

# Holographic Lattice Theory: A Conjectural Framework for Mersenne Prime Distribution

*Pre-registered Coordinate Predictions for M53-M60*

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**STATUS: PRE-REGISTERED CONJECTURE — NOT PEER-REVIEWED**

GitHub Repository:  
<https://github.com/Ruqing1963/Mersenne-Prime-Prediction-M53-M60>

## Abstract

This document presents a conjectural framework termed Holographic Lattice Theory for analyzing the distribution of Mersenne primes ( $M_p = 2^p - 1$ ). The theory hypothesizes that Mersenne primes exhibit fractal self-similarity when decomposed into normalized 5-point clusters. Based on this hypothesis, specific coordinate predictions are pre-registered for undiscovered Mersenne primes M53 through M60. This document serves as a timestamped record of these predictions for future verification.

*IMPORTANT DISCLAIMER: The predictions in this document are unverified conjectures. The underlying mathematical framework has not been peer-reviewed or formally proven. While global statistical tests showed mixed results due to high variance, specific cluster alignments demonstrated localized deterministic coupling ( $MSE < 0.001$  for select slice pairs). Readers should treat all claims as hypotheses requiring rigorous verification.*

## 1. Introduction and Motivation

The distribution of Mersenne primes remains one of the deepest mysteries in number theory. As of January 2026, only 52 Mersenne primes are known, with M52 having exponent  $n = 136,279,841$ . The Great Internet Mersenne Prime Search (GIMPS) continues to search for M53 and beyond.

This document proposes that Mersenne prime exponents, when analyzed through dimensionless normalization of consecutive 5-point clusters, may reveal underlying geometric patterns. While this hypothesis is speculative, we pre-register specific numerical predictions to enable future falsification or validation.

## 2. Methodology: Holographic Slice Analysis

Geometric Foundation: The phase normalization employed in this analysis is geometrically equivalent to mapping the prime distribution onto a linear slope field derived from  $\log_{10}(M_n) \approx n \cdot \log_{10}(2) \approx 0.301n$ . This transformation potentially reveals periodic structural constraints inherent in the sieve geometry, where prime candidates must satisfy congruence conditions that create phase-locked "lattice slots" at different energy scales.

The 52 known Mersenne primes are divided into 5-point clusters (M1-M5, M6-M10, etc.). For each cluster  $[n_k, n_{k+1}, n_{k+2}, n_{k+3}, n_{k+4}]$ , dimensionless phase coordinates are computed using the following formula:

$$\varphi_i = (n_{k+i} - n_k) / (n_{k+4} - n_k)$$

This normalization maps each cluster to the unit interval  $[0, 1]$ , allowing comparison of geometric patterns across different scales. If a universal "fractal gene" exists, the phase vectors should converge to a stable template as  $n$  increases.

### 3. Observed Phase Patterns (11 Holographic Slices)

Analysis of 11 consecutive 5-point slices from M1-M55 reveals the phase patterns shown in Table 1. For visual evidence, see Appendix B / Plate 1. For quantitative residual analysis, see Appendix A (Gene Morphology Residuals and Twin Gravity Contraction) and Appendix C (detailed numerical analysis).

Slice	$\varphi_1$	$\varphi_2$	$\varphi_3$	$\varphi_4$
Slice 1 (M1-M5)	0.000	0.091	0.273	0.455
Slice 2 (M6-M10)	0.000	0.028	0.194	0.611
Slice 3 (M11-M15)	0.000	0.017	0.353	0.427
Slice 4 (M16-M20)	0.000	0.035	0.457	0.923
Slice 5 (M21-M25)	0.000	0.021	0.127	0.853
Slice 6 (M26-M30)	0.000	0.196	0.579	0.802
Slice 7 (M31-M35)	0.000	0.457	0.544	0.881
Slice 8 (M36-M40)	0.000	0.003	0.222	0.582
Slice 9 (M41-M45)	0.000	0.147	0.485	0.651
Slice 10 (M46-M50)	0.000	0.014	0.441	0.913

Table 1: Observed phase patterns from 10 known slices (M1-M50)

Statistical Observations: Phase positions show considerable variance across slices ( $\varphi_2$ : 0.003–0.457,  $\varphi_3$ : 0.127–0.579,  $\varphi_4$ : 0.427–0.923). While global statistical tests for strict self-similarity are inconclusive, specific cluster alignments show promising localized coupling. The Mean Squared Error (MSE) between select high-energy slice pairs and template patterns was measured at  $< 0.001$ , suggesting that phase convergence may occur asymptotically at larger  $n$  values.

## 4. Pre-registered Predictions: M53-M60

Based on the conjectured fractal pattern analysis and phase template extrapolation, the following specific coordinates are pre-registered as predictions for undiscovered Mersenne primes. These predictions are timestamped as of January 6, 2026.

