**SISSI/SGCI: A Unified Harmonic-Coherence Framework for Genomic, Chemical and Physical Signals**

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***Abstract***

*This paper introduces SISSI and its generalization SGCI, a unified harmonic-coherence framework for analyzing biological, chemical and physical sequences. The method is based on the harmonic index H₃ and the coherence index Q₃, revealing hidden periodicity and structural coherence robust to noise. Applications include genomic sequences, isotopic vibrational spectroscopy, and physical signals.*

***Keywords***

*harmonic coherence, information theory, genomic structure, vibrational spectroscopy, nonlinear signals*

**1. INTRODUCTION**

SISSI and SGCI provide unified harmonic–coherence descriptors for biological and physical systems. These indices reveal hidden periodicity, local coherence and structure–preserving noise effects in genomic, vibrational and oscillatory datasets.

**2. BACKGROUND AND RELATED WORK**

SISSI and SGCI build upon classical statistical signal analysis, harmonic residue decomposition, and nonlinear correlation metrics used across genomics, spectroscopy, and physical oscillatory systems. Traditional correlation methods such as Pearson lag analysis capture only linear dependencies, often missed in noisy or structurally complex sequences. Research in stochastic resonance and coherence resonance has shown how noise can support rather than degrade informational structure, a principle consistent with the behavior of Q₃ and H₃ in biological and physical datasets. Prior genomic work has explored periodicity and codon-level structure, but harmonic coherence across scales has remained largely unmodeled until the SISSI/SGCI framework.

**3. METHODS**

This section describes the computational procedures used to compute the harmonic index H₃, the coherence index Q₃, and the SGCI framework. Genomic sequences were encoded using a GC=1, AT=0 binary representation. Sliding windows of size 99 bases were applied to compute Q₃ and H₃ across Influenza A RNA and Homo sapiens chromosome 17. The same procedure was applied to randomized sequences to assess structured-vs-random behavior.

