MOLECULAR MOTION MOVIES AND GEOMETRY RECONSTRUCTION USING BAYESIAN STATISTICS

by

ALI RAMADHAN

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AUTHOR DECLARATION

I hereby declare that I am the sole author of this thesis. This is a true copy of the thesis, including any required final revisions, as accepted by my examiners.

I understand that my thesis may be made electronically available to the public.

ABSTRACT

Ever since the early days of Coulomb explosion imaging, the direct imaging of the structure and dynamics of individual molecules has been promised; however, in practice no one has been able to accurately retrieve this structure and all imaging relies on plotting the momentum vectors of the fragments in different ways to infer crude changes in geometry. The momentum vectors tell a large part of the story but do not provide a clear picture of the molecular dynamics everyone seeks so an accurate method of retrieving the structure is highly desirable. I use Bayesian inference and Markov chain Monte Carlo methods to elucidate the molecular geometries, allowing for the study of larger systems than before and for the inclusion of measurement error in these studies for the first time. Using this method, the ultrafast isomerization of carbonyl sulfide and acetylene is imaged in position-space and showcased as a molecular movie. The method, however, is much larger in scope and is generalized to any problem involving a physical system described by a system of ordinary differential equations, where the final conditions are experimentally measured and inference of the initial conditions is desirable.

ACKNOWLEDGMENTS

Hi everyone, thanks!

DEDICATION

Look mom and dad! I got my name on a thesis!

Also dedicated to you, the reader, for reading 0.05% of this thing!

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INTRODUCTION

To image the dynamics of a molecule by destroying it seems paradoxical. As we shall see, the molecule's structure is encoded in the atmoic shrapnel left behind after an explosion. However, to destroy one of nature's simplest creations is no easy task. Molecules are held together by strong chemical bonds. Our best line of attach is to shoot them with a short laser pulse—engulfing the molecule in an intense oscillating electric field will strip away its electrons and cause it to break up quickly. In these first few chapters, I will discuss how to create a short laser pulse and how these pulses interact with matter. Then I will introduce the technique of pump-probe Coulomb explosion imaging, which we will use to probe the dynamic structure of small molecules by studying the atomic fragments resulting from the explosion.

1.1 MOTIVATION

The scope of this imaging method is to make measurements of the geometries of single molecules on a timescale faster than that of molecular motion (10^{-15} seconds). Ultimately these images can be recorded in sequence to image the dynamics of a molecule. It works well for small molecules in the gas phase, a regime in which no other method has been viable.

The method involves shooting a molecule in a vacuum chamber with two laser pulses, a pump pulse followed by a probe pulse after some time delay $\tau \geq 0$. The pump causes the molecule to undergo some change, then the more intense probe pulse strips off enough electrons from the molecule such that the molecule's individual atoms separate and repel each other "explosively" due to Coulomb repulsion. The further apart the atoms are repelled, the weaker the repulsion and eventually every atom reaches an asymptotic state of constant velocity. This all takes place in a constant electric field that accelerates all the atoms towards a time and position-sensitive detector. The detector can tell us how much time each atom took to reach it, and the position where the atom hit it. From this information, the atom's (asymptotic) momentum can be calculated and then provided we know how to simulate the experiment in reverse, we can determine the initial geometry of the molecule just before it was hit by the pump pulse. By picking different values of τ and repeating the experiment many times for each τ we get a "frame" of the molecule's

geometry at each τ , which may be placed in sequence to form a "molecular movie" of the change induced by the pump pulse.

1.2   RESEARCH PROBLEM

Determining these geometries is a computationally difficult task. Almost every study dodges the problem entirely and relies on the momentum vectors to infer information about the geometries. The momentum vectors carry a lot of information but that is certainly not the structural imaging promised by Coulomb explosion imaging that is talked about. It also does not capture all the dynamics possible. When geometry reconstruction is done, it is usually done in a hand wavy way that sidesteps the nuances of the problem and ignores uncertainty, rendering it unreliable. I am working on a rigorous method to perform the geometry reconstruction that may be used (and improved) by my group and others.

