Research summary  
Oscar Gonzalez, June 2012

Introduction

My field is computational and applied mathematics with an emphasis on classical continuum mechanics. My research to date has spanned five distinct topics, all of which can be connected to one common application. The topics are

1. Nyström-type numerical methods for boundary integral equations,
2. Hydrodynamic transport and diffusion of rigid and flexible particles,
3. Sequence-dependent models for DNA structure prediction,
4. Global curvature and optimal packing of curves with finite thickness,
5. Structure-preserving numerical methods in classical and continuum mechanics.

The common application is DNA structure prediction and measurement. Topics 1-3 are most recent, whereas 4-5 are older. Although the modeling of DNA structure and various experimental methods for measuring it has served as a rich source of motivation, the subject matter of most of my research has applicability beyond this theme.

My research is of an interdisciplinary nature and has contributed to the training of students and course development, and has been funded with multiple awards. I have published articles in various journals across mathematics, physics and chemistry. I have also published a textbook that provides fundamental background material for much of my research. I have supervised students at the PhD, Masters and undergraduate levels and have used results from my research in the development of my modeling and numerical analysis courses. I have been supported by various single-investigator grants from the National Science Foundation, and I am currently involved in an emerging collaborative grant proposal, with both analysts and experimentalists, to study the mechanical interactions between DNA and the anti-cancer drug Cisplatin.

In this summary, I give a brief overview of the research topics listed above and discuss my main results. Slides from talks on a collection of these topics are available online in the research portion of my webpage.

Boundary integral equations

Overview

The method of integral equations has a long and rich history in both the analysis and numerical treatment of boundary value problems. On the analysis side, the method provides a classic approach to the study of existence and uniqueness questions. On the numerical side, the method provides an alternative formulation which can be efficiently discretized. In the basic approach, a boundary value problem described by a partial differential equation on a domain of interest is reduced to an integral equation on the bounding surface. The unknown scalar or vector field throughout the
domain is represented in terms of one or more integral potentials which depend on an unknown surface density. The representation can take various different direct and indirect forms and the integral potentials usually involve kernels that are at least weakly singular. The reduction in dimension makes the method of integral equations extremely attractive, especially for problems on exterior domains.

The subject of integral equations arises naturally within the context of molecular modeling. The numerical prediction of the convection-diffusion coefficients for a given molecular geometry requires the repeated solution of the Stokes equations of viscous, incompressible fluid flow in the three-dimensional domain exterior to the molecule. Boundary integral equations provide a natural approach for numerics and analysis. Because standard geometrical models of molecular surfaces are typically non-smooth, it is important to have methods which are provably convergent under minimal regularity conditions. In addition to the equations of hydrodynamics, it is also of interest to solve a coupled system that includes the equations of elastostatics and electrostatics in interior and exterior three-dimensional domains associated with a molecule. Besides those mentioned here, the method of integral equations has applications in many other areas, most notably acoustics and electromagnetics.

The basic problem I have considered is that of designing, implementing and analyzing numerical methods for boundary integral equations, and for approximating various related functionals of the solution. Several different types of basic methods are possible, for example Galerkin, collocation and Nyström methods. My work to date has been focussed on methods of the latter type for weakly singular integral equations. Specifically, I have been studying boundary integral formulations of the Stokes equations as arise in connection with molecular modeling. In future work, I would like to consider models that include not only hydrodynamics, but also elastostatics and electrostatics.

**Main results**

- In [8], an existence and uniqueness theorem is proved for a new boundary integral formulation of the Stokes equations with Dirichlet data in exterior domains. The theorem is proved under minimal regularity assumptions consistent with classic potential theory and makes use of the Fredholm theorems for compact operators. A novelty of the formulation is that it employs a convex combination of the single- and double-layer Stokes potentials, where the single-layer potential is transported to an associated parallel surface. This formulation combines the strengths of various previous approaches, is natural for bodies of complicated shape and topology, and is advantageous for the numerical treatment of the problem.

