. Pat. (x2) | 0.3\% |  |
| Maternal Maternal | 0.1\% |  |
| G- Aunt/Uncle/Niece/Nephew |  | 1.1\% |
| Paternal Paternal | 0.4\% |  |
| Pat. Mat. or Mat. Pat. (x2) | 0.3\% |  |
| Maternal Maternal | 0.1\% |  |
| 1st Cousin |  | 0.8\% |
| Paternal Paternal | 0.3\% |  |
| Pat. Mat. or Mat. Pat. (x2) | 0.2\% |  |
| Maternal Maternal | 0.1\% |  |
| Aunt/Uncle/Niece/Nephew |  | 0.1\% |
| Paternal | 0.1\% |  |

## Close family predictions from SegcM

- dna-sci.com

cMs


## Submit

| Relationship Type | Probability | Group |
| :---: | :---: | :---: |
| Grandparent/Grandchild |  | 100.0\% |
| Paternal | 100.0\% |  |

a dna-sci.com

$1,741 \mathrm{cMs}$ and 18 segments

| Relationship Type | Probability | Group |
| :--- | ---: | ---: |
| Grandparent/Grandchild |  | $\mathbf{1 0 0 . 0} \%$ |
| Paternal | $100.0 \%$ |  |

There's only one possibility for these two!

## Close family predictions from SegcM


$1,763 \mathrm{cMs}$ and 49 segments

| Relationship Type | Probability | Group59.4\% | Relationship | Probability | Group |
| :---: | :---: | :---: | :---: | :---: | :---: |
| Aunt/Uncle/Niece/Nephew |  |  | Aunt/Uncle/N |  | 62.7\% |
| Maternal | 38.5\% |  | Maternal | 35.1\% |  |
| Paternal | 20.9\% |  | Paternal | 27.6\% |  |
| Half-Sibling |  | 40.6\% | Half-Sibling |  | 37.3\% |
| Maternal | 40.6\% |  | Maternal | 37.3\% |  |

Newly discovered paternal aunt and uncle

## Close family predictions from SegcM



## Maternal close family predictions from SegcM



## How can we compare predictors?

| 100\% | a dna-sci.com |  |  |
| :---: | :---: | :---: | :---: |
|  | 1887 <br> 36 <br> cMs <br> \# of Segs. |  |  |
| 6 relationships | Submit |  |  |
| $\sim=17 \%$ per relationship | 1,887 cMs and 36 segments |  |  |
|  | Relationship Type | Probability | Group |
|  | Half-Sibling |  | 46.8\% |
|  | Paternal | 46.3\% |  |
|  | Maternal | 0.5\% |  |
| Grandparent Aunt / Uncle Half Sibling Niece / Nephew | Grandparent/Grandchild | 46.0\% |  |
|  | Maternal | 45.9\% |  |
|  | Paternal | 0.1\% |  |
| Grandchild | Aunt/Uncle/Niece/Nephew | 7.3\% |  |
| ** Sibling | Paternal | 6.5\% |  |
|  | Maternal | 0.8\% |  |

## 1st cousins once removed and half 1st cousins

## 1C1R and half 1C are usually thought to have the same properties of shared DNA: <br> 6.25\% average

| - dna-sci.com |  |  |
| :---: | :---: | :---: |
| 516 cMs and 31 segments |  |  |
| Relationship Type Pro | Probability | Group |
| 1st Cousin, Once Removed |  | 77.3\% |
| 1st Cousin |  | 6.9\% |
| Maternal Maternal | 4.1\% |  |
| Pat. Mat. or Mat. Pat. (x2) | 1.0\% |  |
| Paternal Paternal | 0.8\% |  |
| G- Aunt/Uncle/Niece/Nephew |  | 3.8\% |
| Maternal Maternal | 2.2\% |  |
| Paternal Paternal | 0.6\% |  |
| Pat. Mat. or Mat. Pat. (x2) | 0.5\% |  |
| Half- Aunt/Uncle/Niece/Nephew | hew | 3.6\% |
| Maternal Maternal | 2.7\% |  |
| Pat. Mat. or Mat. Pat. (x2) | 0.4\% |  |
| Paternal Paternal | 0.1\% |  |
| Half-1C Group |  | 3.2\% |
| Half-1C, Half-G or 2 G Aunt/Uncle/Niece/Nephew | 3.2\% |  |
| G-Grandparent/G-Grandchild |  | 0.8\% |
| Maternal Maternal | 0.6\% |  |
| Pat. Mat. or Mat. Pat. (x2) | 0.1\% |  |
| 2C Group |  | 0.3\% |
| 2C, 1C2R, Half-1C1R, Half-2GAunt/Uncle/Niece/Nephew | - $0.3 \%$ |  |