1.3   APPROACH TAKEN

We are only interested in the molecular geometry, i.e. the relative positions of the atoms, not the absolute position of every atom. This reduces the dimensionality of our problem from $3n$ to $3n - 6$ in both the geometry $\mathbf{g}$ and momentum vector $\mathbf{p}$. The geometry "vector" $\mathbf{g} \in \mathbb{R}^{3n-6}$ contains the molecule's bond lengths and bond angles, and the momentum "vector" $\mathbf{p} \in \mathbb{R}^{3n-6}$ is a concatenation of momentum values in a specific convention. They both do not transform like vectors.

Having destroyed a molecule and measured the momentum of each of its atomic fragments, we are left with the inverse problem of inferring its structure. While explosions proceed in a deterministic fashion, that is structures map bijectively to momentum measurements, the converse is not true. Two very different structures may produce the same momentum measurements. To make matters worse, there is no analytic solution to the problem and as the molecule grows, the problem of finding its structure becomes increasingly high dimensional. To combat this problem we will require the use of various mathematical and statistical methods. I first discuss some results from the theory of inverse problems to shed some general insight on these problems. I then follow with a discussion of optimization methods which may be used to tackle the problem for very small molecules. However, for full imaging of larger polyatomic molecules with an analysis of measurement error, Bayesian inference using Markov chain Monte Carlo methods is the way to go, which I discuss in the last chapter of this part.

To find the initial geometry $\mathbf{g}_0$ that produced the measured asymptotic momentum $\mathbf{p}_\infty$, we make use of the fact that simulating the

Coulomb explosion forward in time is easy. Let $\mathbf{p}(\mathbf{g}) : \mathbb{R}^{3n-6} \to \mathbb{R}^{3n-6}$ map an initial geometry $\mathbf{g}$ onto the asymptotic momentum vector $\mathbf{p}_\infty$ such a geometry produces upon Coulomb explosion. It simulates the explosion forwards in time by solving a set of $6n - 12$ coupled first-order ODEs. Then casting this as an optimization problem, we seek the geometry $\mathbf{g}$ that minimizes the objective function $\|\mathbf{p}(\mathbf{g}) - \mathbf{p}_\infty\|_2^2$.

1.4 THESIS OUTLINE

Chapter 2 will provide a brief history of molecular movies and geometry reconstruction attempts, with a particular focus on attempts employing Coulomb Explosion imaging (CEI). The history and achievements of CEI will also be briefly reviewed.

Chapter 3 will provide a more detailed description of CEI including the experimental schemes generally employed, such as pump-probe CEI and Femtosecond Multiple Pulse Length Spectroscopy (FEMPULS). Focusing on the experimental apparatus used for this work, we will also go through the process of how data is collected for each atmoic fragment following a Coulomb explosion event. We will then discuss how to computationally simulate a Coulomb explosion using Hamiltonian mechanics, which is an essential step in reconstructing molecular geometris. Finally we will discuss some neccessary conventions for describing molecular geometries and momentum vectors.

Chapters 4-6 constitute the main portion of this thesis as they detail the three different approaches taken to geometry reconstruction. Chapter 4 discusses the somewhat limited lookup table approach, while chapter 5 formulates the task as an optimization problem with some success in making point estimates of the geometries, and chapter 6 uses Bayesian inference to infer the distribution of the molecular geometries taking measurement uncertainty into account.

A BRIEF HISTORY

2.1 GEOMETRY RECONSTRUCTION

2.2 MOLECULAR MOVIES

2.3 COULOMB EXPLOSION IMAGING

The idea that Coulomb explosion imaging could be used to produce so-called molecular movies has permeated the literature ever since the technique's emergence. The goal of observing

CEI was first performed by VAGER, NAAMAN, and KANTER (1989) whereby the Coulomb explosion was initiated by passing the molecule through a thin carbon film at high velocities.