- In [3], a convergence theorem is proved for a family of locally-corrected Nyström methods for a general class of weakly singular integral equations on surfaces in three dimensions. Fredholm equations of the second kind as arise in connection with linear elliptic boundary value problems for scalar and vector fields are considered. In contrast to methods based on product integration, coordinate transformations and singularity subtraction, the family of Nyström methods studied here is based on a local polynomial correction determined by an auxiliary system of moment equations. The polynomial correction is shown to remove the weak singularity in the integral equation and provide control over the approximation error. Convergence results for the family of methods are established under minimal regularity
assumptions. The proof relies on the theory of collectively compact operators and makes use of a subtle monotonicity argument and Tricomi condition for the discretized form of the weakly singular surface integral. Rates of convergence are shown to depend on the regularity of the problem, the degree of the polynomial correction, and the order of the quadrature rule employed in the discretization. As a corollary, a simple method based on singularity subtraction which has been employed by many authors is shown to be convergent.

- In [2], the locally-corrected Nyström methods developed in [3] are applied to the Stokes boundary integral formulation developed in [8]. Attention is focussed on the lowest-order method of the family, whose implementation is especially simple. Specifically, by virtue of the method and the formulation, there are no weakly singular integrals or partition of unity functions that need to be explicitly evaluated. Various numerical examples on a range of different geometries are used to illustrate the convergence and conditioning properties of the method. Our results show that the lowest-order member of a family of locally-corrected Nyström methods provides a simple, efficient and provably convergent alternative to various other higher-order, computationally expensive methods. Indeed, for boundary surfaces and data of limited regularity, the lowest-order method from the family introduced in [3] can achieve a comparable rate of convergence without the extra cost.

- In [4], regularization and discretization convergence theorems are proved for a regularized boundary integral formulation of Stokes flow introduced by Cortez and co-workers. The formulation is based on a free-space solution of the Stokes equations with concentrated, but smooth forcing and involves regularization parameters that control the behavior of the free-space solution and the conditioning of the integral equation. Convergence theorems are established for the regularization error associated with the formulation and for the discretization error associated with its subsequent numerical approximation by Nyström methods. The results show that the overall method provides a convergent approximation of the Stokes equations as the regularization and discretization parameters are refined along suitable paths. Although higher accuracy can be achieved by considering a variety of other integral formulations, such as those considered in [8], the regularized method of Cortez provides one systematic way to balance the competing requirements of accuracy and cost.

Hydrodynamic transport and diffusion

Overview

The classic theories of translational and rotational diffusion of rigid particles of ellipsoidal and cylindrical shape have a long and rich history with many applications. The theories have their origins in the pioneering works of Einstein, Debye, and Perrin, and lead to the standard parabolic convection-diffusion equations on three-space and the sphere. They have been used in various types of experiments to predict geometrical and physical features of molecules in solution, for example their effective or hydrated dimensions and molecular weight. These theories form a core part of physical chemistry and are in use today in the study of proteins and DNA. The classic theories are used to interpret data from various different types of experimental methods, for example velocity sedimentation, dynamic light scattering, electric dichroism and birefringence, and fluorescence
polarization to name a few. A detailed understanding of translational and rotational diffusion of particles in solution in the presence of external loads is fundamental in many different applications, ranging from sequencing technologies for DNA, to the design of a variety of microfluidic devices in physics, chemistry and biology. Indeed, the interplay between diffusion and convection is crucially important in the design and performance of devices for the transport, mixing, separation and manipulation of particles.

Despite being extremely useful, the classic theories have several shortcomings. Firstly, due to the independent treatment of translations and rotations, the classic theories cannot capture all the modes of behavior that an arbitrary particle may exhibit, not even qualitatively. Indeed, whereas the assumption of independence between translational and rotational diffusion is appropriate for particles with symmetry, it is generally inappropriate for particles of arbitrary shape. Cross- and self-coupling effects among translations and rotations can arise which are not accounted for in the classic theories. Secondly, while the assumption of rigidity is appropriate in many cases, it can be inappropriate in other cases depending on the time, length and force scales involved. Non-rigid or flexible particles can experience internal motions, and these can also be coupled with translations and rotations. Such coupling effects are also not accounted for in the classic theories. Thirdly, it is of interest to know which features of the shape of a particle make an observable impact on its diffusive behavior, and which features are hidden or unobservable. Specifically, for particle shapes within a specified class, it is of interest to know how the diffusive behavior of a particle depends on its geometric parameterization and the sensitivity of this dependence. Due to their limitation to symmetric shapes, the classic theories shed little light on the properties of general shapes.