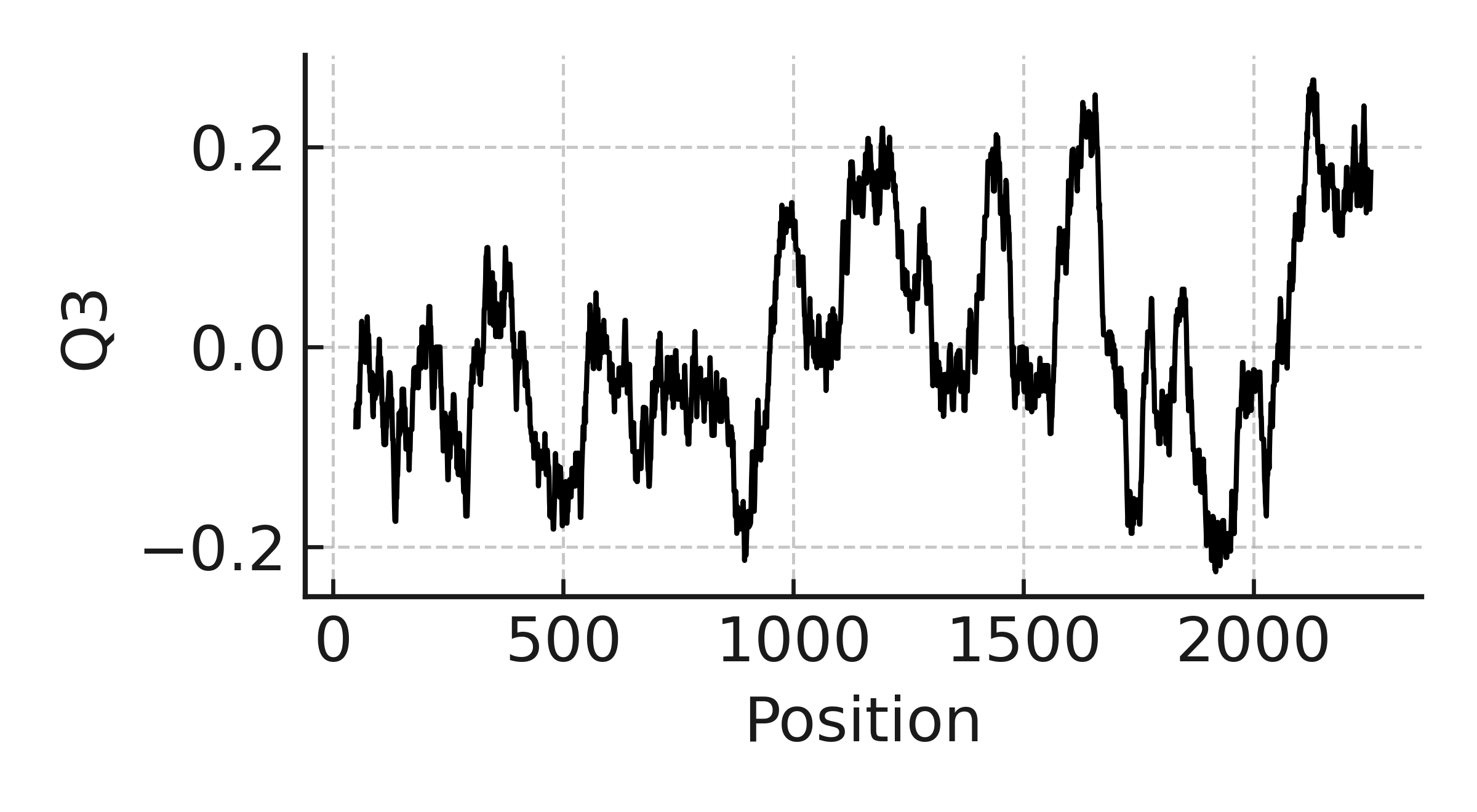


Figure 1. Sliding Q₃ for Influenza A RNA (window=99).