There exist other methods of initiating CEI, among them thin foils, free-electron lasers, highly-charged ion impact, single X-ray photons from a synchrotron source.

Surprisingly, an attempt was made to arrive at an analytical solution for calculating geometries from measured momentum data. NAGAYA and BANDRAUK (2004) are able to derive so-called classical imaging formulas giving the position wavefunction squared for the Coulomb explosion of a diatomic molecule and a linear triatomic molecule (the cases of symmetric and asymmetric Coulomb explosion are treated).

LÉGARÉ et al. (2005a,b) was the first to use Coulomb explosion imaging and report molecular structures. To obtain structures, they assume the explosion proceeds under a purely Coulombic potential and use optimization methods to make guesses at the structure that most accurately reproduces the observed data consistent with minimizing a least-squares objective function. Unfortunately they provide very minimal information regarding their methods and there is a complete lack of discussion acknowledging the shortcomings of this method. Using 8 fs laser pulses they report on the structure of D_2O and SO_2 (LÉGARÉ et al., 2005b). They also claim to have imaged vibrating D_2+ and dissociating SO_2^{2+} and SO_2^{3+} however they provide no more than a couple of dissociation frames and infer the transient D_2+ bond length from kinetic energy release ratios as a function of pump-probe time delay (LÉGARÉ et al., 2005a).

GAGNON et al. (2008) reported the reconstruction of dichloromethane (CH_2Cl_2) using a home-made stochastic-based simulated annealing algorithm that globally optimizes the molecular spatial configuration.

They seem to have worked hard to find an analytical solution but their unsaid conclusion seems to be that it is an intractable problem and their group went silent on this problem.

The main shortcomings being degenerate solutions and the fact that they employ convex optimization methods to a problem that is not convex. It is not clear if they even knew about these issues.

There is nothing wrong with writing your own code here but nonconvex optimization algorithms are tricky to get right and the reliance should be on

They discuss uncertainties but are only able to obtain the structure in five cases. [1]

The best effort so far has probably been the one by KUNITSKI et al. (2015) in which they use a lookup table approach to image the Efimov state of the helium trimer.

Molecular movies are of course not only of interest in physics and chemistry as a means of probing fundamental processes, but also in the biological sciences where molecular structure play a crucial role in determining the function of biomolecules such as proteins. However, the molecules of interest there are much too large to be studied by any of the previous techniques. Thus molecular movies in the biological sciences tend to be annotated computer simulations amalgamated from multiple studies. That said, they are very impressive pieces of work.

A particularly impressive movie by CHEUNG and CRAMER (2012) showcases the process of RNA polymerase transcription and goes on for over six minutes.

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1 See BOCHAROVA et al. (2011) for a discussion of optimization algorithms.

COULOMB EXPLOSION IMAGING

3.1   OUTLINE OF THE EXPERIMENT

3.1.1   *Pump-probe Coulomb explosion imaging*

In pump-probe Coulomb explosion imaging (CEI) one ultrashort laser pulse is split into two pulses through the use an asymmetric beamsplitter. One of the pulses, the pump pulse, is usually much weaker than the other, the probe pulse. A time delay τ between the pulses is then created such that the pump pulse goes first and the probe pulse second. The job of the pump pulse will be to initiate some change in the molecule. One example could include an isomerization of the molecule. Thus the pump pulse "pumps" the molecule into some excited state. The job of the powerful probe pulse is to engulf the molecule in an intense enough laser field such that multiple electrons are stripped off of it. The molecule's individual atoms are left in a highly-charged state and begin to behave as individual point charges in a purely Coulombic potential. The entire process occurs in the presence of a constant electric field and so the positively-charged ions all accelerate upwards towards a time- and position-sensitive detector. Thus the probe pulse allows for the "probing" of the excited state.