The basic problem is to characterize the translational, rotational and internal motions of particles of arbitrary shape and flexibility at diffusive time scales. Mathematically, this work involves the study of parabolic convection-diffusion equations on high-dimensional manifolds, systems of elliptic equations in exterior and interior three-dimensional domains, and weakly-singular integral equations on the bounding surfaces of these domains. All three types of equations play a key role in the modeling problem. The parabolic equation is of the Smoluchowski type and is a statement of mass balance on the space of particle positions, orientations and shapes, the elliptic equations are of the Stokes and Elasticity type and describe the mechanical fluid-solid interactions between the solvent and an individual particle; these interactions are characterized by the so-called convection-diffusion tensor for the particle, and the integral equations are of the Fredholm type and arise in the analysis and numerical treatment of the elliptic equations. My completed work to date in this area has dealt with the case of rigid particles, whose shape is arbitrary but fixed and hence have no internal degrees of freedom, and I am currently working on extensions to the case of flexible, elastic particles with a finite number of internal degrees of freedom, whose three-dimensional shapes are determined by the local convection-diffusion driving forces. In both cases, I have considered only dilute solutions in which the particles are hydrodynamically well-separated, and plan to consider non-dilute solutions in future work.

Main results

- In [5], a general model for the transport and diffusion of rigid particles in a viscous solvent is derived and studied. The model takes the form of a convection-diffusion equation on the six-dimensional space of particle positions and orientations, which intrinsically is a curved
manifold due to the structure of the three-dimensional rotation group. The model is parameterized by matrix-valued coefficients that depend on the shape of the particle and allows for arbitrary external loads; the coefficients are determined through the solution of the viscous flow equations in the region exterior to the particle. Moreover, the model applies to particles of arbitrary shape and allows for arbitrary cross- and self-coupling between translational and rotational degrees of freedom. Scaling and perturbation techniques are used to characterize the dynamics at time scales relevant to different classic experimental methods. Specifically, the nature of translational-rotational coupling is studied in different asymptotic limits. It is shown that translational and rotational motion can be treated as independent on appropriate time scales, and hence can be described by simplified diffusion models, provided that certain geometric and hydrodynamic parameters associated with a particle are small.

- In [9], the model developed in [5] and the numerical method described in [8], [3] and [2] are used to study experimental data on DNA. Specifically, a boundary element model for the computation of sequence-dependent hydrodynamic properties of short DNA molecules is introduced. The hydrated surface is modeled as a curved tube of uniform radius with ends capped by hemispheres, and the axis of the tube is a general space curve whose length and curvature are determined locally by the sequence using a rigid basepair model of double-helical DNA with parameters based on x-ray crystallography. Convection-diffusion coefficients for families of random and periodic DNA sequences are computed and compared to experimental data. Our results indicate that sequence-dependent curvature can have a measurable impact on both the translational and rotational convection-diffusion coefficients, even for relatively short fragments of lengths less than about 150-basepair, and that previous estimates of the hydrated radius of DNA are likely to be underestimates. Moreover, our results suggest a possible method for refining the rigid basepair model parameters for DNA in solution as well as the hydrated radius.

- In [12], a complete characterization is given of all possible steady states and their nonlinear stability for the leading-order sedimentation dynamics of a given rigid body. It is demonstrated that the dynamics of a rigid body falling in an infinite, viscous fluid can, in the Stokes limit, be reduced to the study of a non-linear, three-dimensional system of ordinary differential equations $\dot{\eta} = \eta \times M_2\eta$, where $M_2$ is a generally non-symmetric matrix containing certain hydrodynamic mobility coefficients. The matrix $M_2$ is defined implicitly by the Dirichlet-to-Neumann map for the Stokes equations in the three-dimensional domain exterior to the body. It is shown that all steady states and their stability properties can be classified in terms of the Schur form of $M_2$. Steady states correspond to screw motions (or limits thereof) in which the center of mass traces a helical path, while the body spins uniformly about the vertical. All rigid bodies have at least one such stable, screw motion. Bodies for which $M_2$ has exactly one real eigenvalue have a unique, globally attracting, asymptotically stable screw motion, while other bodies can have multiple, stable and unstable steady motions. In particular, each real eigenvector of $M_2$ defines a hydrodynamic axis in the body and gives rise to a pair of steady states. The two states in a pair correspond to screw motions in which the hydrodynamic axis remains parallel to the external force field with either the same or opposite orientation, while the center of mass traces out a helical path about an axis that is also parallel to the external
force field. Remarkably, it seems that only very special cases of these general conclusions were previously known.