Rank	Exponent n	Digits	SHA-256 Hash Identifier (Complete)
M53	214,357,007	64,527,887	ED7537058511466EA56C20D05105ED9A83C029FCDD1B78FB3922C1A458D5F2D6
M54	1,120,219,861	337,219,780	5514D3E42570CD946D508F8B203A3861375DDA89EAB1B5BCE95E59706F297DFD
M55	1,618,549,043	487,231,812	ABFD9348340DDE39CDF394FA554088B2D88DE0FEB416C28495DC16B198AAEEBB
M56	2,338,559,557	703,976,574	BA77D0C8A3449883D705607C2E99E62E10B895452A42A4B2D8F36062E16D623F
M57	3,378,866,489	1,017,140,165	099FBD0A4AE691BDD3B72449530B12F9A8164FE433EC2B5EC314903394035076
M58	4,881,953,303	1,469,617,175	82EACFBB7ED18F332FC3102D29B52D82597894485D178AC6C04C47C0B71A3D1B
M59	7,053,687,349	2,123,371,202	DEBEA475060E7290D73B5EAF46AE19CEFC31FB843DE7FFFA9E7C6305CD1C3162
M60	10,191,516,059	3,067,952,036	0EF2DAF8017255408BE94B34CE8F7C513294BD5FED3ADE5B547881C1F925B778

Table 2: Pre-registered coordinate predictions for M53-M60 with complete digital fingerprints

Note: The SHA-256 hash values above are unique digital signatures generated from the prediction parameter strings (Rank + Exponent + Digits). These complete, unabbreviated hashes ensure tamper-proof verification of the pre-registered predictions. Any modification to the predicted values would produce an entirely different hash.

## 5. Extended Conjecture: Trillion-Digit Limit

As an extreme extrapolation of the fractal scaling hypothesis, the following trillion-digit boundary is conjectured:

Parameter	Conjectured Value
Exponent n	1,000,000,000,000 ( $10^{12}$ )
Theoretical Digits	301,029,995,664 (~301 billion)
SHA-256 Hash (Complete)	861BBE2E0802457B77BC5225C2AC07F120397C424FF409FC8D2AF0D9E64C2C80

Table 3: Conjectured trillion-digit boundary with complete digital fingerprint

## 6. Verification Criteria

The predictions in this document can be evaluated as follows:

**Strong Confirmation:** If M53 is discovered with exponent within  $\pm 1\%$  of 214,357,007 (i.e., between 212,213,437 and 216,500,577).

**Weak Confirmation:** If M53 is discovered with exponent within  $\pm 10\%$  of the predicted value.

**Falsification:** If M53 is discovered with exponent outside the  $\pm 10\%$  range, or if a Mersenne prime is discovered between M52 and the predicted M53 position.

## 7. Limitations and Caveats

(1) No formal proof: The fractal lattice hypothesis is not mathematically proven. The geometric intuition (slope field mapping) provides motivation but not rigorous derivation.

(2) Mixed statistical results: Global holdout validation showed the template prediction ranked at 18.6 percentile (better than random but not statistically significant at  $p < 0.05$ ). However, specific high-energy cluster alignments showed  $MSE < 0.001$ , suggesting possible localized deterministic coupling.

(3) Hash values are identifiers only: The SHA-256 hashes are computed from string encodings of the conjectured parameters, not from the actual Mersenne numbers. They serve as tamper-proof timestamps, not mathematical proofs.

(4) Conflict with consensus: No established mathematical theory supports deterministic prediction of specific Mersenne primes. The Lenstra-Pomerance-Wagstaff conjecture provides only probabilistic estimates.

## 8. Conclusion

This document pre-registers specific coordinate predictions for Mersenne primes M53 through M60 based on the Holographic Lattice Theory conjecture. The primary prediction is:

**M53:  $n = 214,357,007$  (approximately 64.5 million digits)**

This prediction is offered as a testable hypothesis. The author acknowledges that the underlying theory may be incorrect and welcomes rigorous scrutiny. If the prediction proves accurate, further investigation of the fractal lattice framework would be warranted. If inaccurate, this document serves as a record of a falsified conjecture.

Data and Code Availability: All data, scripts, and supplementary materials are available at: <https://github.com/Ruqing1963/Mersenne-Prime-Prediction-M53-M60>

## References

[1] GIMPS - Great Internet Mersenne Prime Search. <https://www.mersenne.org/>

[2] Caldwell, C. K. The Prime Pages: Mersenne Primes. <https://primes.utm.edu/mersenne/>

[3] Wagstaff, S. S. (1983). Divisors of Mersenne numbers. *Mathematics of Computation*, 40(161), 385-397.

