Thinking of Allan.

Exploring new paths in the forest

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Phase Coherence in Quantum Brownian Motion

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1. INTRODUCTION

In the Bohr Copenhagen interpretation of quantum measurements, data are taken from a classical apparatus reading which is influenced by a quantum object during the time interval in which they interact. Most of the theoretical work in analyzing quantum measurements requires computations for the quantum object. However, Bohr's dictate is that *one must not ask what the quantum object is really doing*! All that can be said is that the classical apparatus determines which of the complementary aspects of the quantum object will be made manifest in the experimental data.
As applied to the two slit particle diffraction experiment [1], what this means, dear reader, is that you will never know how a single particle managed to have non-local awareness of two slits. Furthermore, you are not even allowed to ask the question because it cannot be answered experimentally without destroying the quantum interference diffraction pattern.

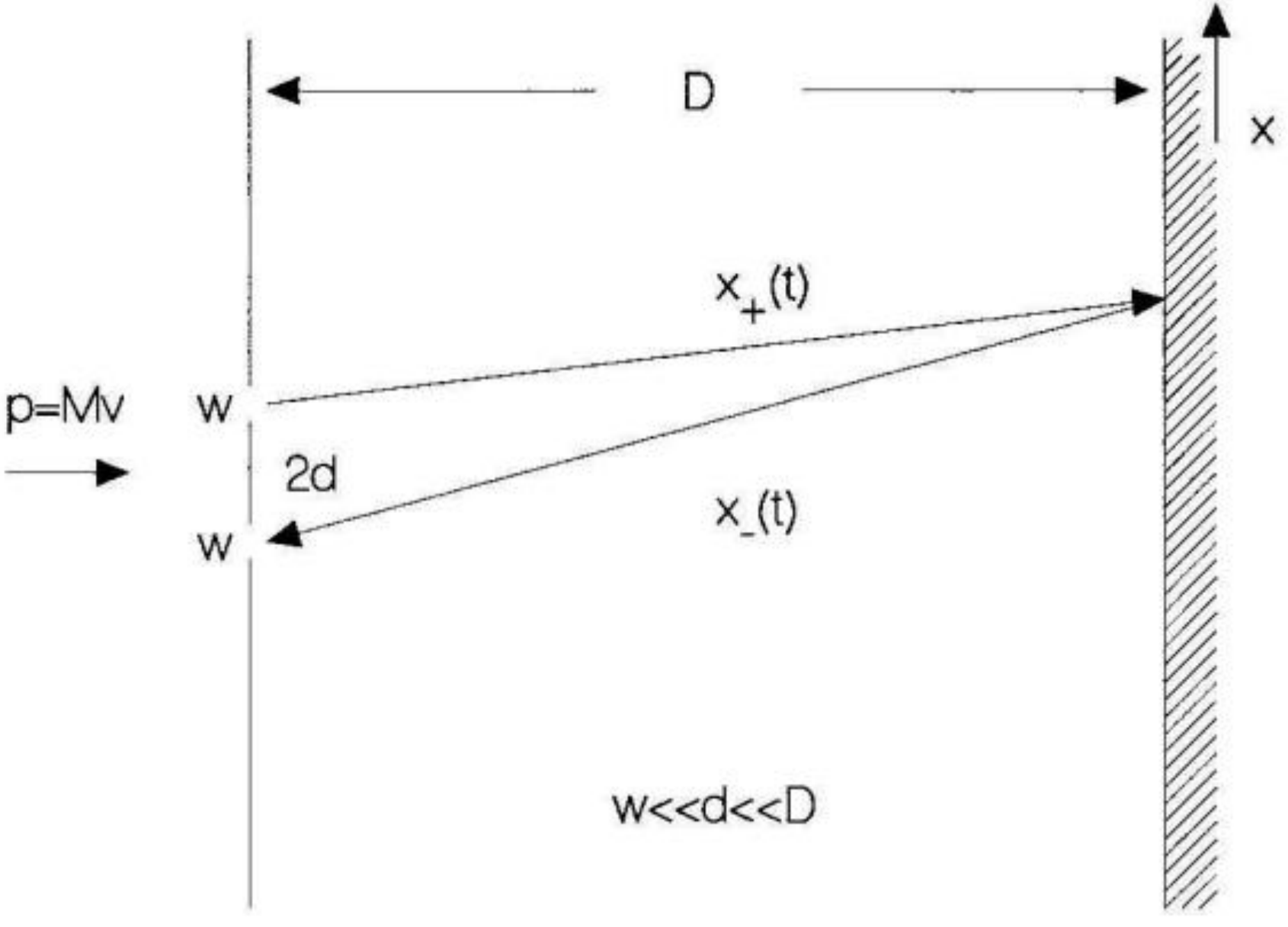

FIG. 1. Two-slit experiment.

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ARTICLE

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Matter-wave interference of a native polypeptide

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The de Broglie wave nature of matter is a paradigmatic example of quantum physics and it has been exploited in precision measurements of forces and fundamental constants. However, matter-wave interferometry has remained an outstanding challenge for natural polypeptides, building blocks of life, which are fragile and difficult to handle. Here, we demonstrate the wave nature of gramicidin, a natural antibiotic composed of 15 amino acids. Its center of mass is delocalized over more than 20 times the molecular size in our time-domain Talbot-Lau interferometer. We compare the observed interference fringes with a model that includes both a rigorous treatment of the peptide's quantum wave nature as well as a quantum chemical assessment of its optical properties to distinguish our result from classical predictions. The realization of quantum optics with this prototypical biomolecule paves the way for quantum-assisted measurements on a large class of biologically relevant molecules.