3.1.2 *Femtosecond Multiple Pulse Length Spectroscopy*

3.2 EXPERIMENTAL APPARATUS

3.3 DATA ANALYSIS

3.3.1 *Time and position measurement*

The position is then calculated using

$$x = \frac{Q_1 + Q_2}{Q_1 + Q_2 + Q_3 + Q_4}, \quad y = \frac{Q_1 + Q_3}{Q_1 + Q_2 + Q_3 + Q_4} \qquad (3.1)$$

3.3.2 *Calculating the atomic fragments' momenta*

The components of the three-dimensional momentum vector $\mathbf{p} = (p_x, p_y, p_z)$ for each atom are then calculated as

$$p_x = \frac{m(x - x_0)}{t}, \quad p_y = \frac{m(y - y_0)}{t}, \quad p_z = \frac{qV}{2\ell}\left(\frac{t_0^2 - t^2}{t}\right) \qquad (3.2)$$

where m is the atom's mass, (x, y) is the location the atom collided with the MCP detector, and (x_0, y_0) is the location that the Coulomb explosion originated. The location $(0, 0)$ corresponds to the physical center of the MCP detector. q is the net charge of the atom, V is the value of constant electric potential the atom is subjected to, and ℓ is the distance from the location of the Coulomb explosion to the detector. t is measured time of flight (between Coulomb explosion and detection) of the atom and

$$t_0 = \sqrt{\frac{2d\ell}{V}\left(\frac{m}{q}\right)} \qquad (3.3)$$

is the atom's time of flight assuming no external forces act on it during its trip to the detector.

3.3.3 *Measurement uncertainty in the momenta*

For any relation $f = f(x_1, x_2, \ldots, x_n)$, assuming independent variables, the absolute uncertainty in f, denoted Δf, may be calculated as

$$\Delta f = \sqrt{\sum_{i=1}^{n}\left(\frac{\partial f}{\partial x_i}\Delta x_i\right)^2} \qquad (3.4)$$

where Δx_i is the uncertainty in the independent variable x_i.

Using this we may calculate the uncertainty in the measured momentum values, which will we different for each component. In our

case, $p_x = p_x(m, x, x_0, t)$ and $p_y = p_y(m, y, y_0, t)$, however, the uncertainty in the atomic mass m is orders of magnitude smaller than the uncertainty in the other variables and so we will ignore its effects. Thus we get that

$$(\Delta p_x)^2 = \frac{\partial p_x}{\partial x}\Delta x + \frac{\partial p_x}{\partial x_0}\Delta x_0 + \frac{\partial p_x}{\partial t}\Delta t \tag{3.5a}$$

$$(\Delta p_y)^2 = \frac{\partial p_y}{\partial y}\Delta y + \frac{\partial p_y}{\partial y_0}\Delta y_0 + \frac{\partial p_y}{\partial t}\Delta t \tag{3.5b}$$

where the partial derivatives can be calculated from (3.2) as

$$\frac{\partial p_x}{\partial x} = \frac{m}{t}, \quad \frac{\partial p_x}{\partial x_0} = \frac{m}{t}, \quad \frac{\partial p_x}{\partial t} = -m\frac{x - x_0}{t^2} \tag{3.6a}$$

$$\frac{\partial p_y}{\partial y} = \frac{m}{t}, \quad \frac{\partial p_y}{\partial y_0} = \frac{m}{t}, \quad \frac{\partial p_y}{\partial t} = -m\frac{y - y_0}{t^2} \tag{3.6b}$$

and so

$$\left(\frac{\Delta p_x}{p_x}\right)^2 = \left(\frac{\Delta x}{x - x_0}\right)^2 + \left(\frac{\Delta x_0}{x - x_0}\right)^2 + \left(\frac{\Delta t}{t}\right)^2 \tag{3.7a}$$

$$\left(\frac{\Delta p_y}{p_y}\right)^2 = \left(\frac{\Delta y}{y - y_0}\right)^2 + \left(\frac{\Delta y_0}{y - y_0}\right)^2 + \left(\frac{\Delta t}{t}\right)^2 \tag{3.7b}$$