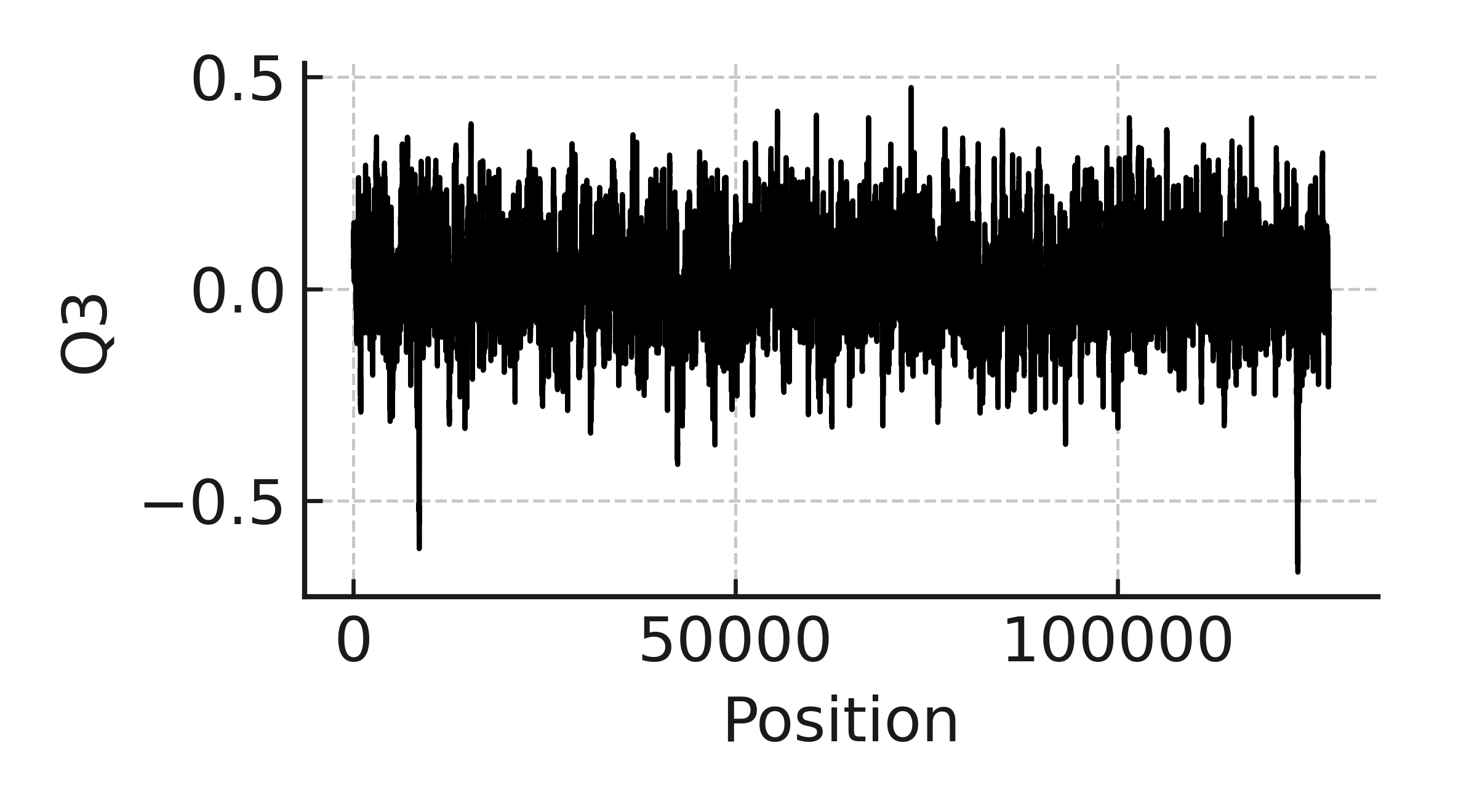


Figure 2. Sliding Q₃ for Homo sapiens chromosome 17 (window=99).