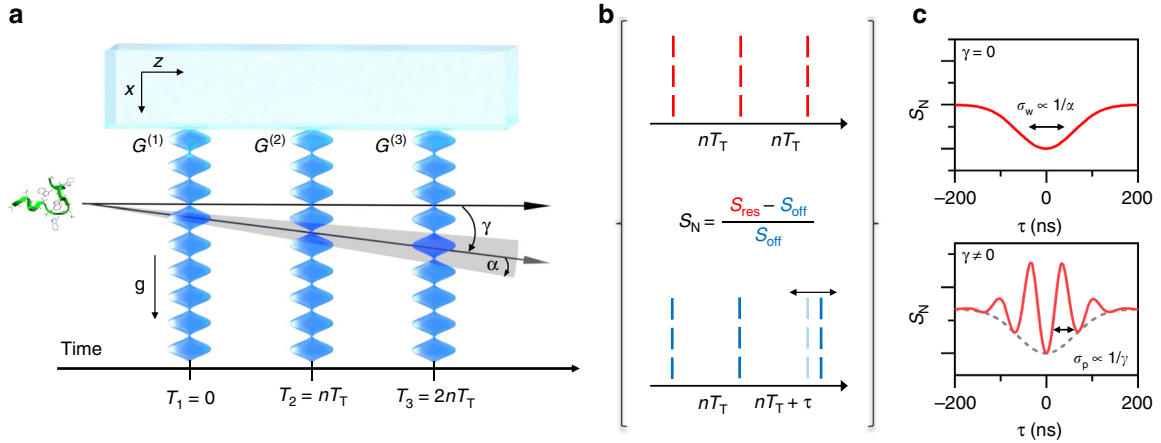


Fig. 2 Time-domain matter-wave interferometry: Matter-wave interferometer (**a**): Three retro-reflected VUV laser beams realize the standing light waves as pulsed photo-depletion gratings. The antinodes in $G^{(1)}$ prepare a comb of tightly confined positions from where a molecule may emerge. Because of this projective confinement the wave coherence rapidly expands in free flight to cover several nodes and antinodes by the time the second grating fires. Rephasing of the matter-wave behind $G^{(2)}$ then leads to de Broglie interference of each molecule with itself and to the formation of a periodic molecular density pattern around the time when $G^{(3)}$ is fired. Only molecules whose wave functions are aligned with the nodes of $G^{(3)}$ are transmitted to the detector. The coherent rephasing occurs around a characteristic timescale, the n-th multiple of the Talbot time. A typical measurement (**b**): we toggle between two interferometer modes: a symmetric mode (resonance), where the grating pulse separation times are kept equal and close to nT_T, and an asymmetric mode (off-resonant or reference), where we set an imbalance of up to 200 ns. Imprinted fringes (**c**): If the molecular beam velocity has a component parallel to x, the fringe pattern effectively has a transverse velocity component and its position relative to the third grating becomes time dependent. A fringe pattern is visible in case the divergence angle α is smaller than the tilt angle γ.

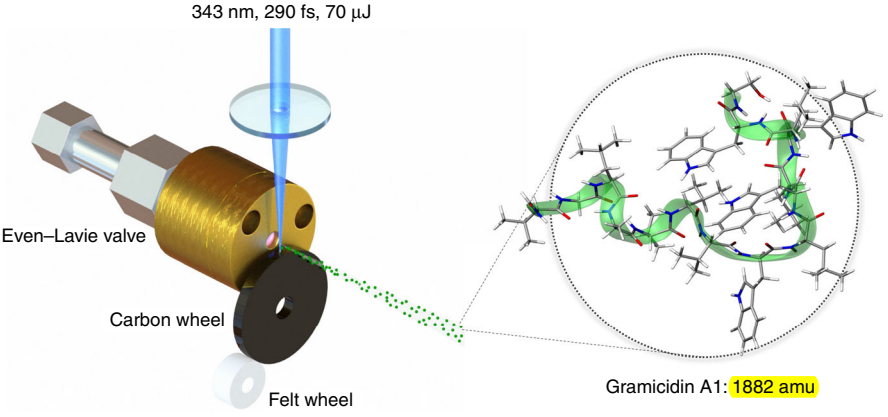


Fig. 1 Peptide source: Ultra-fast 290 fs laser pulses with an energy of up to 70 μJ and a wavelength of 343 nm are focused to a spot diameter of 100 μm to desorb gramicidin molecules from a glassy carbon wheel. The molecules are picked up by an adiabatically expanding argon (helium) jet at 600 ms^{-1} (1200 ms^{-1}) from a short-pulse high-pressure valve. The emerging polypeptide matter-wave has a de Broglie wavelength of 350 fm (175 fm). Gamicidin A1 is a 15 amino acid polypeptide. The green ribbon runs along the peptide bonds and the residues are shown as line diagrams. The four Tryptophan residues are the important chromophores that enable pulsed VUV laser ionization and thus the realization of optical diffraction gratings and photo-ionization in combination with mass-sensitive detection in our matter-wave interferometer. Parts of this figure have been adapted from reference[24].