Repeating the process for $p_z = p_z(q, V, \ell, t_0, t)$ but ignoring the tiny uncertainties in q, V, and ℓ, we get

3.4 COMPUTATIONALLY SIMULATING A COULOMB EXPLOSION

To simulate an explosion of a molecule containing n atoms, we must solve the classical equations of motion for each ion right after the explosion. We choose to use Hamiltonian mechanics here to acquire a system of first-order differential equations which may be easily solved by numerical methods such as the ubiquitous fourth-order Runge-Kutta. Assuming a purely electromagnetic potential for each ion, the Hamiltonian of the molecular system is

$$\mathcal{H}(\mathbf{r}_i, \mathbf{p}_i, t) = \sum_{i=1}^{n} \frac{\mathbf{p}_i^2}{2m_i} + \frac{1}{4\pi\epsilon_0} \sum_{\substack{\{i,j\} \\ i \neq j}} \frac{q_i q_j}{|\mathbf{r}_i - \mathbf{r}_j|} \tag{3.8}$$

where $i, j \in \{1, 2, \ldots, n\}$ and so the second summation is over all i, j pairs where $i \neq j$. Calculating Hamilton's equations for the system, we get

$$\frac{d\mathbf{r}_i}{dt} = \frac{\partial\mathcal{H}}{\partial\mathbf{p}_i} = \frac{\mathbf{p}_i}{m_i} \tag{3.9a}$$

$$\frac{d\mathbf{p}_i}{dt} = \frac{\partial\mathcal{H}}{\partial\mathbf{r}_i} = \frac{1}{4\pi\epsilon_0} \sum_{j, j \neq i} \frac{\mathbf{r}_i - \mathbf{r}_j}{|\mathbf{r}_i - \mathbf{r}_j|^3} \tag{3.9b}$$

where i is held fixed over the second summation. With appropriate initial conditions this system of $6n$ scalar first-order ordinary differential equations may be easily solved using, for example, the classical fourth-order Runge-Kutta method for numerically solving ordinary differential equations. The atoms are assumed to be at rest so that $\mathbf{p}_i(t = 0) = 0$, while the initial positions, $\mathbf{r}_i(t = 0) = 0$, are chosen to correspond to the molecular geometry.

Discuss the validity of the at rest assumption.

One way to think of the problem being tackled in this thesis is: which initial geometry $\mathbf{r}_i(t = 0) = 0$ results in the momentum values measured at the detector? The atoms are far enough apart after just a few nanoseconds that by the time they arrive at the detector, they feel almost no forces due to each other and their momenta attain asymptotic values which we can denote $\mathbf{p}_i(t \to \infty)$.

3.5   CONVENTIONS FOR GEOMETRIES AND MOMENTA

3.5.1   *Describing molecular geometries by a Z-matrix*

3.5.2   *A homemade convention to describe momentum vectors*

GEOMETRY RECONSTRUCTION BY LOOKUP TABLE

We begin our attempts at reconstructing geometries by taking a very simple approach.

4.1 LOOKUP TABLES: WHAT ARE THEY GOOD FOR?

As the name would suggest, a lookup table catalogues a relationship between two sets such that anyone wishing to obtain the mapping between the sets may simply find the object of interest. Lookup tables tend to be more useful in one direction.

The most familiar lookup table may be the multiplication times table that every elementary school student is familiar where sets of two integers are mapped to their product. Lookup tables have been employed since antiquity and one of the earliest surviving examples is a 98-column multiplication table from 493 A.D. attributed to the Roman, Victorius of Aquitaine (MAHER and MAKOWSKI, 2001). Before the advent of the calculator and for much of scientific history, extensive logarithm tables were used to look up their values to several decimal places and to speed up computations. The earliest such tables date back to the ancient greeks although they have since been lost, and the earliest surviving one is a sine table by the ancient Indian mathematician Āryabhaṭa circa 499 C.E. (HAYASHI, 1997).