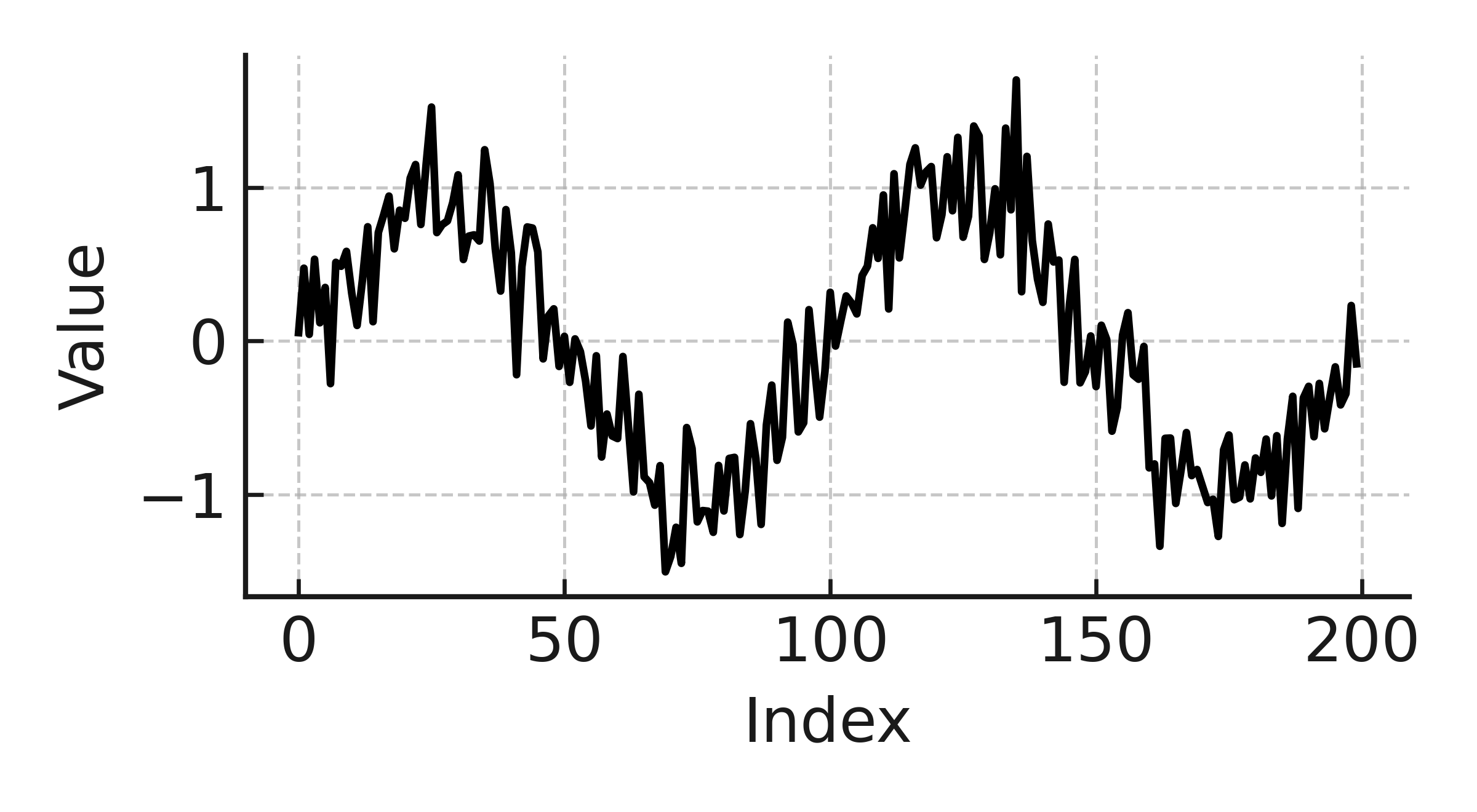


Figure 3. Example harmonic input sequence with noise.

