# Unified Charge-Oscillatory Genomics Framework: Multi-Scale Integration



HIERARCHICAL CHARGE-OSCILLATORY GENOMICS FRAMEWORK

Level 1: METABOLISM → Level 2: CHARGE SCREENING → Level 3: CHROMATIN → Level 4: TRANSCRIPTION → Level 5: SPLICING
[ATP], [Mg²⁺]                Debye Length λ_D            Accessibility          mRNA Production          Isoform Selection
[K⁺], pH                     Electric Field Φ           Nucleosome Breathing   Burst Dynamics           PKM1/PKM2 Ratio
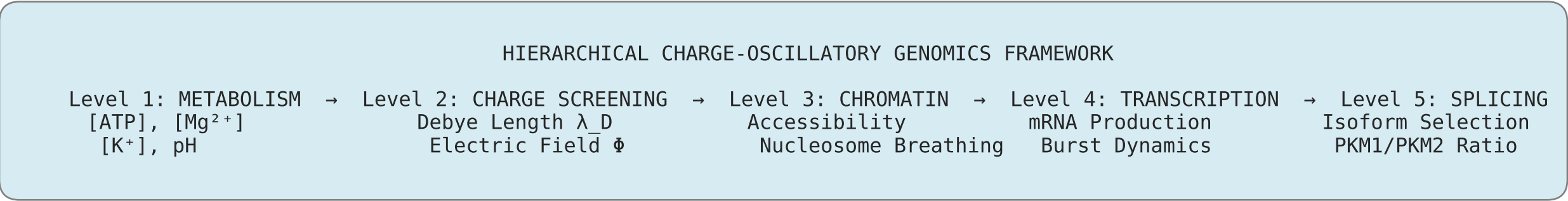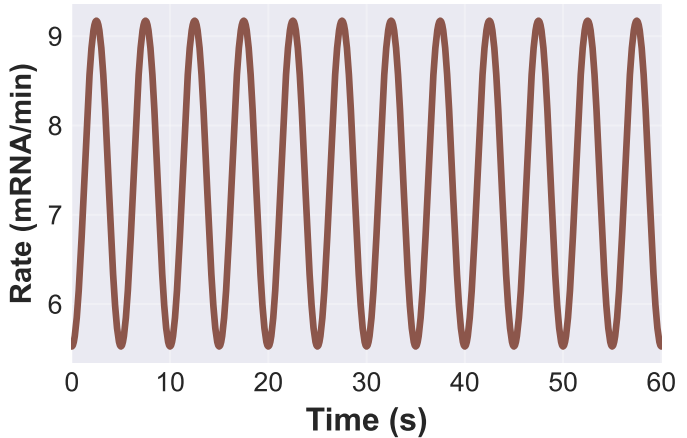
**A. Level 1: Metabolic Oscillations**
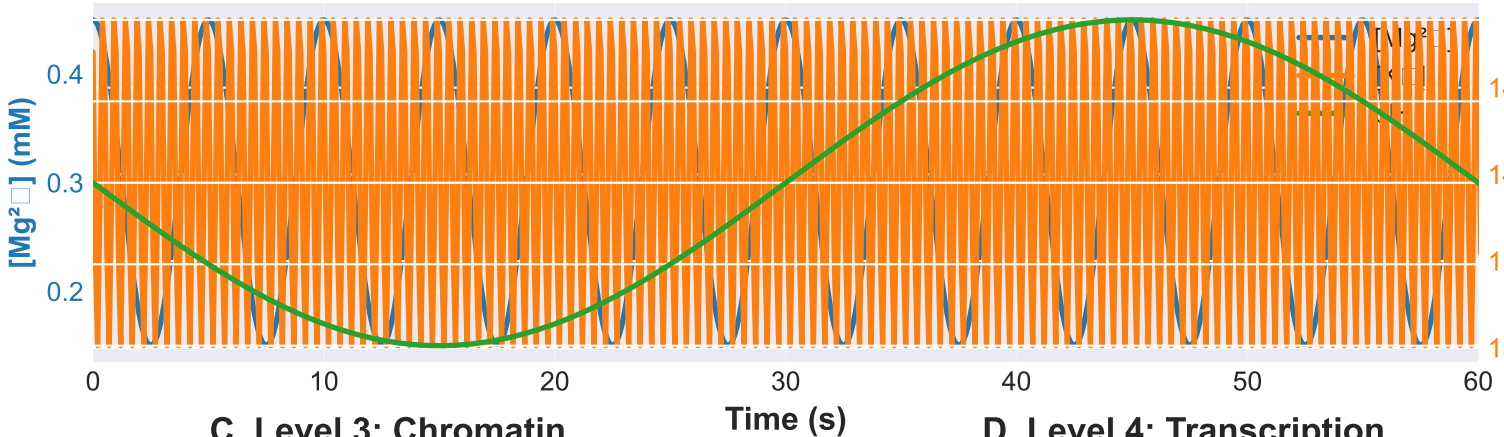
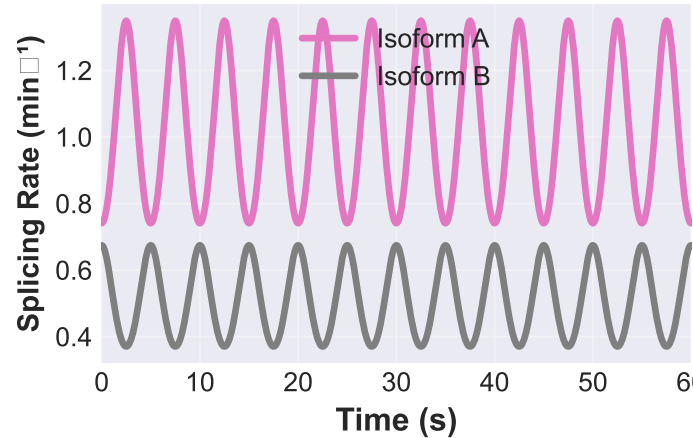**B. Level 2: Charge Screening Length**
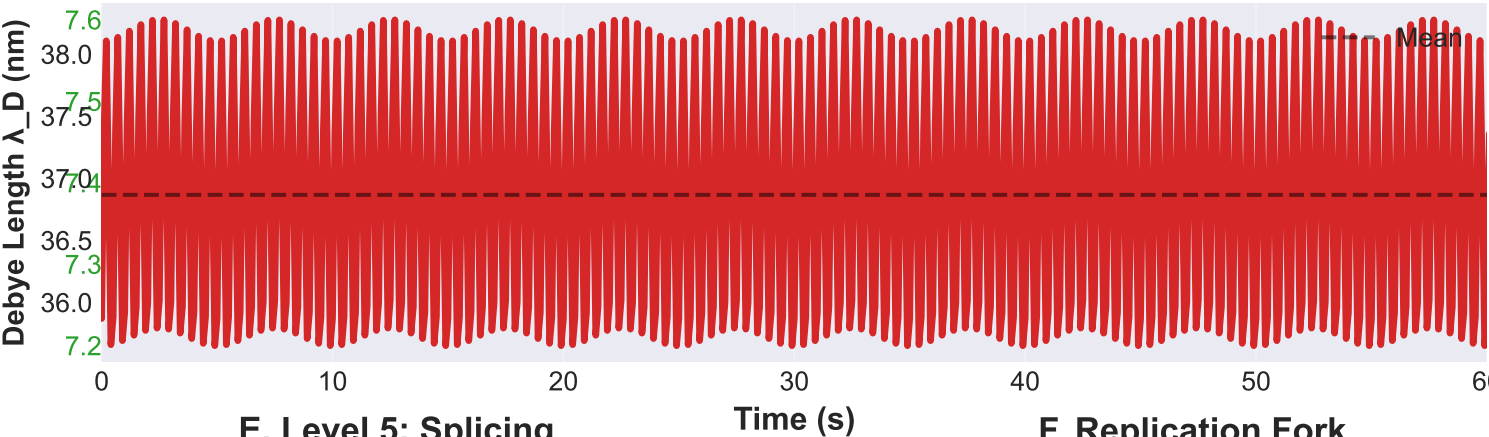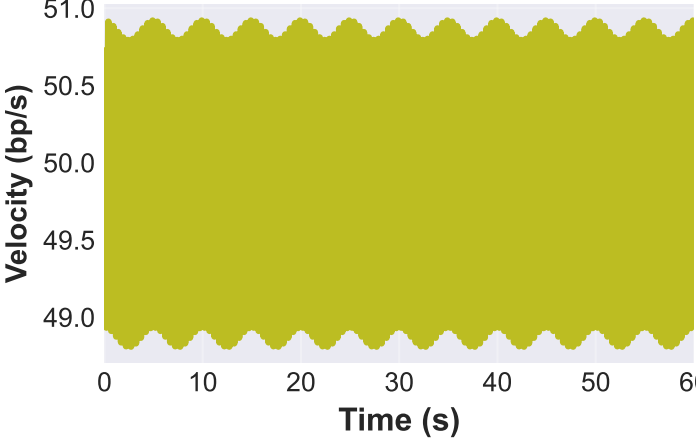
**C. Level 3: Chromatin Accessibility**
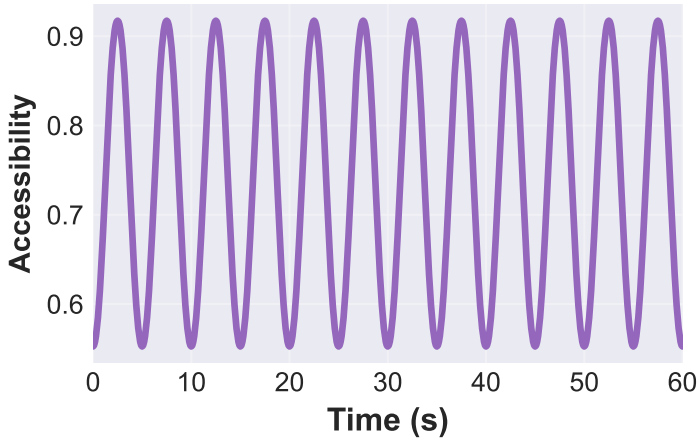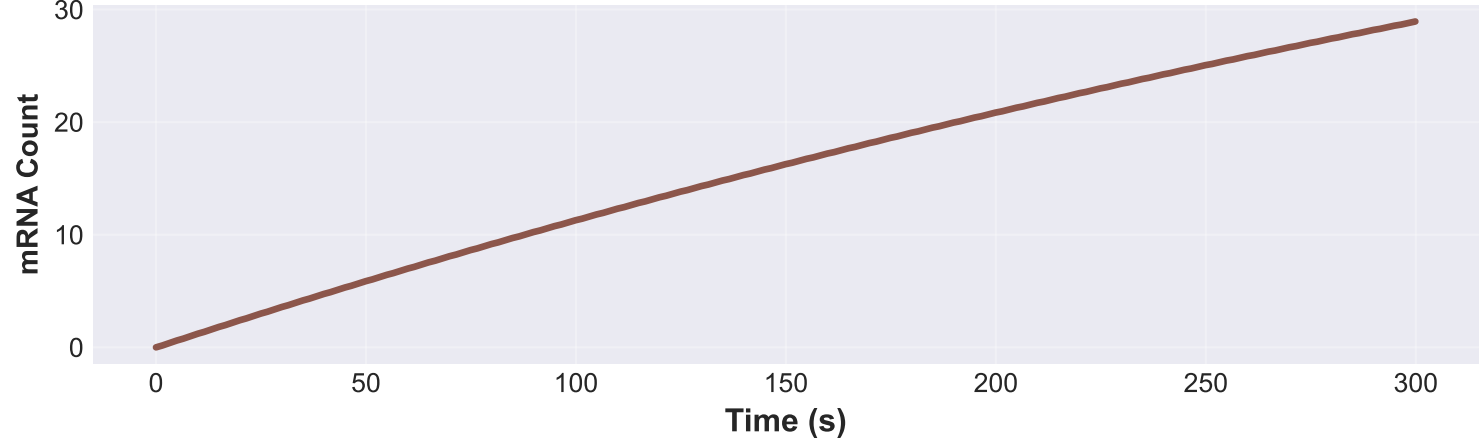
