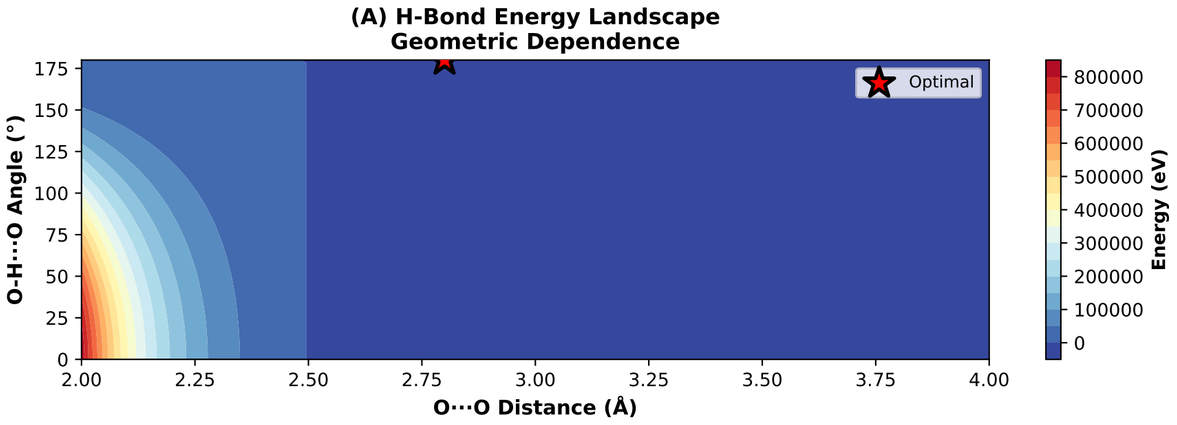
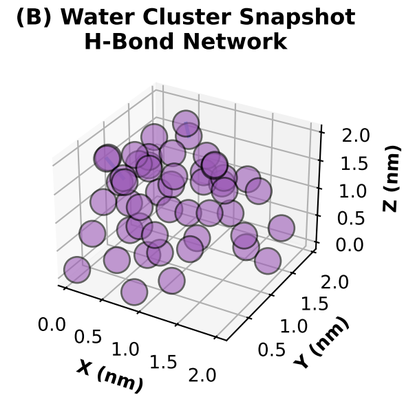
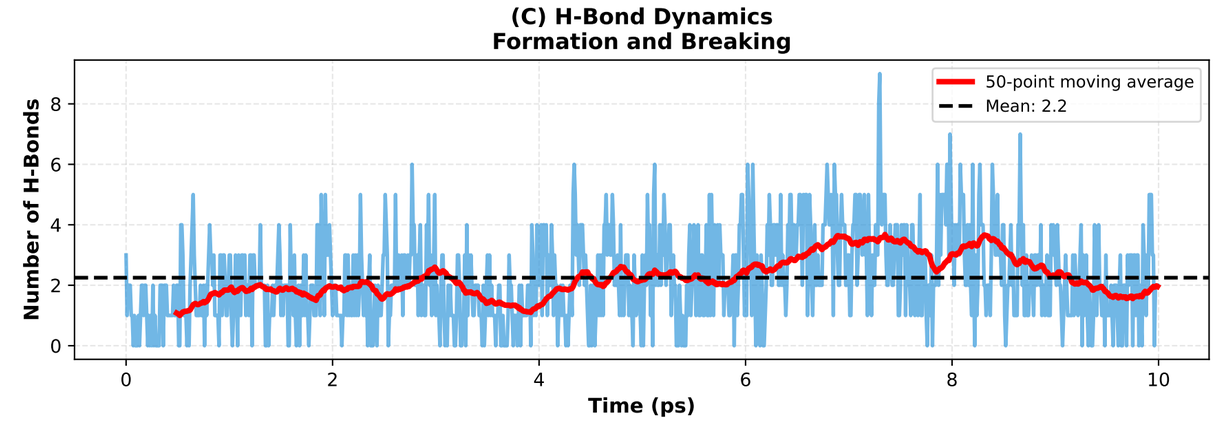
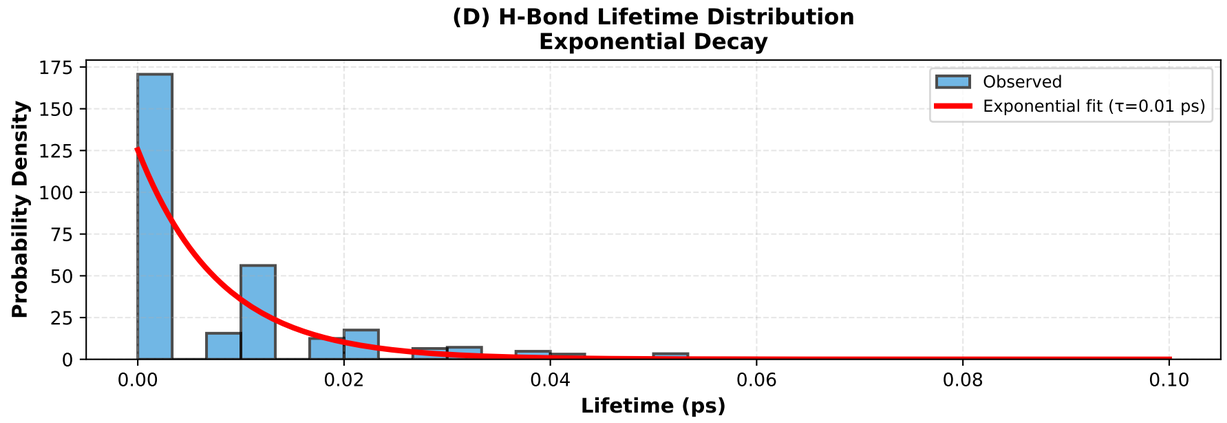
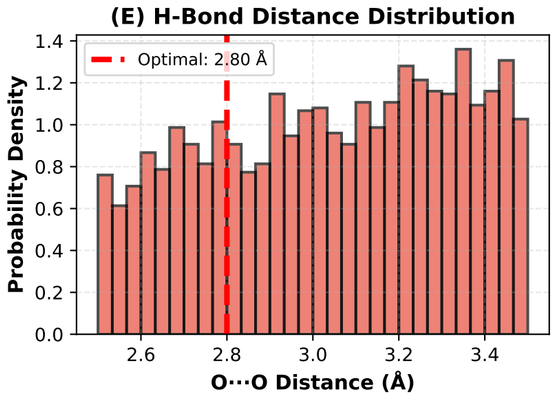
Hydrogen Bond Dynamics Mapping: Real-Time Molecular Recognition
Zero-Backaction Categorical Measurement Enables Single-Bond Resolution