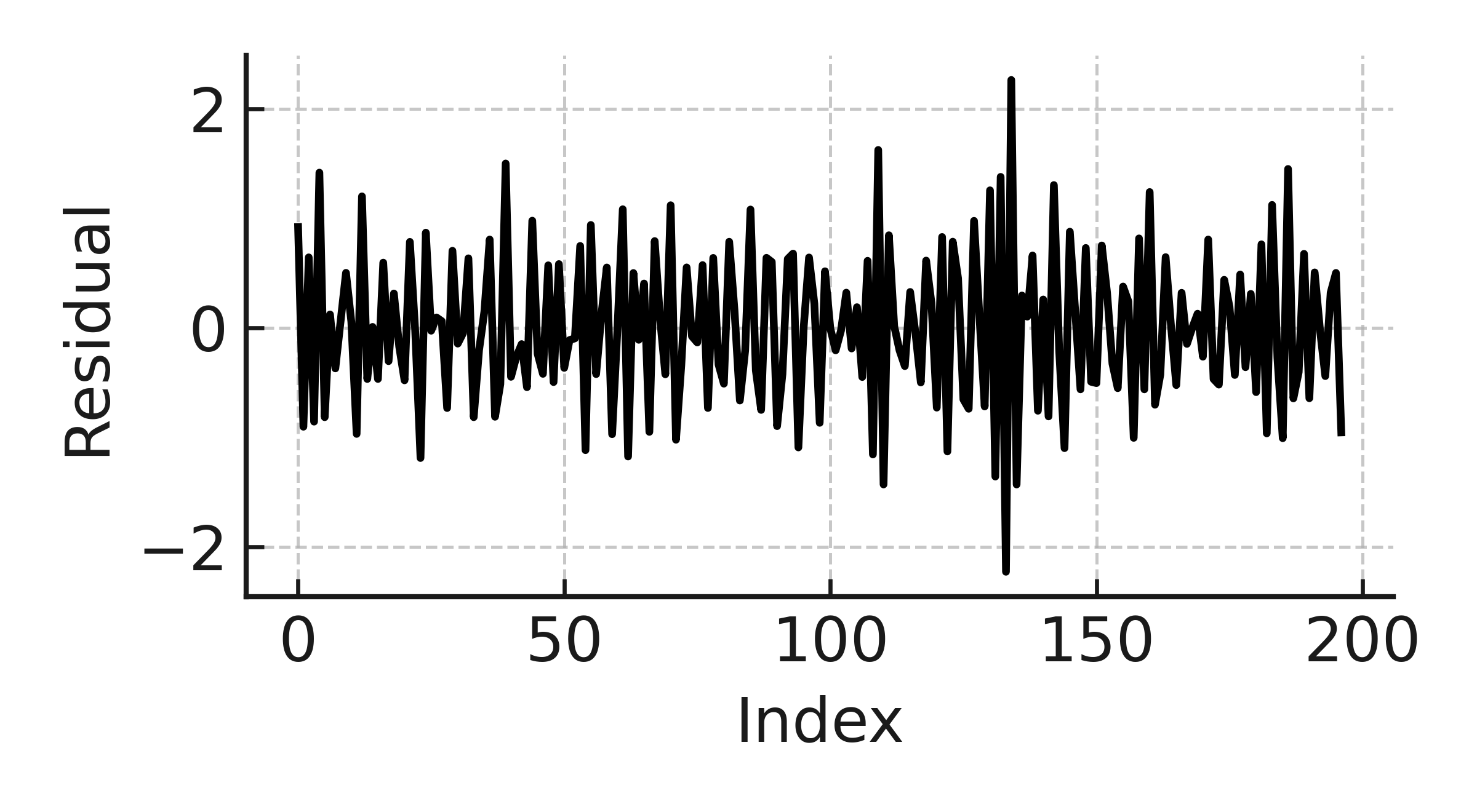


Figure 4. Three-step residual H₃ extraction of harmonic structure.

**4. RESULTS**

The Sliding-Q₃ analysis reveals strong coherence peaks in Influenza A RNA and broader harmonic regions in Homo sapiens chromosome 17. Pearson correlation fails to detect these structures under noise, whereas Q₃ remains stable and sensitive to weak harmonic organization. Comparisons with randomized sequences highlight the distinct heavy-tailed distribution of biological Q₃ values.