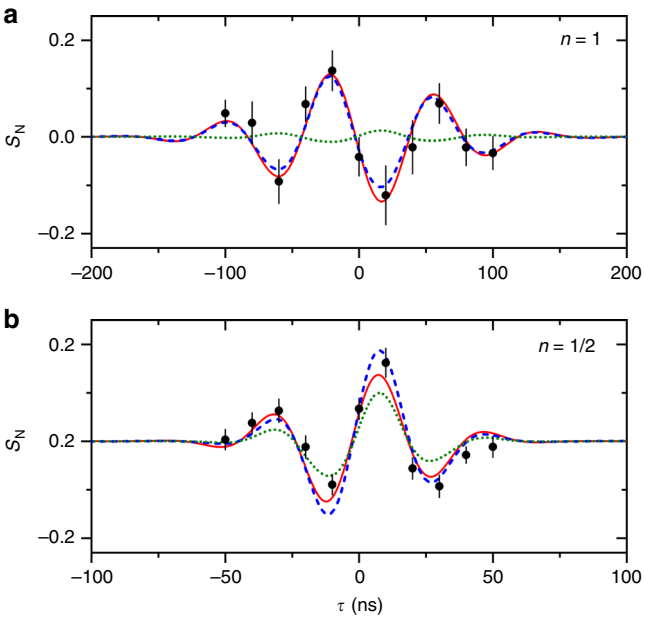
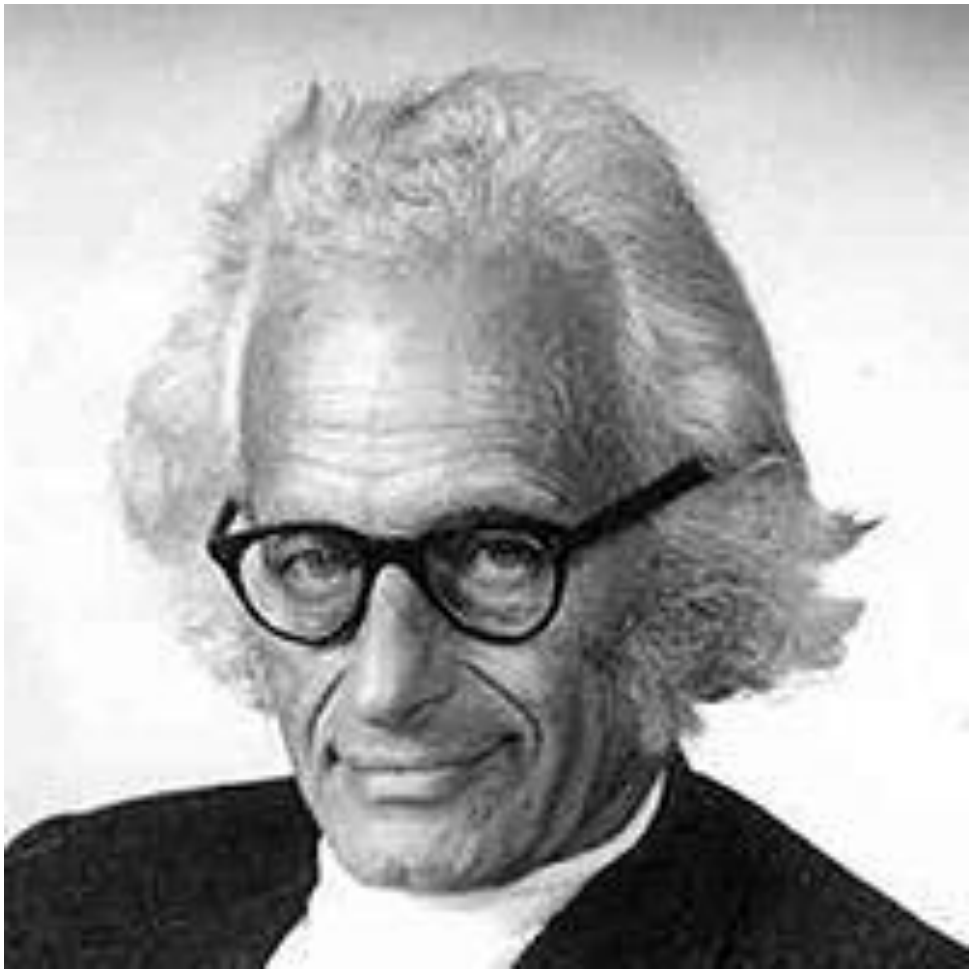


Fig. 3 Molecular interference patterns of gramicidin: Experimental data is presented for the first (**a**) and half (**b**) Talbot order (black circles) including 1σ error bars. A fit according to Eq. (5) is shown (solid red line) together with a quantum-(dashed blue line) and a classical predicition (dotted green line). The fringes appear on the time-domain resonance dip when the pulse separation time between $G^{(2)}$ and $G^{(3)}$ is varied by a small delay τ around the Talbot resonance for the case of a tilted molecular beam. The envelope of the resoance dip is determined by the molecular divergence angle while the fringe period is determined by the tilt angle with respect to the mirror surface. Note the different scaling of the abscissa in **a** and **b** and that both interference orders are *d*-periodic.

