

# **T-Model Fingerprint Calculator ©**

**Version 3.0.3**

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# Instructions for Quick Start

Print out below fingerprint data tables<sup>1</sup>. Use the data to make entries in the calculator's open fields. The open fields are highlighted in green. If less than 20 ridge features are found in the latent v. exemplar fingerprint impressions then enter "1" in the "Total Value" for each unused field.

After the values for all ridge features have been entered, e.g., quantitatively interpreted and qualitatively assessed, hit "Enter". The Likelihood Ratio and Fingerprint Match Probability values are automatically calculated.

In order to calculate the conservative, upper-bound, number of look-alikes estimated to exist in the fingerprint population, enter the "relevant fingerprint population" for the case at hand. In general, relevant fingerprint population is defined as the number of people who could have plausibly committed the crime at hand multiplied by 10.

After entering the relevant fingerprint population value, hit "Enter". The estimated number of look-alikes is automatically calculated. If the number of look-alikes is more than 1, inclusive of the latent fingerprint, then the final conclusion is "No Identification". If the number of look-alikes is less than or equal to 1, inclusive of the latent fingerprint, then the final conclusion is "Positive Identification".

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<sup>1</sup> New data tables for Ridge Feature Clarity / Ridge Reliability Grade Scale and Quality of Agreement Grade Scale presented in T-Model v. 3.0.1 are used.

# RIDGE FEATURE VALUES

## Ridge Feature Shape

Use the following data table to enter the quantitative weights for ridge feature shapes, e.g., ridge feature types:

<b>1.</b>	<b>Continuous ridge unit</b>	<b>=</b>	<b>1.15</b>
<b>2.</b>	<b>Pore</b>	<b>=</b>	<b>5</b>
<b>3.</b>	<b>Ending ridge unit in funnel</b>	<b>=</b>	<b>10.00</b>
<b>4.</b>	<b>Ending Ridge Not in funnel</b>	<b>=</b>	<b>14.25</b>
<b>5.</b>	<b>Ending/bifurcating ridge unit in funnel</b>	<b>=</b>	<b>14.375</b>
<b>6.</b>	<b>Bifurcating ridge unit in funnel</b>	<b>=</b>	<b>18.75</b>
<b>7.</b>	<b>Ending/bifurcating ridge unit not in funnel</b>	<b>=</b>	<b>20.50</b>
<b>8.</b>	<b>Bifurcating ridge unit not in funnel</b>	<b>=</b>	<b>26.75</b>
<b>9.</b>	<b>Single ridge unit (dot)</b>	<b>=</b>	<b>98</b>
<b>10.</b>	<b>Core area (1mm x 1mm)</b>	<b>=</b>	<b>209</b>
<b>11.</b>	<b>Delta (1mm x 1mm)</b>	<b>=</b>	<b>453</b>
<b>12.</b>	<b>Crease</b>	<b>=</b>	<b>634</b>
<b>13.</b>	<b>Trifurcating ridge unit</b>	<b>=</b>	<b>23,136</b>
<b>14.</b>	<b>Scar</b>	<b>=</b>	<b>26,224</b>
<b>15.</b>	<b>Other</b>	<b>=</b>	<b>23,136</b>

## **Ridge Feature Position**

Use the following data table to enter the quantitative weights for ridge feature positions, e.g., intervening ridge count to the nearest Level II neighbor:

<b>1. 0-1 intervening ridges to nearest neighbor</b>	<b>=</b>	<b>1.0</b>
<b>2. 2 intervening ridges to nearest neighbor</b>	<b>=</b>	<b>2.5</b>
<b>3. 3 intervening ridges to nearest neighbor</b>	<b>=</b>	<b>9.5</b>
<b>4. 4 intervening ridges to nearest neighbor</b>	<b>=</b>	<b>26.5</b>
<b>5. 5 intervening ridges to nearest neighbor</b>	<b>=</b>	<b>50.0</b>
<b>6. 6 intervening ridges to nearest neighbor</b>	<b>=</b>	<b>188.5</b>
<b>7. 7 intervening ridges to nearest neighbor</b>	<b>=</b>	<b>377.5</b>