## Extended family to 1st cousins, group probabilities

| Actual | Totala cms | $\begin{aligned} & \text { \#of } \\ & \text { Segments } \end{aligned}$ | $\begin{aligned} & \text { SegcM Group } \\ & \text { Prob. } \end{aligned}$ | Orogen Group Prob | DNA Painter |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 10 | ${ }^{823}$ | ${ }^{31}$ | 99\% | 98\% | 96\% |  |
| Haf niece | 744 | 25 | 95\% | 91\% | 84\% |  |
| Haff 1018 | 522 | 17 | 1\% | 1\% | 3\% |  |
| 1018 | 478 | 24 | 91\% | 95\% | 89\% |  |
| Parents 10 | 477 | ${ }^{23}$ | 91\% | 95\% | 89\% | SegcM highest: 63\% |
| 2 C | 460 | 17 | 3\% | 4\% | 10\% | SegcM highest. 63 |
| 1018 | 410 | 16 | 89\% | 88\% | 77\% |  |
| 1018 | 382 | 17 | 84\% | 79\% | ${ }^{69 \%}$ | Orogen 2nd highest: 73\% |
| Half grat-nephew | 379 | 16 | 82\% | 77\% | 68\% |  |
| Half grat-nephew | 330 | 13 | 54\% | 53\% | 46\% |  |
| 2 ClR | 223 |  | 13\% | 21\% | 37\% | Ancestry simulated data: |
| Haff great-nephew | ${ }^{218}$ | 10 | 7\%\% | ${ }^{5 \%}$ | 7\% | lowest probability $68 \%$ of |
| ${ }^{20}$ | ${ }^{213}$ | ${ }^{9}$ | 78\% | 68\% | 49\% |  |
| $12^{2}$ | 183 | ${ }^{8}$ | 71\% | 53\% | 50\% | the time |
| $\begin{aligned} & \left.\quad \begin{array}{l} 30 \\ 20 \end{array}\right) \end{aligned}$ | 167 156 | 6 7 | 9\% | 9\% | 13\% |  |
| 2 C | 151 | ${ }^{9}$ | 32\% | 32\% | 24\% |  |
| ${ }^{\text {sc }}$ | 103 | 5 | 34\% | 34\% | 30\% |  |
| - $2_{2618}$ | 87 | 7 | 29.0\% | 29.0\% | 30\% |  |
| ( Average |  |  | 52\% | 51\% | 47\% |  |

Data obtained from here: https://dna-explained.com/category/cm-explainer/

## Extended family to 1st cousins, individual relationships

## SegcM highest: 50\%

Orogen 2nd highest: 90\%
Ancestry simulated data: lowest probability $68 \%$ of the time

| Actual Relationship | Total cMs | \# of Segments | SegcM Ind. Prob. | Orogen Ind. Prob. | DNA Painter Ind. Prob. | SegcM Group Prob. | Orogen Group Prob. | DNA Painter Group Prob. |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 1 C | 823 | 31 | 46\% | 28\% | 24\% | 99\% | 98\% | 96\% |
| Half niece | 744 | 25 | 26\% | 22\% | 21\% | 95\% | 91\% | 84\% |
| Half 1C1R | 522 | 17 | 1\% | 1\% | 2\% | 1\% | 1\% | 3\% |
| 1C1R | 478 | 24 | 76\% | 48\% | 45\% | 91\% | 95\% | 89\% |
| Parent's 1C | 477 | 23 | 73\% | 48\% | 45\% | 91\% | 95\% | 89\% |
| 2C | 460 | 17 | 3\% | 4\% | 5\% | 3\% | 4\% | 10\% |
| 1C1R | 410 | 16 | 47\% | 45\% | 39\% | 89\% | 88\% | 77\% |
| 1C1R | 382 | 17 | 53\% | 41\% | 35\% | 84\% | 79\% | 69\% |
| Half great-nephew | 379 | 16 | 34\% | 37\% | 34\% | 82\% | 77\% | 68\% |
| Half great-nephew | 330 | 13 | 45\% | 25\% | 23\% | 54\% | 53\% | 46\% |
| 2C1R | 223 | 8 | 13\% | 21\% | 37\% | 13\% | 21\% | 37\% |
| Half great-nephew | 218 | 10 | 7\% | 3\% | 4\% | 7\% | 5\% | 7\% |
| 2 C | 213 | 9 | 78\% | 68\% | 49\% | 78\% | 68\% | 49\% |
| 1C2R | 183 | 8 | 71\% | 53\% | 50\% | 71\% | 53\% | 50\% |
| 3C | 167 | 6 | 9\% | 9\% | 13\% | 9\% | 9\% | 13\% |
| 2C | 156 | 7 | 35\% | 35\% | 26\% | 35\% | 35\% | 26\% |
| 2C | 151 | 9 | 32\% | 32\% | 24\% | 32\% | 32\% | 24\% |
| 3C | 103 | 5 | 34\% | 34\% | 30\% | 34\% | 34\% | 30\% |
| 2C1R | 87 | 7 | 29\% | 29\% | 30\% | 29.0\% | 29.0\% | 30\% |
| Average |  |  | 37\% | 31\% | 28\% | 52\% | 51\% | 47\% |