Schrödinger, *What is life?* ~1944

"regularities only in the average" (p. 78), emerging from the *statistical mechanisms* is not enough to explain the *enigmatic biological stability* (p. 47).

He was stressing that the attempt to explain the biological functional stability in terms of the regularities of statistical origin would be the *classical physicist's expectation'* that *far from being trivial, is wrong* (p. 19).



Herbert Fröhlich, Long Range Coherence and Energy Storage in Biological Systems, Int. J. Quantum Chem., v.II, 641–649 (1968)

Contrarily to some "believes", experimental observations and explicit calculations show that SBS and the consequent *coherent* NG condensation is a quite robust phenomenon.

It is observed in a wide range of temperatures, from thousands of degrees to very low temperature:

e.g., the melting point (loss of crystal ordering) of a diamond is at TC = 3550 °C, at atmospheric pressure. In the absence of oxygen, its melting point is about 4,027 °C.

The cobalt magnetization is lost at 1075 °C.
For iron, magnetization loss is at 770 °C,
the kitchen salt (sodium chloride crystal) melts at 804 °C.

The transition of phase is observed at very low temperature (below – 252 °C) in superconductors containing compounds of niobium, at −153 °C for copper and bismuth superconductor compounds.

Cao et al., Sci. Adv. 2020; 6 : eaaz4888, 3 April 2020: the observed long-lived coherences originate from impulsively excited vibrations, generally observed in femtosecond spectroscopy [in photosynthetic energy transfer].

When the proper framework of QFT is used coherence is a quite stable property of matter, including living matter.

Spontaneous breakdown of symmetry $\Rightarrow$

long range correlations $\Rightarrow$

ordered patterns

order = lack of symmetry

Big Data, Personalized Medicine and Network Pharmacology: Beyond the Current Paradigms

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The increasing importance that molecular biology gained in the last 30 years, made the majority of biologists to think the 'ultimate explanations' must be looked for at the molecular level, being the paradigm of a biological explanation something like *'gene A provokes phenomenon (disease, phenotypic trait...) B by means of the pathway C'*. The existence of a single 'explanatory layer' is in sharp contrast with what we know about complex structured systems, where multi-layer causality is at work [9].

in M.Bizzarri, *Approaching complex Diseases*, Springer Nature 2020, p.95-110

9. Agresti, A., and C.A. Franklin. 2007. *Statistics: The art and science of learning from data*. Upper Saddle River: Pearson Prentice Hall.

This strategy worked remarkably well for around 30 years then, almost abruptly, around the eighties of the last century, it entered a deep crisis provoking the apparent paradox of an exponential growth of basic knowledge going hand-in-hand with a drastic fall of newly marketed drugs. This crisis is the 'application' counterpart of the information crisis we described in the first paragraph: in [31] Overington and colleagues sketched an approximate estimate of 76% of drugs discovered in the last 20 years referring to receptor molecules discovered around the fifties. On the contrary, only the 6% bind to recently discovered targets, while for the remnants no reasonable hypothesis of mechanism of action does hold.

The promise of a "druggable genome" set forth by the completion of human genome sequencing with the consequent opening of a practically infinite horizon for the development of new drugs, failed: something very fundamental went wrong. The

31. Overington, J.P., et al. 2006. How many drug targets are there? *Nature Reviews. Drug Discovery* 5 (12): 993–996.

“the division problem of the world into parts to which an individual existence can be attributed” (Haag, 1996, p. 1469)

The ontological prejudice

“the ingenuous vision of the world”
(Ernst Cassirer, *The Problem of Knowledge*, 1919).

Coherent states:
infinitely many particles sharing the same phase

(Klauder, Glauber, Sudarshan,…1963…; ~~ Schrödinger, 1926)

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