**D. Level 4: Transcription Rate**
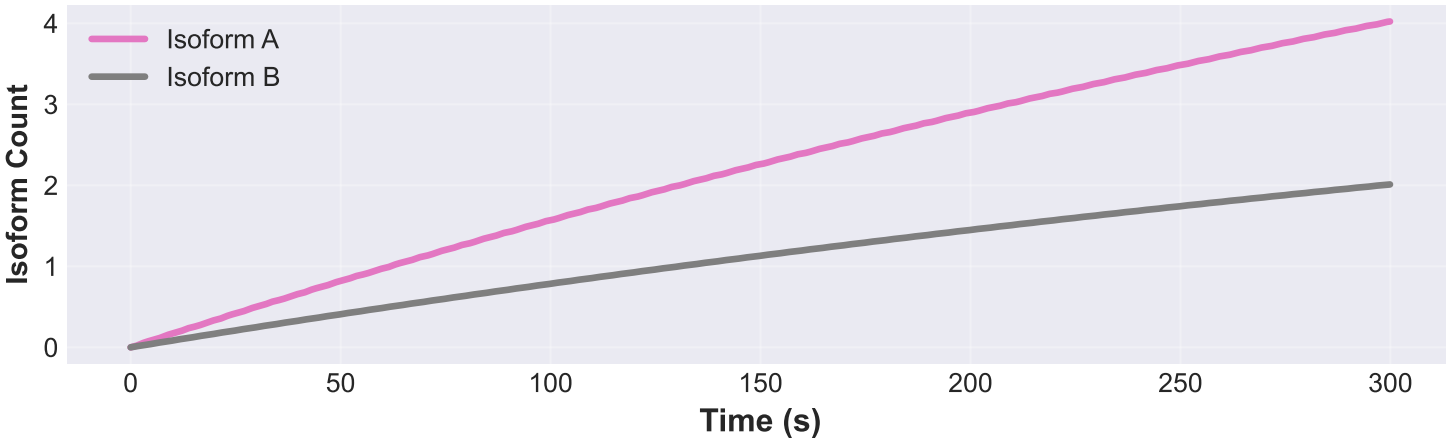
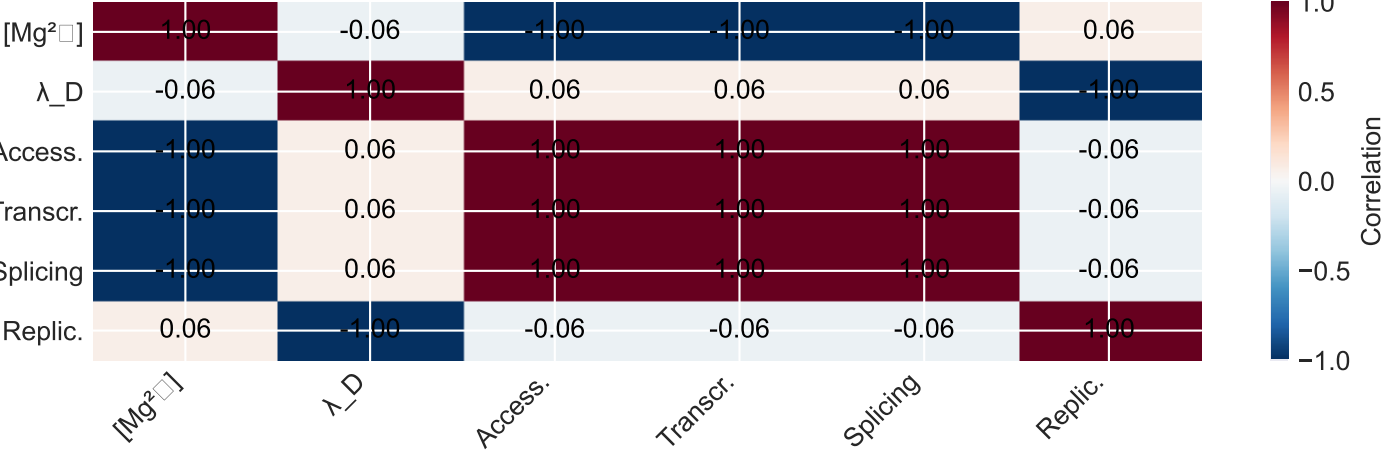**E. Level 5: Splicing Rates**

**F. Replication Fork Velocity**

**G. Total mRNA Accumulation**

**H. Isoform Dynamics**

**I. Cross-Level Correlation Matrix**

UNIFIED FRAMEWORK STATISTICS

Oscillation Amplitudes:
• [Mg²⁺]: 50.0%
• λ_D: 3.6%
• Accessibility: 24.8%
• Transcription: 24.8%
• Splicing A: 29.8%

Key Correlations:
• [Mg²⁺] vs λ_D: r = -0.060
• λ_D vs Access.: r = 0.060
• Access. vs Transcr.: r = 1.000
• [Mg²⁺] vs Splicing: r = -0.997

Mean Values:
• [Mg²⁺]: 0.300 mM
• λ_D: 36.867 nm
• Accessibility: 0.736
• Transcription: 7.36 mRNA/min
• Replication: 49.9 bp/s

Dominant Frequencies:
• ATP synthesis: ~5 s
• Na⁺/K⁺-ATPase: ~0.5 s
• Glycolysis: ~60 s

Integration:
All genomic processes coupled through
charge-dependent electrostatic interactions