Of course since then lookup tables have found an enormous number of uses in computer science. Arrays are ubiquitous objects in procedural programming languages and so is the more general dictionary object, especially in Python. Sine tables are still stored in calculators for quick trigonometric computations using the CORDIC algorithm and 3D lookup tables are used in image processing to store colormaps. In each case the speed offered by a lookup table once it has been generated is the main reason for their use.

4.2   IMPLEMENTATION TO RECONSTRUCT TRIATOMIC MOLECULES

In this approach, many Coulomb explosions are simulated (see secton 3.4) using a wide variety of molecular structures as the initial condition, and the resulting momentum vectors from each simulation are stored. Thus you have a mapping from molecular structures to momentum vectors. To determine the structure belonging to a certain set of observed momentum vectors, you simply read the table in reverse. This approach is simple to implement, very quick by design, and front-loads the computation which may be desirable for large data sets. However, of course, it has an exponential time and space complexity $\mathcal{O}(e^{3N-6})$ where N is the number of atoms.

4.3   RECONSTRUCTIONS OF CARBON DIOXIDE AND CARBONYL SULFIDE

4.4   COMPUTATIONAL COMPLEXITY

4.5   ADVANTAGES, DISADVANTAGES AND PROBLEMS

4.6   LESSONS LEARNT

GEOMETRY RECONSTRUCTION AS AN OPTIMIZATION PROBLEM

Much progress was made over the lookup table by treating the geometry reconstruction problem as a constrained nonlinear convex optimization such that MATLAB's `fmincon` function an be relied on. It relies on trust regions and uses an interior-point algorithm. This worked especially well in the case of triatomic molecules however four-atom systems proved incredibly difficult to tackle here. This was due to the exponential increase in the number of saddle points with dimensionality making the problem highly non-convex and unsuitable for `fmincon`.

Recall that triatomic molecules have three degrees of freedom resulting in a problem of dimension 3 while four-atom systems have six. That is, $3N + 6$ for an N-atom system.

5.1 OPTIMIZATION PROBLEMS

5.2 PREVIOUS WORK EMPLOYING A SIMPLEX ALGORITHM

BRICHTA, SEAMAN, and SANDERSON (2009) proposed the reconstruction of small triatomic molecules using a simplex algorithm. Unfortunately they only report on the reconstruction of molecular structures based on simulated data for carbon dioxide and formaldehyde. I could not use this algorithm to find the geometries of CO_2 or OCS from real data.

5.3 CURRENT IMPLEMENTATION

5.4 RECONSTRUCTIONS OF CARBON DIOXIDE AND CARBONYL SULFIDE

5.5 ADVANTAGES, DISADVANTAGES AND PROBLEMS

5.6 LESSONS LEARNT

6

GEOMETRY RECONSTRUCTION USING BAYESIAN INFERENCE

7

CONCLUSIONS

7.1 GEOMETRY RECONSTRUCTION AND MOLECULAR MOVIES

7.2 FUTURE DIRECTIONS

BIBLIOGRAPHY

BOCHAROVA, I. et al. (2011). Charge Resonance Enhanced Ionization of CO_2 Probed by Laser Coulomb Explosion Imaging. *Physical Review Letters* **107**, 063201.

BRICHTA, J.-P., SEAMAN, A. N., and SANDERSON, J. H. (2009). Ultrafast imaging of polyatomic molecules with simplex algorithm. *Computer Physics Communications* **180**, 197–200.

CHEUNG, A. and CRAMER, P. (2012). A Movie of RNA Polymerase II Transcription. *Cell* **149**, 1431–37.