[^0]
## A 2nd cousin pair from Roberta's dataset

Most distant common ancestor
Assuming no pedigree collapse or endogamy, and that you're related in just ne way, the furthest back you might need to go to find common ancestors for a match of 213 cM is 3rd-Great-Grandparent level or generation 6 on your pedigree chart.
The connection may be closer.
Relationship probabilities (based on stats from The DNA Geek) Slick on any relationship to view a histogram
New: View these relationships in a tree

| $49 \%$ | Half GG-Aunt / Uncle $2 C$ | Half 1C1R | $1 C 2 R$ |
| ---: | :--- | :--- | :--- | :--- |
|  | Half GG-Niece / Nephew |  |  |

https://dnapainter.com/tools/sharedcmv4

## MyHeritage predictions



Most probable relationships: Uncle/Aunt, Nephew/Niece

## Possible relationships

| Relationship | Probability | Most Recent Common Ancestor(s) |  |
| :--- | :---: | :---: | :---: |
| Uncle/Aunt | $29.2 \%$ |  | Grandparents |
| Nephew/Niece | $28.6 \%$ |  | Parents |
| Grandchild | $14.3 \%$ |  | You |
| Grandparent | $14.3 \%$ |  | Grandparent |
| Half sibling ? | $13.6 \%$ |  | Parent |

Show fewer possible relationships ^

## Comparing MyHeritage to other predictors

\(\left.\begin{array}{|l|}\hline Close Family Relationships <br>
\hline Half Sibling <br>
\hline Aunt/Uncle <br>
\hline Niece/Nephew <br>
\hline Grandparent <br>

\hline Grandchild\end{array}\right\}\)|  |
| :--- |

There are still only three major relationships

- Grandparent/Grandchild has two different perspectives for which ages matter
- Aunt/uncle/niece/nephew has two different perspectives
- Half sibling only has one perspective


## MyHeritage and SegcM for a maternal uncle



## MyHeritage and SegcM for my maternal half sibling



## MyHeritage and Ancestry for my maternal half sibling

## Most distant common ancestors

Assuming no pedigree collapse or endogamy, and that you're related in just one way, the furthest back you might need to go to find common ancestors for a match of 1932cM is Grandparent level.
The connection may be closer. Also, depending on your family, this match could be a close younger generation relative, such as the descendant of your sibling.

Relationship probabilities (based on stats from The DNA Geek) New: View these relationships in a tree
100\% Grandparent Aunt / Uncle Half Sibling
Niece / Nephew Grandchild
Shared DNA (cM)
1932

Your age

## Redacted

Optional

Match's age
Redacted
Submit

Optional

Possible relationships

99.72\%

## Population weights

| Relationship | Number (SR = 2) | Number (SR = 2.5) |  |
| :--- | :--- | :--- | :--- |
| Full Sibling | 1 | 1.5 |  |
| Aunt/Uncle | 2 | 3 |  |
| X4 <br> each <br> gen. | 1st Cousin | 4 | 7.5 |
|  | 2nd Cousin | 16 | 38 |
|  | 3rd Cousin | 64 | 190 |
|  | 4th Cousin | 256 | 940 |
|  | 5th Cousin | 1,024 | 4,700 |
|  | 6th Cousin | 4,096 | 23,000 |