## **Ridge Feature Clarity [and Reliability] and Quality of Agreement**

Use the below data tables to enter the qualitative reduction factors for ridge features bearing reduced levels of visual clarity, ridge reliability, and/or for corresponding ridge features found in the latent v. exemplar bearing reduced levels of quality of agreement:



# Ridge Feature Quality of Agreement Grade Scale - COMPARISON

Ridge Feature Type: Continuous ridge unit, ending ridge unit, bifurcating ridge unit, dot, pore, core, delta, crease, scar, etc.

Ridge Path: Feature ridge unit slants to the right, left, or not; angle of feature ridge unit is narrow, normal, wide, etc.

Spatial Relationship: Less than or equal to a friction ridge skin elasticity threshold of 20% as measured from exemplar.  
To Nearest Neighbor(s)

NOTE: 1/P denotes neutralization of ridge feature weight, e.g. a ridge feature quantitative-qualitative agreement value of 1.

Verbal Statement	Grade	Ridge Type Agrees (Connectivity)	Ridge Path Agrees (Slant/Angle)	Spatial Relationship to Nearest Neighbor(s) Agrees			Reduction Factor
				1	2	3	
<b>Excellent</b>	<b>A</b>	<b>Yes</b>	<b>Yes</b>	<b>Yes</b>	<b>Yes</b>	<b>Yes</b>	<b>1.00</b>
<b>Above Average</b>	<b>B1</b>	<b>Yes</b>	<b>Yes</b>	<b>Yes</b>	<b>Yes</b>	<b>No</b>	<b>0.75</b>
	<b>B2</b>	<b>Yes</b>	<b>No</b>	<b>Yes</b>	<b>Yes</b>	<b>Yes</b>	
<b>Average</b>	<b>C1</b>	<b>Yes</b>	<b>Yes</b>	<b>Yes</b>	<b>No</b>	<b>No</b>	<b>0.50</b>
	<b>C2</b>	<b>Yes</b>	<b>No</b>	<b>Yes</b>	<b>Yes</b>	<b>No</b>	
	<b>C3</b>	<b>No</b>	<b>Yes</b>	<b>Yes</b>	<b>Yes</b>	<b>Yes</b>	
<b>Below Average</b>	<b>D1</b>	<b>Yes</b>	<b>Yes</b>	<b>No</b>	<b>No</b>	<b>No</b>	<b>0.25</b>
	<b>D2</b>	<b>Yes</b>	<b>No</b>	<b>Yes</b>	<b>No</b>	<b>No</b>	
	<b>D3</b>	<b>No</b>	<b>No</b>	<b>Yes</b>	<b>Yes</b>	<b>Yes</b>	
	<b>D4</b>	<b>No</b>	<b>Yes</b>	<b>Yes</b>	<b>Yes</b>	<b>No</b>	
<b>Fail</b>	<b>F1</b>	<b>Yes</b>	<b>No</b>	<b>No</b>	<b>No</b>	<b>No</b>	<b>1/P</b>
	<b>F2</b>	<b>No</b>	<b>No</b>	<b>Yes</b>	<b>Yes</b>	<b>No</b>	
	<b>F3</b>	<b>No</b>	<b>Yes</b>	<b>Yes</b>	<b>No</b>	<b>No</b>	

## RELEVANT FINGERPRINT POPULATION

The following sample conservative, upper-bound fingerprint population groups are based on recent US Census Bureau estimates and AFIS database sizes and may be considered appropriate in order to calculate what is the estimated, conservative, upper-bound number of fingerprint look-alikes for the case at hand:

1. Greater San Francisco Bay Area of 18-65 year olds = 77,000,000
2. California Department of Justice Criminal AFIS Database = 100,000,000
3. State of California of 18-65 year olds = 228,000,000
4. FBI IAFIS Database = 550,000,000
5. United States of 18-65 year olds = 1,116,000,000
- 6. United States Total = 3,000,000,000 (default)<sup>2</sup>**
7. World 18-65 year olds = 24,552,000,000

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<sup>2</sup> In the event the relevant fingerprint population is unknown, for purposes of conservatism a default fingerprint population group of 3 billion, the total number of people in the United States, is recommended.