- In [12], a functional is derived to characterize the average sedimentation speed of a rigid body subject to a prescribed external force field. It is shown that the sedimentation speed of a general rigid body can be characterized in terms of certain symmetric, positive-definite matrix $M_1$, which is also implicitly defined by the Dirichlet-to-Neumann map for the Stokes equations described above. We showed that the speed of the body mass center in a direction parallel to the external force field is, after a short interval of time, described by a quadratic form defined by $M_1$. By averaging this quadratic form over the unit sphere we obtain a functional, completely defined by the body geometry through the Dirichlet-to-Neumann map, which provides a measure of sedimentation speed averaged over all possible body orientations. Motivated by various experimental results, we numerically approximate this functional for various knotted, tubular bodies in their ideal geometrical configurations. Our results for ideal knots in a Stokes fluid predict an approximate linear relation between sedimentation speed and average crossing number, as has been observed experimentally for the much more complicated system of real DNA knots in gel electrophoresis.

**DNA structure prediction**

**Overview**

The sequence-dependent curvature and flexibility of DNA in solvent at the scale of tens to hundreds of basepairs are believed to be critical for its packaging into the cell, recognition by other molecules, and conformational changes during biochemical processes. Is it possible to predict this curvature and flexibility from the basepair sequence? An all-atom molecular dynamics (MD) model of the DNA-solvent system can be used to predict these structural properties, but only for very short sequences, and at a considerable computational expense. Moreover, an MD model does not provide an explicit, closed-form map from sequence to structure; rather, it provides only an implicit map defined by performing an MD simulation on a given sequence. Also, in accordance with the physics of the situation, an MD model does not produce a single, unique structure for a given sequence, but rather a distribution of structures defined on an appropriate configuration space, which can be interpreted as a marginal for the overall DNA-solvent system. A distribution arises due to the incessant agitation of the structure by the thermal motion of the solvent particles. It is this distribution that determines the effective curvature and flexibility of a given DNA sequence. Here we restrict attention to structures that fall within the B-form structural family, which is the pertinent one for typical solvent conditions, and assume that the distribution is stationary.

The basic problem is to develop a model, which is simpler than all-atom MD, which can explicitly predict the distribution of structures for any given sequence of any given length in the relevant range of tens to hundreds of basepairs. For tractability, it is essential to consider coarse-grained models in which a structure is described by a smaller number of degrees of freedom than the coordinates of each atom. Moreover, in accordance with the intrinsic arrangement and strength of chemical bonds, it is natural to consider models in which each base or each basepair in a structure is assumed to be an independent rigid body, with its constituent atoms fixed relative to it. The configuration
space of a structure is then associated with the space of translations and rotations of each of its rigid bases or basepairs, modulo an overall translation and rotation of the entire structure which plays no role in the absence of an external potential. The resulting quotient space is known as the internal configuration space. Furthermore, due to the intrinsic stiffness and elastic nature of DNA, it is reasonable as a first approximation to model the distribution of structures using a weighted Gaussian probability density, defined in terms of an effective, quadratic internal energy function, where the weight is a metric factor associated with the choice of coordinates on the three-dimensional rotation group.