GAGNON, J, LEE, K. F., RAYNER, D. M., CORKUM, P. B., and BHARDWAJ, V. R. (2008). Coincidence imaging of polyatomic molecules via laser-induced Coulomb explosion. *Journal of Physics B: Atomic, Molecular and Optical Physics* **41**, 215104.

HAYASHI, T. (1997). Āryabhaṭa's Rule and Table for Sine-Differences. *Historia Mathematica* **24**, 396–406.

KUNITSKI, M. et al. (2015). Observation of the Efimov state of the helium trimer. *Science* **348**, 551–55.

LÉGARÉ, F., LEE, K., LITVINYUK, I., DOOLEY, P., BANDRAUK, a., VILLENEUVE, D., and CORKUM, P. (2005a). Imaging the time-dependent structure of a molecule as it undergoes dynamics. *Physical Review A* **72**, 052717.

LÉGARÉ, F. et al. (2005b). Laser Coulomb-explosion imaging of small molecules. *Physical Review A* **71**, 013415.

MAHER, D. W. and MAKOWSKI, J. F. (2001). Literary evidence for Roman arithmetic with fractions. *Classical Philology* **96**, 376–399.

NAGAYA, K. and BANDRAUK, A. D. (2004). Laser Coulomb explosion imaging of linear triatomic molecules. *Journal of Physics B: Atomic, Molecular and Optical Physics* **37**, 2829–53.

VAGER, Z., NAAMAN, R., and KANTER, E. P. (1989). Coulomb explosion imaging of small molecules. *Science* **244**, 426–31.
This is a classic of linguistics.

A

BAYESIAN STATISTICS

A.1 FUNDAMENTALS OF PROBABILITY THEORY

A.2 BAYESIAN INFERENCE

A.3 MARKOV CHAIN MONTE CARLO

A.4 INVERSE PROBLEMS

Lorem ipsum at nusquam appellantur his, ut eos erant homero concludaturque. Albucius appellantur deterruisset id eam, vivendum partiendo dissentiet ei ius. Vis melius facilisis ea, sea id convenire referrentur, takimata adolescens ex duo. Ei harum argumentum per. Eam vidit exerci appetere ad, ut vel zzril intellegam interpretaris.

More dummy text.

Theorems can easily be defined

Definition A.1. *Let f be a function whose derivative exists in every point, then f is a continuous function.*

Theorem A.1 (Pythagorean theorem)**.** *This is a theorema about right triangles and can be summarised in the next equation*

$$x^2 + y^2 = z^2$$

Proof. The theorem can be proved algebraically using four copies of a right triangle with sides a, b, and c, arranged inside a square with side c as in the top half of the diagram. The triangles are similar with area $\frac{1}{2}ab$, while the small square has side $b - a$ and area $(b-a)^2$. The area of the large square is therefore

$$(b-a)^2 + 4\frac{ab}{2} = (b-a)^2 + 2ab = a^2 + b^2$$

But this is a square with side c and area c^2, so $c^2 = a^2 + b^2$. □

And a consequence of theorem B.1 is the statement in the next corollary.

MATHEMATICAL OPTIMIZATION

B.1 LINEAR OPTIMIZATION

B.2 CONVEX OPTIMIZATION

B.3 NONLINEAR OPTIMIZATION

Lorem ipsum at nusquam appellantur his, ut eos erant homero concludaturque. Albucius appellantur deterruisset id eam, vivendum partiendo dissentiet ei ius. Vis melius facilisis ea, sea id convenire referrentur, takimata adolescens ex duo. Ei harum argumentum per. Eam vidit exerci appetere ad, ut vel zzril intellegam interpretaris.

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$$(b - a)^2 + 4\frac{ab}{2} = (b - a)^2 + 2ab = a^2 + b^2$$

But this is a square with side c and area c^2, so $c^2 = a^2 + b^2$. □

And a consequence of theorem B.1 is the statement in the next corollary.

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