# T-Model Formulae

## Inference for identification to a Single Source

Inference of fingerprint identification to a single source is established when, first, the likelihood ratio or total quantitative-qualitative weight or value (T) is calculated for the particular aggregate arrangement of ridge formations found in agreement between two impressions. Second, the estimated number of parts (P) that the total value (T) must be raised exponentially in order to equal the value for the average flat/latent fingerprint (see the below two (2) formulae). Subsequently, if the FMP is less than the probability for 1 out of the total number of parts per fingerprint in the relevant fingerprint population, then positive identification to a single source can be inferred with an reasonable degree of scientific certainty.

## Number of Fingerprint Parts (P)

Fingerprint source attribution can be made on partial, fragmented “parts” of whole, complete fingerprints. The following formula defines the value for the number of parts “P” for any aggregate amount of matching ridge features found in two impressions:

$$T ^ P = 10 ^ {240}$$

Where,

T = T-Value or total match probability for an aggregate amount of ridge feature.

P = The number that the value (T) must be raised to equal the value for the average flat/latent fingerprint, and thereby defining the conservative number of parts in the average fingerprint a look-alike can exist.

F =  $10^{240}$  (the total weight for the average flat fingerprint)<sup>3</sup>

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<sup>3</sup> The total weight for the average flat fingerprint was defined as  $2.45 \times 10^{239}$ . For purposes of conservativeness this figure is rounded up to the nearest factor of 10 and defined as  $10^{240}$ . The log of  $10^{240}$  divided by the log of the total value (T) for the aggregate quantitative - qualitative volume of ridge formations found in agreement between a latent fingerprint impression and an exemplar establishes the numbers of parts (P) where the part represents the amount of ridge detail, for example, in a latent. P is the exponential power that T must be raised to equal the value for the average flat fingerprint (F).

# Number of Look-alikes Calculator

$$L = (P) (R)/T$$

Where,

**L = Number of Look-alikes**

**R = Relevant Fingerprint Population**

**P = The number that the value (T) must be raised to equal the value for the average flat/latent fingerprint, and thereby defining the conservative number of parts in the average fingerprint a look-alike can exist.**

**T = T-Value or total quantitative-qualitative value or weight for the particular arrangement of ridge formations in a single impression or in agreement in two impressions**

The number of look-alikes (L) present in a given fingerprint population is calculated by multiplying relevant fingerprint population (R) to the number of parts (P) divided by the T-Value (T) for the latent or pair of corresponding impressions. The above formula is used to define the number of look-alikes (L) likely to exist in a given fingerprint population.

## Inference for Positive identification

The T-Model infers positive identification based on the definition for “identification” as to mean one person, however, it should not be confused with “uniqueness” or one and only one to the exclusion of all others that exist, have existed, or will exist in the world. When deducing positive identification there often is little need to establish that a fingerprint sample is found in only one person in the entire world. Instead, source attribution is considered in the context of the case, and rarely would the entire world’s population be considered as the pool of plausible contributors of any fingerprint evidence sample. *Inference for positive identification depends on relevant population.* For purposes of accuracy, especially when dealing with small known population groups, the variable for relevant fingerprint population remains an open field to be defined based on the case at hand. In general, however, inference for positive identification is defined as follows:

If  $L > 1$ , then **No Identification**

If  $L \leq 1$ , then **Positive Identification**

Where,

L equals the estimated, conservative (lower-bound) number of fingerprint “look-alikes” in a given fingerprint population.