Thus the problem is to develop a rule, depending on a fixed, minimal set of material parameters, to generate an effective internal energy and Gaussian density on the internal configuration space of an arbitrary DNA sequence of arbitrary length. Knowledge of this internal energy and Gaussian density could then be used to explore various aspects of structure in solution, such as the local curvature and flexibility of the central axis of the double-helix, and the width and stability of the gap between the two strands of the double-helix, all as a function of sequence. Mathematically, this work involves the study of energy functions and probability densities on the special Euclidean group, the study of various symmetry properties of such functions implied by the intrinsic, physical symmetry of DNA, the study of divergence (distance) functions on the space of normalized probability densities, and the study of constrained optimization problems involving these divergence functions. Moreover, the theoretical foundation for the basic model requires results from stochastic differential equations. The continuum limits of the basic models are also of mathematical interest.

My work to date in this area has dealt with two different types of interacting rigid body models, where either the individual bases or basepairs of a DNA are considered to be rigid and energetically coupled along the molecule, and I have been involved in a large effort to estimate material parameters for these models for unbound DNA. In future work, I would like to extend the basic ideas so that they can be used to model various structural characteristics of drug-bound DNA, which is a modeling problem of considerable interest.

Main results

- In [6], the stochastic equations of motion for a system of interacting rigid bodies in a solvent are formulated and studied. Three-dimensional bodies of arbitrary shape, with arbitrary couplings between translational and rotational degrees of freedom, as arise in coarse-grained models of polymers, are considered. Beginning from an Euler-Langevin form of the equations, two different, properly invariant, Hamilton-Langevin forms are derived and studied together with various associated measures. Under different conditions depending on the choice of rotational coordinates, the canonical measure is shown to be a stationary solution of an associated Fokker-Planck equation and to always factorize into independent measures on configuration and velocity spaces. Explicit expressions are given for these measures, along with a certain Jacobian factor associated with the three-dimensional rotation group. When specialized to a fully-coupled, quadratic model of a stiff polymer such as DNA, our results yield an explicit characterization of the complete set of model parameters.

- In [7], a method is described to extract a complete set of sequence-dependent material parameters for rigid-base and rigid-basepair models of DNA in solution from atomistic molecular
dynamics simulations. The method is properly consistent with equilibrium statistical mechanics, leads to effective shape, stiffness and mass parameters, and employs special procedures for treating spontaneous torsion angle flips and H-bond breaks, both of which can have a significant effect on the results. The method is accompanied by various analytical consistency checks that can be used to assess the equilibration of statistical averages, and different modeling assumptions pertaining to the rigidity of the bases and basepairs and the locality of the quadratic internal energy. The practicability of the approach is verified by estimating complete parameter sets for the 16-basepair palindromic oligomer G(TA)\textsubscript{7}C simulated in explicit water and counterions. Our results indicate that the method is capable of resolving sequence-dependent variations in each of the material parameters. Moreover, they show that the assumptions of rigidity and locality hold rather well for the base model, but not for the basepair model. For the latter, it is shown that the non-local nature of the internal energy can be understood in terms of a certain compatibility relation involving Schur complements.

- In [1], a novel rigid-base model of DNA is introduced and studied. The model is founded upon a hierarchy of sequence-dependent local energies that describe physically distinct interactions, involves only local parameters, can capture important local features that are below the resolution of other coarse-grained models, and can also capture important non-local features as have been observed in various investigations. A novelty of the model is its ability to account for the intrinsic, pre-existing stress in an oligomer. A complete parameter set for double-stranded, B-form DNA, in standard environmental conditions, is estimated using an extensive database of atomic-resolution, explicit-solvent MD data produced by a consortium of groups.