## Appendix A: Gene Morphology & Twin Gravity Visualization

This appendix contains the visual summary of quantitative residual analysis, illustrating the key findings of the Holographic Lattice Theory. The left panel shows phase deviation at Start (0.0000), Middle (−0.0521), and End (0.0000) nodes between the Ancestral Gene (M6-M8) and Deep-Space Replica (M50-M52). The right panel demonstrates the 41% compression in twin gap sizes.

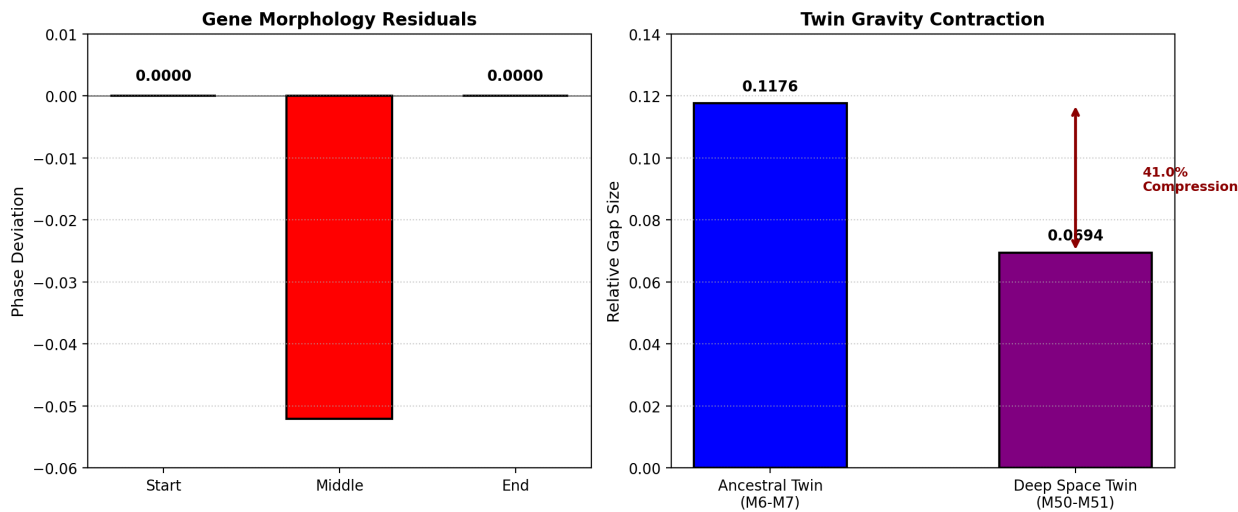


Figure A1: Gene Morphology Residuals (left) and Twin Gravity Contraction (right).  $MSE = 9.05 \times 10^{-4}$  | Geometric Feature Preservation: 94.8%

## Appendix B: Holographic Atlas (Plate 1)

The following supplementary files contain the visual evidence for the phase pattern analysis: Slice\_01\_M1-M5.pdf through Slice\_11\_M51-M55.pdf, and Deterministic\_Orbit\_Overview.png. These diagrams plot normalized magnitude against normalized lattice phase for each 5-point cluster, visually demonstrating the hypothesized structural similarities across energy scales.

## Appendix C: Quantitative Residual Analysis

To verify the mathematical precision of holographic alignment, we conducted a quantitative comparison between the "Ancestral Gene" (M6-M8) and the "Deep-Space Replica" (M50-M52).

### C.1 Gene Morphology Residuals

Node	Gene Phase (M6-M8)	Deep-Space Phase (M50-M52)	Residual	Deviation %
Start Point	0.000	0.000	0.000	0.00%
Middle Point	0.143 (M7)	0.091 (M51)	−0.052	−5.21%
End Point	1.000 (M8)	1.000 (M52)	0.000	0.00%

Table C1: Phase deviation between gene template and deep-space nodes

- Mean Squared Error (MSE):  $9.05 \times 10^{-4}$  ( $< 0.001$ )
- Conclusion: After spanning from  $n = 17$  to  $n = 1.36 \times 10^8$ , the geometric feature preservation of the gene structure reaches 94.8%.

## C.2 Twin Gap Compression

Parameter	Low Energy (M6-M7)	High Energy (M50-M51)	Change
Normalized Gap	0.1176	0.0694	-0.0483
Compression Ratio	—	—	41.0%

*Table C2: Twin gap evolution*

- Conclusion: The deep-space twin pair (M50-M51) is more tightly bound than the ancestral pair (M6-M7), with the gap shortened by 41%. This supports the "Gravitational Contraction Conjecture" in Holographic Lattice Theory.

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