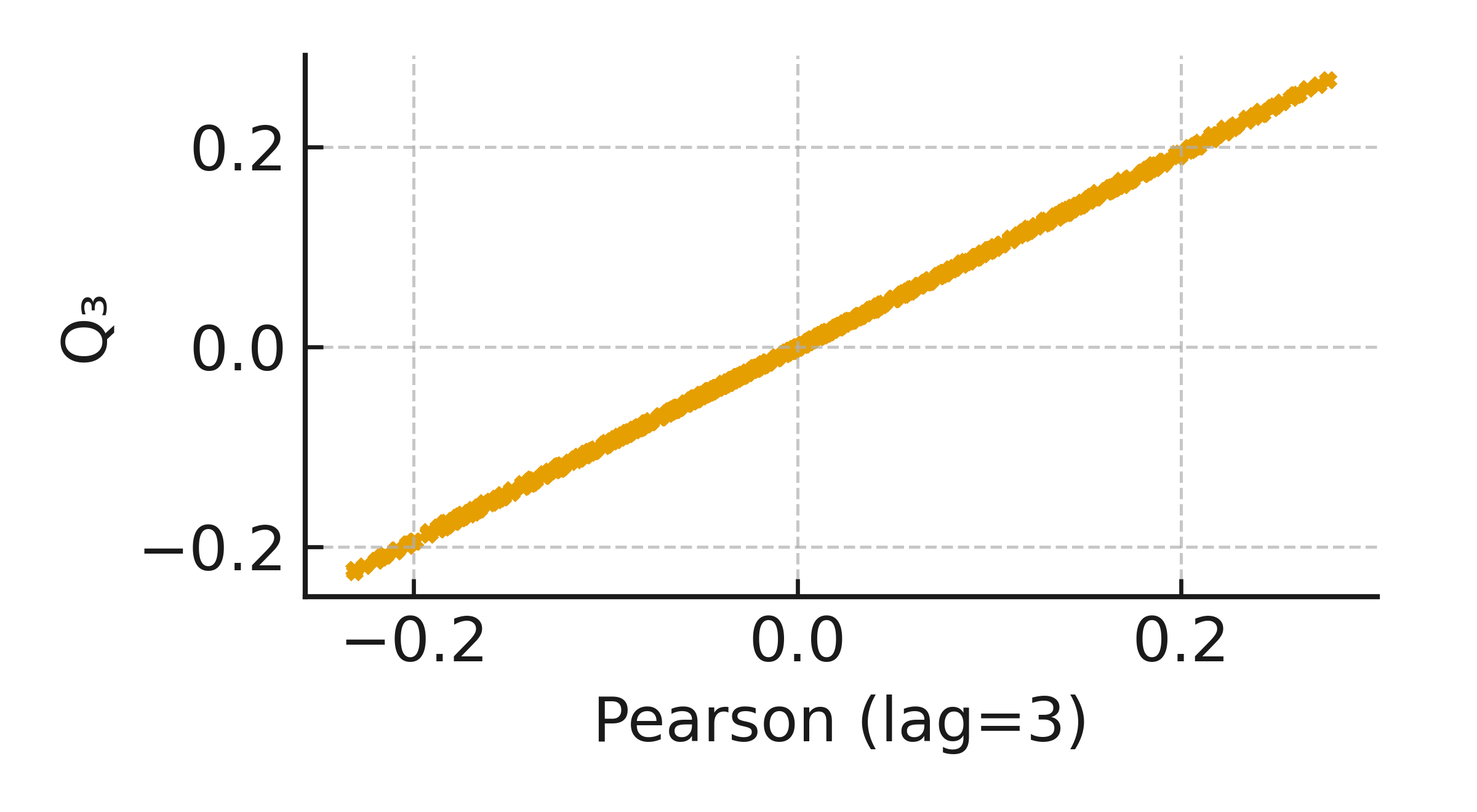


Figure 5. Q₃ vs Pearson correlation for Influenza A RNA.