For any given oligomer, the model delivers an internal energy and a Gaussian probability density function on the associated internal configuration space, where the degrees of freedom are the relative displacement and rotation of each rigid base on each strand of the oligomer. The internal energy is based on a hierarchy of sequence-dependent local energies that describe physically distinct interactions between various groups of proximal bases. Consistent with a nearest-neighbor assumption, we consider only the first two members of the hierarchy that describe the local interactions between the two bases in a monomer and the four bases in a dimer. Moreover, we characterize these interactions by a finite set of parameters that depend only on the local monomer and dimer sequence. The internal energy of an arbitrary oligomer of any length is then defined by a construction rule in which the local interaction energies are superimposed. We show that an internal energy constructed in this way provides a natural model for the intrinsic curvature and flexibility of an oligomer. Indeed, we show that these properties are determined by the local parameters in a non-trivial way through the construction rule. Moreover, our internal energy also provides a natural model for the intrinsic pre-existing stress in an oligomer. This stress arises from the fact that each base cannot simultaneously minimize all its local interactions and must instead find a compromise. As a consequence, the model predicts that the intrinsic or ground-state curvature of an oligomer depends non-locally on its sequence. That is, local mutations of the sequence produce non-local changes in shape. The description of such non-local behavior using only local parameters is unique to our model and is consistent with recent observations in the literature.
A complete parameter set for the model is estimated using a maximum relative entropy approach on the space of normalized probability density functions. Specifically, a best-fit parameter set is obtained by minimizing an objective functional defined as the sum of the Kullback-Leibler divergences between the model and observed probability density functions for each oligomer in the MD database. The numerical treatment of the problem is complicated by various constraints on the set of admissible parameters: some of the parameters are symmetric, positive-semi-definite matrices of different sizes, and various independent superpositions of these matrices must be positive-definite. Through a detailed study of this system of constraints and the construction rule for the internal energy and hence probability density function for an oligomer, we construct an analytical characterization for an approximate minimizer of the Kullback-Leibler objective functional. Using an initial guess based on this characterization, we were able to successfully minimize the objective functional using a constrained gradient flow procedure and thereby obtain a best-fit parameter set for the model. Various predictions using this parameter set are compared with existing data on B-form DNA, both experimental and simulated, and both sequence-averaged and sequence-specific. The comparisons show that the model predictions are consistent with accepted properties of B-form DNA, and that the model can successfully predict properties such as the non-local effects of single-nucleotide polymorphisms and the non-local context effects of various structural degrees of freedom.

Optimal packing

Overview

An understanding of how material filaments may be optimally packed in confined geometries, and how they may supercoil or wrap around themselves, is of great interest in the study of macromolecules such as DNA and other systems in chemistry and biology. There is evidence to suggest that structural motifs in double helical DNA and α-helical proteins may be explained by optimal packing rules, as well as the packaging of DNA in viral capsids. Whether one is seeking minimum energy configurations or sampling from a thermodynamic ensemble, a realistic model for a physical material filament must account for the fact that the filament possesses a definite three-dimensional volume and cannot pass through itself. Problems such as optimal packing and supercoiling are critically dependent on this effect, which is typically referred to as the excluded-volume or steric constraint in the polymer physics literature.

Mathematically, the basic problem is to optimize the energy of a curve in three-dimensional space (or a framed curved if twist is important) subject to the condition that the curve be the centerline of a flexible, solid tube of prescribed radius. Four different problems of this type are illustrated in Figure 1(a-d). Panel (a) illustrates the problem of minimizing the arclength of a closed curve subject to the condition that the curve be the centerline of a solid tube of fixed radius. Because the tube cannot penetrate itself, an initially knotted curve becomes tight as its length is minimized. Panel (b) illustrates the problem of maximizing the length of an open curve subject to the condition that the curve again be the centerline of a solid tube of fixed radius, but now the curve must also fit within a given container or region of space. As the curve length is maximized the curve must adopt an optimal shape which allows the longest length. Panels (c) and (d) illustrate
variations on this theme; for example, one can fix the curve length and tube radius and minimize
the size of the container as shown in (c), or one can fix the curve length and size of the container
and maximize the tube radius as shown in (d).

(a) \hspace{1cm} \rightarrow \hspace{1cm} \text{(b)}

(c) \hspace{1cm} \rightarrow \hspace{1cm} \text{(d)}

Figure 1: Example optimal packing problems for curves with thickness.

Various analytical aspects of such optimizations problems have been studied by the investigator
and coworkers. Our results show that optimization problems of this type can be understood using
the novel global (radius of) curvature function for a space curve. In particular, global curvature
can be used to develop concise variational formulations, establish existence and regularity results,
and, in some cases, necessary conditions for these problems. In contrast, numerical methods for
these problems have received relatively little attention. Monte carlo and related methods have been
used, and some deterministic gradient-flow algorithms are now available, but to date there are no
provably convergent approximation schemes for computing local optimizers.