## How to tell which predictors have population weights

## DNA-Sci Weighted

## DNA-Sci Unweighted

## Ancestry 2019 (Beta)

MyHeritage

- dna-sci.com

| 8 cMs at Ancestry, FTDNA, or MyHeritage |  |  |
| :---: | :---: | :---: |
| Relationship Type Pro | Probability | Group |
| 8C1R Group |  | 20.9\% |
| 8C1R, Half-8C, Half-7C2R, 7C3R | 3R 20.9\% |  |
| 8C Group |  | 16.4\% |
| 8C, 7C2R, Half-7C1R, Half-6C3R | 3R 16.4\% |  |
| 7C1R Group |  | 13.8\% |
| 7C1R, Half-7C, Half-6C2R, 6C3R | 3R 13.8\% |  |
| 7C Group |  | 13.2\% |
| 7C, 6C2R, Half-6C1R, Half-5C3R | $3 \mathrm{R} \quad 13.2 \%$ |  |
| 6C1R Group |  | 10.4\% |
| 6C1R, Half-6C, Half-5C2R, 5C3R | 3R 10.4\% |  |
| 6C Group |  | 8.1\% |
| 6C, 5C2R, Half-5C1R, Half-4C3R | C3R 8.1\% |  |
| 5C1R Group |  | 6.8\% |
| 5C1R, Half-5C, Half-4C2R, 4C3R | C3R 6.8\% |  |
| 5C Group |  | 4.8\% |
| 5C, 4C2R, Half-4C1R, Half-3C3R | R 3 - 4.8 |  |
| 4C1R Group |  | 3.1\% |
| 4C1R, Half-4C, Half-3C2R, 3C3R | 3R 3.1\% |  |
| 4C Group |  | 1.7\% |
| 4C, 3C2R, Half-3C1R, Half-2C3R | 3R 1.7\% |  |
| 3C1R Group |  | 0.7\% |
| 3C1R, Half-3C, Half-2C2R, 2C3R | 3R 0.7\% |  |
| 3C Group |  | 0.1\% |
| 3C, 2C2R, Half-2C1R, Half-1C3R | C3R 0.1\% |  |



8C1R Group
8C1R, Half-8C. Half-7C2R. 7C3R

## Most distant common ancestors

A match of 8 cM has a wide range of possible relationships. The connection may be within 8th-Great-Grandparent level, but the common ancestors could also be 20 or more generations back.

Relationship probabilities (based on stats from The DNA Geek) New: View these relationships in a tree

| 21\% | 4C Half 3C1R 3C2R |
| :---: | :---: |
| 19\% | Half 3C 3C1R Half 2C2R 2C3R |
| 17\% | 6C 6C1R 6C2R 5C1R 7C 5C2R 7C1R 4C3R 5C3R 8C or more distant |
| 17\% | 4C1R Half 3C2R 3C3R |
| 12\% | 5C 4C2R |
| 10\% | 3C Half 2C1R 2C2R Half 1C3R |
| 1\% | * GGGG Aunt / Uncle <br> Great-Great-Great-Great-Aunt / Uncle <br> Half Great-Great-Great-Aunt / Uncle 1C3R <br> 2C1R Half 1C2R Half 2C |

$0.50 \%$ * Great-Great-Great-Grandparent Great-Great-Great-Grandchild GGG Aunt / Uncle
Great-Great-Great-Aunt / Uncle
Half GG-Niece / Nephew Half GG-Aunt / Uncle Half Great-Great-Niece / Nephew
Half Great-Great-Aunt / Uncle Half Great-Great-Niece / Nephew 1C2R 2C Half 1C1R
*this set of relationships has a positive probability for 8 CM in thednageek's table of probabilities, but falls outside the bounds of the shared CM project (99th percentile)
https://dnapainter.com/tools/sharedcmv4-beta

Shared DNA (CM)
8
Your age
Optional

## Possible relationships

| Relationship | Probability |
| :---: | :---: |
| 5th cousin | 19.9\% |
| 4th cousin's child | 16.2\% |
| Parent's 4th cousin | 16.2\% |
| 6 th cousin | 12.5\% |
| 5th cousin's child | 6.2\% |
| Parent's 5th cousin | 6.2\% |
| 4th cousin's grandchild | 6.0\% |
| Grandparent's 4th cousin | 6.0\% |
| 4th cousin | 5.4\% |
| 3 rd cousin's child | 1.5\% |
| Parent's 3rd cousin | 1.5\% |
| 3 rd cousin's grandchild | 1.2\% |
| Grandparent's 3rd cousin | 1.2\% |
| Show fewer possible relationships ^ |  |
|  | ed from |