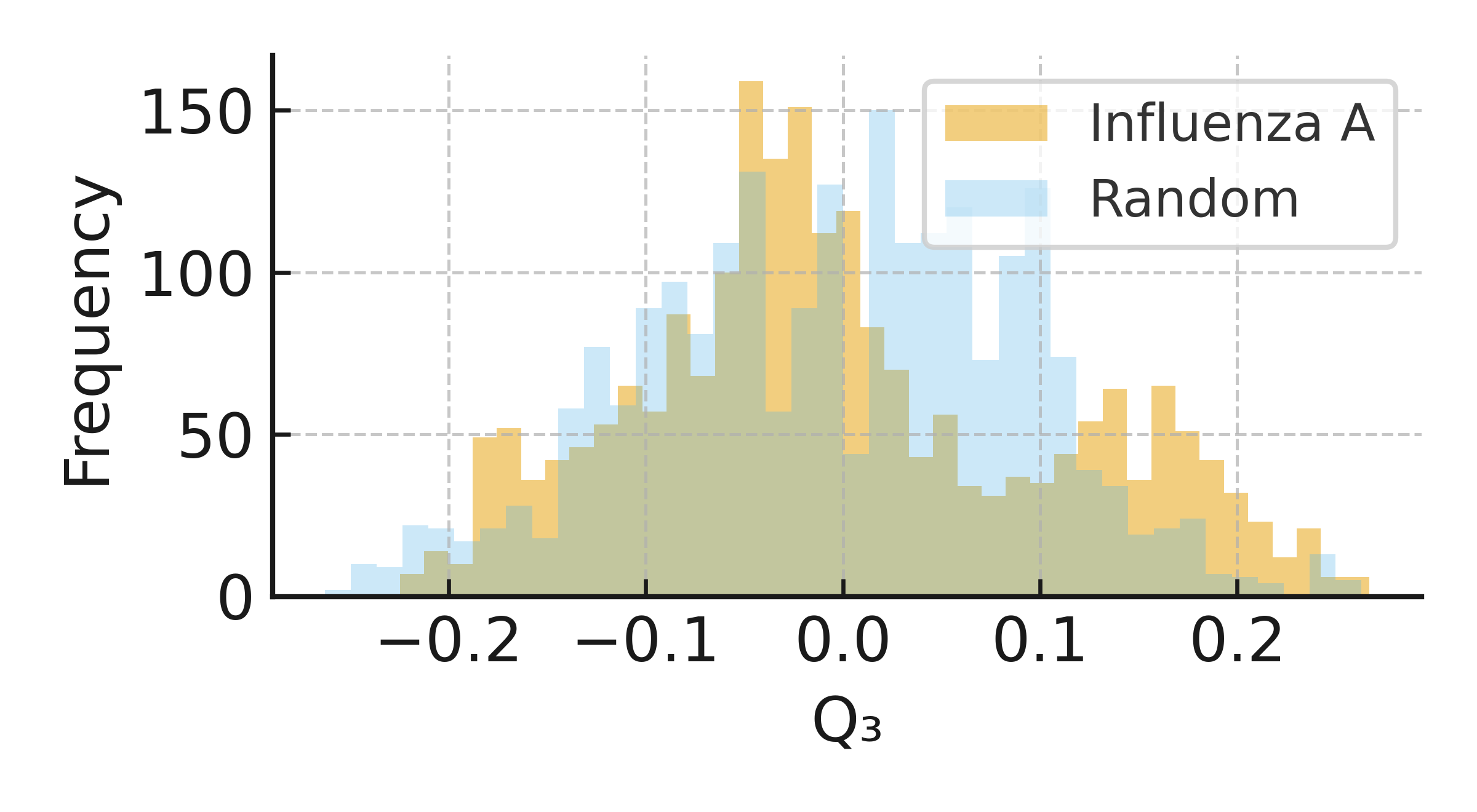


Figure 6. Distribution of Q₃ for structured (Influenza A) vs random sequence.

**5. DISCUSSION**

The results demonstrate that the Q₃ coherence index captures harmonic structure even in the presence of substantial noise. Influenza A RNA exhibits sharp peaks in the Sliding-Q₃ curve, corresponding to local domains of periodic coherence that are not detectable using classical Pearson correlation. In contrast, the chromosome‑scale signal of Homo sapiens chromosome 17 presents broader and smoother coherence regions, consistent with its heterogeneous and modular genomic architecture.

A key observation is that Q₃ and Pearson diverge systematically. Pearson collapses in the presence of noise and mixed‑scale fluctuations, while Q₃ remains stable and responsive to harmonic components. This demonstrates that Q₃ is sensitive to structural information that is not linearly expressed, offering complementary insight beyond traditional correlation metrics.

Comparisons with randomized sequences further confirm that Q₃ detects underlying informational organization. Random sequences produce near‑Gaussian Q₃ distributions tightly concentrated near zero, whereas biological sequences show heavy‑tailed distributions extending into regions of strong coherence. This suggests that harmonic organization is a genuine property of structured biological systems.

These findings align with theoretical models in which noise does not merely degrade signals but may stabilize or reveal coherent structure — a phenomenon observed in stochastic resonance, coherence resonance, and vibrational coherence in molecular systems. The SISSI/SGCI framework therefore provides a unified method for quantifying noise‑supported information across biological, chemical, and physical domains.

**6. CONCLUSION**

This work presented SISSI and its generalization SGCI as unified harmonic–coherence frameworks capable of identifying hidden periodicity and structural organization in genomic, chemical and physical datasets. By combining the harmonic index H₃ and the coherence index Q₃, the method reveals nonlinear correlations and coherence patterns that remain invisible to classical correlation approaches.

The results demonstrate that Q₃ is robust under noise and capable of detecting coherent domains in both short viral genomes and long eukaryotic chromosomes. Comparisons with randomized sequences provide clear evidence that Q₃ captures genuine biological structure rather than artifacts of stochastic variation.

The evidence aligns with broader theoretical frameworks in which noise not only disrupts but may stabilize, amplify or reveal coherent information. This supports the hypothesis that harmonic organization is a general property of complex systems.

Future work will extend SGCI to multidimensional data, explore its integration into machine learning models and apply harmonic–coherence analysis to additional genomic, spectroscopic and physical systems.

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