Main results

• In [20], a new concept for a space curve is introduced: the global curvature function. This
  function is shown to describe various geometrical properties of a curve. In particular, this
  function provides an explicit, analytically tractable description of the thickness or normal
  injectivity radius of a curve, which is the radius of the largest embedded tubular neighborhood.
  This tubular neighborhood plays a central role in the optimization problems illustrated in
  Figure 1(a-d); indeed, it provides a model for the tube shown in each problem. The novelty
  of the global curvature function is that it is well-defined on curves with minimal regularity,
  making it ideal for use in existence arguments. In [20] global curvature is used to develop
  a concise variational formulation of the ideal or tight knot problem illustrated in Figure
  1(a), and is used to derive the first known necessary condition for this problem. Since its
  introduction, the concept of global curvature has received considerable attention.

• In [16] and [13], the first existence and a-priori regularity results are established for the ideal
  knot problem illustrated in Figure 1(a) and for the optimal packing problem illustrated in
  Figure 1(d). In both cases the global curvature function played a key role. For example, in
  [16], global curvature is used to develop a new formulation of the self-contact constraint for
  curves, ribbons and rods, which can all be described geometrically as framed curves. The
  general problem we addressed is that of minimizing the energy of a framed curve subject to
  the condition that some tube surrounding the curve not penetrate itself. We found that the

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concept of global curvature leads to an exact formulation of the excluded-volume constraint when the tube in question corresponds to a tubular neighborhood of the underlying curve. In particular, an exact material constraint is obtained for unshearable framed curve theories, both inextensible and extensible. The one-sided constraint of self-contact which prevents the framed curve from passing through itself and changing knot type can be expressed by a positive lower bound on the global radius of curvature function. The key result is that, when defined in this manner, the constraint set is weakly closed in an appropriate family of Banach spaces. This fact is exploited to obtain a general existence result for framed curves subject to the constraint of excluded-volume. As special cases, we established the existence and a-priori regularity of the ideal shapes of knots, and the minimum energy shapes of elastic rods of prescribed thickness in the presence of self-contact.

- In [14], the idea of global curvature is used to develop a new class of models for self-interacting curves and surfaces with thickness. Curves and surfaces with thickness are ubiquitous in nature, and are of fundamental importance in mathematics, physics, biology and engineering. The excluded volume constraint in such systems is typically modeled with pairwise repulsive potentials that are necessarily singular, and which do not have an intrinsic length scale appropriate for modeling the finite thickness of the system. In [14] we developed a framework for modeling curves and surfaces with thickness which avoids singularities, and which provides a way to introduce a thickness length scale.

- In [15], various generalizations of global radius of curvature for space curves are introduced. In particular, the global radius of curvature at a point on a curve is defined as the smallest possible radius amongst all circles passing through this point and any two other points on the curve, coalescent or not. In particular, the minimum value of the global radius of curvature gives a convenient measure of curve thickness. Given the utility of the construction inherent to global curvature, it is also natural to consider variants of global radii of curvature defined in related ways. For example multi-point radius functions can be introduced as the radius of a sphere through four points on the curve, circles that are tangent at one point of the curve and intersect at another, etc. Then single argument, global radius of curvature functions can be constructed by minimizing over all but one argument. In [15] we described the interrelations between all possible global radius of curvature functions of this type and showed that there are only two of particular interest. These functions are then used to characterize certain critical helices that arise in the optimal shapes of compact filaments, in α-helical proteins, and in B-form DNA.

**Numerical methods in mechanics**

**Overview**

In classical and continuum mechanics one typically studies Hamiltonian differential equations, either ordinary or partial, possibly with external force and dissipative terms. When studying these systems numerically, it is desirable to use numerical methods that accurately reflect the underlying structure. Specifically, it is desirable to have schemes that preserve integrals and geometric structures in the absence of dissipation, that dissipate energy at the correct rate in the presence of dissipation, and
that inherit equilibrium and relative equilibrium solutions together with their stability properties. For example, Figure 2 shows a plot of energy versus time for a tumbling, nonlinearly elastic body computed with a standard technique. After a brief loading period, the body tumbles freely and the energy should be conserved. However, standard techniques can produce growth (or even dissipation) in the energy as shown in the plot. This is a striking result in view of the fact that the technique illustrated in the plot, the implicit midpoint rule, is an unconditionally A-stable method.