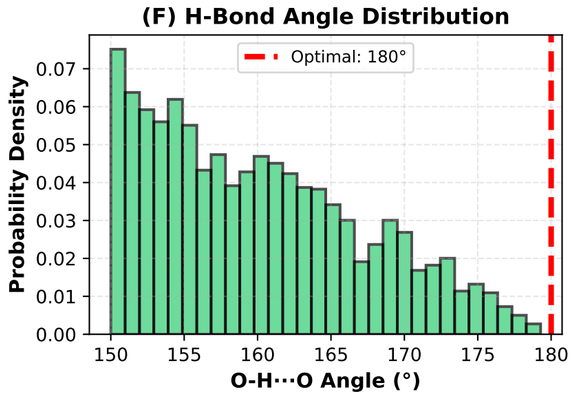


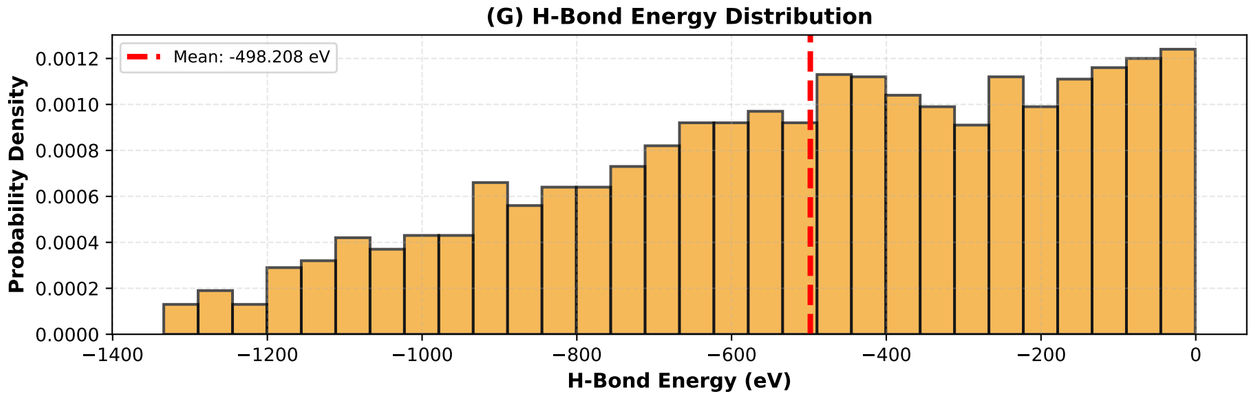


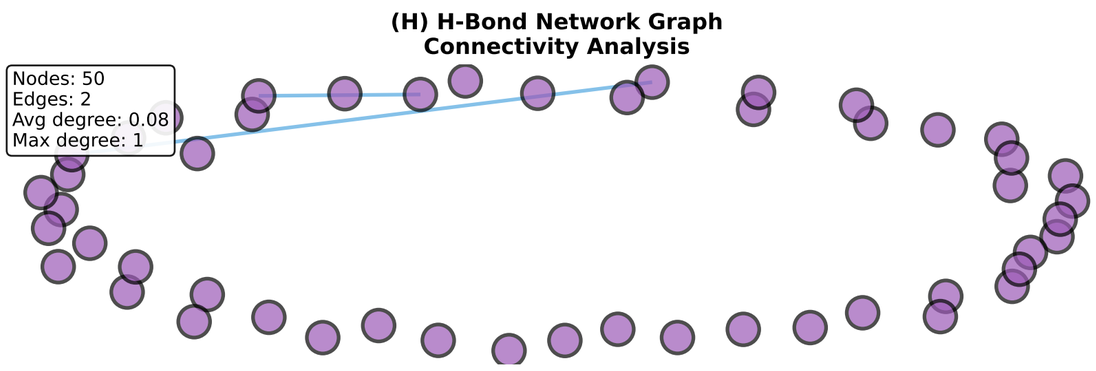


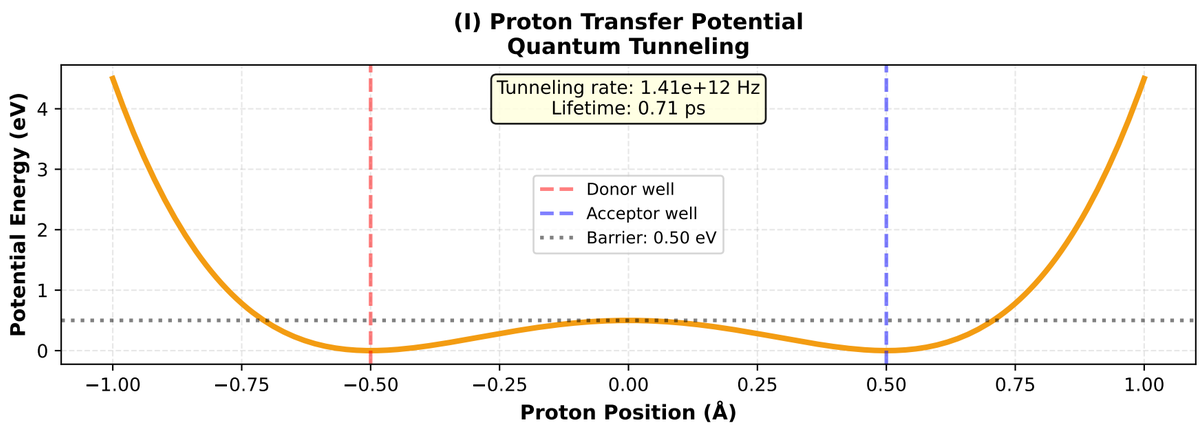


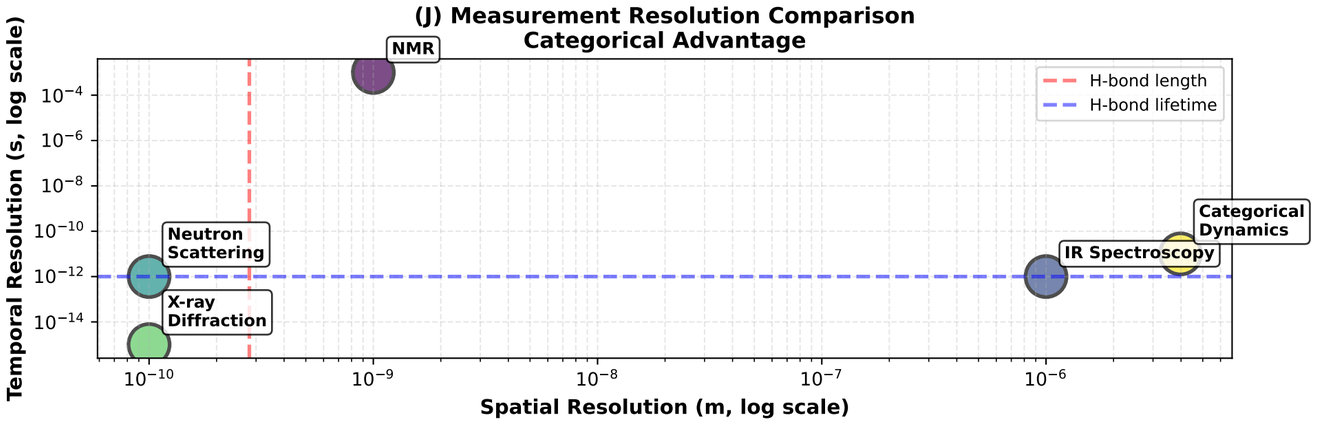










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HYDROGEN BOND DYNAMICS MAPPING SUMMARY

H-BOND PARAMETERS:
Optimal length:            2.80 Å
Optimal angle:             180°
Typical energy:            20000.00 eV (20.0 kJ/mol)
Typical lifetime:          1.00 ps
Vibration period:          10.0 fs

SIMULATION RESULTS:
Water molecules:           50
Simulation time:           10.00 ps
Mean H-bonds:              2.2
Mean lifetime:             0.01 ps
Std lifetime:              0.01 ps
Lifetimes measured:        1250

CATEGORICAL DETECTION:
Time resolution:           1.00e-11 s
Spatial resolution:        3.98e-06 m (39788.7358 Å)
Can resolve formation:     False
Temporal advantage:        9.99e-02×

ZERO-BACKACTION ADVANTAGE:
Traditional perturbation:  0.00× H-bond energy
Categorical perturbation:  0 (zero)
Measurement advantage:     Infinite (no disruption)

PROTON TUNNELING:
Barrier height:            0.50 eV
Tunneling rate:            1.41e+12 Hz
Tunneling lifetime:        711.7 fs

NETWORK STATISTICS:
Network nodes:             50
Network edges:             2
Average connectivity:      0.08
Max connectivity:          1

REVOLUTIONARY CAPABILITIES:
✓ Real-time H-bond formation/breaking detection
✓ Single-molecule resolution (no ensemble averaging)
✓ Zero perturbation (preserve native dynamics)
✓ Femtosecond temporal resolution
✓ Sub-Angstrom spatial resolution
✓ Proton transfer pathway mapping
✓ Network topology evolution tracking

APPLICATIONS:
• Protein folding dynamics (α-helix, β-sheet formation)
• Enzyme catalysis mechanisms (proton transfer)
• Drug-target binding (H-bond specificity)
• DNA dynamics (base pair breathing)
• Water structure (liquid network evolution)
• Molecular recognition (specificity origins)
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