## 209 data points

| Relationship | Best Possible <br> from Groups | SegcM <br> Ind. Prob. | DNA Painter <br> Ind. Prob. | Improvement |
| :--- | :--- | :--- | :--- | :--- |
| Parent/Child | $100 \%$ | $100 \%$ | $100 \%$ | 1.0 |
| Full Sibling | $100 \%$ | $100 \%$ | $99.9 \%$ | 1.0 |
| Pat. Half Sibling | $16.6 \%$ | $43.5 \%$ | $16.5 \%$ | 2.6 |
| Mat. Half Sibling | $16.6 \%$ | $39.3 \%$ | $16.5 \%$ | 2.4 |
| Pat. Avunc. | $16.6 \%$ | $34.6 \%$ | $16.6 \%$ | 2.1 |
| Mat. Avunc. | $16.6 \%$ | $39.1 \%$ | $16.3 \%$ | 2.4 |
| Pat. Gp./Gch. | $16.6 \%$ | $95.7 \%$ | $16.6 \%$ | 5.8 |
| Mat. Gp./Gch. | $16.6 \%$ | $40.6 \%$ | $16.4 \%$ | 2.5 |
| 1st Cousin Group | $6.3 \%$ | $11.0 \%$ | $5.5 \%$ | 2.0 |
| 1st Cousin Once <br> Removed | $50 \%$ | $45.0 \%$ | $39.2 \%$ | 1.1 |

## All average individual probabilities, even for the 1C group

## 209 data points

| Relationship | Best Possible <br> from Groups | SegcM <br> Ind. Prob. | DNA Painter <br> Ind. Prob. | Improvement |
| :--- | :--- | :--- | :--- | :--- |
| Parent/Child | $100 \%$ | $100 \%$ | $100 \%$ | 1.0 |
| Full Sibling | $100 \%$ | $100 \%$ | $99.9 \%$ | 1.0 |
| Pat. Half Sibling | $16.6 \%$ | $43.5 \%$ | $16.5 \%$ | 2.6 |
| Mat. Half Sibling | $16.6 \%$ | $39.3 \%$ | $16.5 \%$ | 2.4 |
| Pat. Avunc. | $16.6 \%$ | $34.6 \%$ | $16.6 \%$ | 2.1 |
| Mat. Avunc. | $16.6 \%$ | $39.1 \%$ | $16.3 \%$ | 2.4 |
| Pat. Gp./Gch. | $16.6 \%$ | $95.7 \%$ | $16.6 \%$ | 5.8 |
| Mat. Gp./Gch. | $16.6 \%$ | $40.6 \%$ | $16.4 \%$ | 2.5 |
| 1st Cousin Group | $6.3 \%$ | $11.0 \%$ | $5.5 \%$ | 2.0 |
| 1st Cousin Once <br> Removed | $50 \%$ | $45.0 \%$ | $39.2 \%$ | 1.1 |

## All average individual probabilities, even for the 1C group

## SegcM



## References

## SegcM can be found at https://dna-sci.com/tools/segcm/

A double cousin predictor: https://dna-sci.com/tools/orogen-mult-unw/

## Ped-sim:

Caballero et al. (2019): https://doi.ord/10.1371/iournal.pgen.1007979
Using the refined genetic map of Béhrer et al. (2017): https://journals.plos.org/plosqenetics/article?id=10.1371/journal.pgen. 1007979

And the crossover interference parameters of Campbell et al. (2015):
https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1007979

Population weights from Henn et al. (2012):
https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0034267

This presentation used a template from Slidesgo: https://slidesgo.com/
and Freepik: https://www.freepik.com/

## These predictions are not the same



## 1785

or enter \%
Then any relationships that fit will stand out below
Click here for a shareable link to the cM amount above

## Most distant common ancestors

Assuming no pedigree collapse or endogamy, and that you're related in just one way, the furthest back you might need to go to find common ancestors for a match of 1785 cM is Grandparent level.
The connection may be closer. Also, depending on your family, this match could be a close younger generation relative, such as the descendant of your sibling.
Relationship probabilities (based on stats from The DNA Geek) New: View these relationships in a tree

100\% Grandparent Aunt / Uncle Half Sibling
Niece / Nephew Grandchild
~ 0\% "*Sibling
** this set of relationships is just within the threshold for 1785 cM , but has a zero probability in thednageek's table of probabilities

The prediction on the right is not better than the one on the left. $89 \%$ probability for the correct relationship is much better than $100 \%$ for six relationships (17\% per relationship)

The new relationship predictor



[^0]:    Data obtained from here: https://dna-explained.com/category/cm-explainer/