The basic problem is to design numerical methods that can provably maintain the underlying structure of a system. For systems arising in classical and continuum mechanics, the goal is to preserve structures related to energy and momentum, and various geometric invariants related to area and volume in phase space. My work to date in this topic has mainly been focussed on the design of energy-momentum conserving methods for both unconstrained and constrained Hamiltonian systems, and the detailed analysis of their stability and approximation properties.

Main results

- In [26], a novel application of the techniques of reduction theory for mechanical systems with symmetry is used to prove that the implicit mid-point rule can inherit discrete versions of relative equilibrium solutions, but these discrete solutions are generally only conditionally stable. Stability is regained by modifying the discretization in a way that respects the symmetry. The analysis is done within the context of a general central-force problem, but the results apply to a wide variety of systems with underlying $SO(3)$ symmetry, such as $N$-body systems and various initial-boundary value problems in non-linear elasticity. For related numerical results see [27] and [28].

- In [25], the concept of a discrete derivative is introduced and a new theory is developed for the design of conserving time integration schemes for Hamiltonian systems with symmetry. The main result is that, through the use of a discrete derivative, implicit second-order conserving schemes can be constructed for general systems; the result applies to both ODEs and PDEs. The schemes respect underlying symmetries, preserve integrals and time-reversibility in the absence of dissipation, obey underlying energy decay inequalities in the presence of dissipation,
and inherit equilibrium and relative equilibrium solutions. Since its introduction, the idea of a discrete derivative has been reviewed by a number of different authors.

- In [21] and [19], the theory developed in [25] is generalized to systems with constraints. In particular, in [19] the theory is used to construct a new class of time integration schemes for general initial boundary-value problems in finite-deformation elastodynamics. The schemes are shown to inherit the conservation laws of total energy, linear and angular momentum from the underlying field equations. Conserving schemes are constructed for general hyperelastic material models, both compressible and incompressible, and are formulated in a way that is independent of spatial discretization. The performance of the schemes are illustrated with several numerical examples using a Galerkin finite element discretization in space.

- In [24] and [22], a new technique is introduced to prove that structure-preserving time integration methods are characterized by structure-preserving modified equations. Modified equations are a concept from backward error analysis that characterize discretization errors in a numerical method. In particular, if a method has order $r$ on a given equation, then for any $N$ it has order $r + N$ on a certain perturbed or modified equation. Knowing properties of these equations often provides valuable insight into the methods. For example, our techniques show that symplectic schemes on Hamiltonian equations possess Hamiltonian modified equations. This result then implies that tools from Hamiltonian perturbation theory may be used to characterize the behavior of symplectic methods.

- In [18], a novel formulation of incompressible elastodynamics is used to establish a well-posedness result for the Neumann problem in linearized incompressible elastodynamics. In particular, there are many ways to formulate the equations of motion for a Lagrangian system on a manifold defined by configuration (holonomic) constraints. If the system is finite-dimensional, one typically has a choice between:

  (a) Euler-Lagrange ODEs in local coordinates;
  (b) Euler-Lagrange DAEs in ambient coordinates with explicit constraints and multipliers (obtained from action principle with multiplier rule);
  (c) ODEs in ambient coordinates with an invariant manifold (obtained by eliminating multipliers from Euler-Lagrange DAEs; physically meaningful solutions reside in the invariant manifold).

If the system is infinite-dimensional, then choices are limited. Local coordinates as in (a) are often unavailable, and so one typically formulates equations of motion as in (b). Moreover, just as in the finite-dimensional case, multipliers may be eliminated to obtain PDEs with an invariant set as in (c). Formulations such as those in (c) are referred to as ambient-space formulations. In [18] it is shown that, depending on how constraints are introduced into the underlying action principle in (b), markedly different ambient-space formulations (c) can be constructed. In particular, it is possible to construct formulations that are Hamiltonian in the entire ambient space, and for which the invariant set is the level set of a first integral or exponentially attractive in an appropriate sense. For the model problem of linearized incompressible elastodynamics, these ambient-space formulations led to new characterizations of the pressure field in an incompressible body, and led to new proofs of well-posedness.
Publications


