



Computing the exact arrangement of circles on a sphere, with applications in structural biology

Frédéric Cazals, Sebastien Lorient

► To cite this version:

Frédéric Cazals, Sebastien Lorient. Computing the exact arrangement of circles on a sphere, with applications in structural biology. [Research Report] RR-6049, INRIA. 2007, pp.56. inria-00118781v4

HAL Id: inria-00118781

<https://inria.hal.science/inria-00118781v4>

Submitted on 18 Sep 2007

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Computing the exact arrangement of circles on a sphere, with applications in structural biology

Frédéric Cazals — Sébastien Lorient

N° 6049 – version 2

version initiale Décembre 2006 – version révisée Septembre 2007

Thème SYM



*apport
de recherche*



Computing the exact arrangement of circles on a sphere, with applications in structural biology

Frédéric Cazals *, Sébastien Lorient *

Thème SYM — Systèmes symboliques
Projet Geometrica

Rapport de recherche n° 6049 – version 2[†] — version initiale Décembre 2006 — version révisée Septembre 2007 56 pages

Abstract: Given a collection of circles on a sphere, we adapt the Bentley-Ottmann algorithm to the spherical setting to compute the *exact* arrangement of the circles. The algorithm consists of sweeping the sphere with a meridian, which is non trivial because of the degenerate cases and the algebraic specification of event points.

From an algorithmic perspective, and with respect to general sweep-line algorithms, we investigate a strategy maintaining a linear size event queue. (The algebraic aspects involved in the development of the predicates involved in our algorithm are reported in a companion paper.)

From an implementation perspective, we present the first effective arrangement calculation dealing with general circles on a sphere in an exact fashion, as exactness incurs a mere factor of two with respect to calculations performed using *double* floating point numbers on generic examples. In particular, we stress the importance of maintaining a linear size queue, in conjunction with arithmetic filter failures.

From an application perspective, we present an application in structural biology. Given a collection of atomic balls, we adapt the sweep-line algorithm to report all balls covering a given face of the spherical arrangement on a given atom. This calculation is used to define molecular surface related quantities going beyond the classical exposed and buried solvent accessible surface areas. Spectacular differences w.r.t. traditional observations on protein - protein and protein - drug complexes are also reported.

Key-words: Arrangement of circles, molecular surfaces, Van der Waals models

* `firstname.name@sophia.inria.fr`

[†] Revision of report 6049, triggered by the publication of the companion report *Design of the CGAL Spherical Kernel and application to arrangements of circles on a sphere*

Calcul de l'arrangement exact induit par des cercles sur une sphère. Applications à la biologie structurale

Résumé : Étant donné un ensemble de cercles sur une sphère, nous présentons une adaptation de l'algorithme de Bentley-Ottmann sur la sphère pour calculer l'arrangement *exact* induit par les cercles. L'algorithme consiste à balayer la sphère avec un méridien, ce qui est non trivial en raison des cas dégénérés et de la spécification algébrique des événements.

D'un point de vue algorithmique dans le registre des algorithmes de balayage, nous développons une stratégie garantissant une taille linéaire de la queue de priorité. (Les aspects algébriques relatifs aux prédicats utilisés par l'algorithme sont présentés dans un travail associé.)

Du point de vue de l'implémentation, cet algorithme est le premier algorithme effectif traitant de façon exacte tous les types de cercles sur une sphère, le surcoût requis pour garantir l'exactitude du résultat étant un facteur deux par rapport à une implémentation avec arithmétique flottante —sur des exemples génériques. En particulier, nous mettons en évidence l'importance de la linéarité de la taille de la queue de priorité afin de n'être pas pénalisé par les échecs de filtres arithmétiques.

Du point de vue applicatif, nous présentons une utilisation de l'arrangement en biologie structurale. Étant données un ensemble de boules atomiques, l'algorithme est adapté de façon à obtenir pour chaque face de l'arrangement sur un atome donné, la liste des boules qui la contiennent. Cette information est utilisée pour définir des quantités allant au-delà des surfaces moléculaires exposées et enfouies. Des différences spectaculaires vis-à-vis des observations classiques sont ainsi obtenues sur des complexes protéine-protéine et protéine-médicament.

Mots-clés : Arrangement de cercles, surface moléculaire, modèle de Van der Waals

1 Introduction

1.1 Atoms, spheres, and multi-body interactions

Balls and their boundaries i.e. spheres are amongst the simplest geometric objects, and are ubiquitous in science and engineering. Among their many uses, maybe the most interesting and surprising one is found in bio-chemistry, as in modeling (macro-)molecules with Van der Waals (VdW) models, an atom is represented by a ball whose radius depends on the atomic properties and its covalent environment. The physical accuracy of a ball to model an atom is certainly limited, but as collections of thousands of atoms are not amenable to quantum mechanic calculations, VdW models provide a compromise between accuracy and tractability. Such models are actually instrumental in a number of structural biology problems, amongst which characterizing *hot spots* [RTVC04], modeling solvation and the hydrophobic effect [EM86, Cha05], investigating electrostatic properties [LFSB03], defining *scoring functions* [MJ85, AT97, GK01], etc.

As most (if not all) of the classical algorithms on spheres required by the afore-mentioned applications on VdW models have reached their geometric maturity, the next stage consists of improving the bio-chemistry models, which will in turn require new geometric developments. One such cycle was possibly initiated in a recent paper dedicated to the investigation of interfaces in protein - protein complexes [CPBJ06]. To state the problem briefly, consider the HP model where each atom is tagged as Hydrophobic or Polar. In investigating *interfaces* of protein - protein complexes in this model, it turns out that pairwise contacts across the interface follow a random distribution given the propensities of the two species, while one naturally expects more H-H (P-P) contacts from the hydrophobic *core* (hydrophilic *rim*) of the interface. This simple observation calls for the development of geometric models quantifying multi-body interactions, so as to account for the complexity of atomic environments. As the neighbors of a given atom intersect its sphere along circles, one way to tackle this problem consists of investigating the equivalence classes of arrangements of circles induced by the neighbors of this atom. To do so, the first step consists of computing an arrangement of circles on a sphere so as to decompose the whole atomic surface, and the second one consists of reporting the atomic balls covering a given face of this arrangement. This decomposition features regions exposed on the molecular surface —which may be retrieved from α -shapes. But it also contains regions which are not exposed on the boundary, and encode higher order multi-body contacts.

Illustrations of insights gained from arrangement based models on protein - protein and protein - drug complexes are provided on Figs. 1 and 2 –refer to section 10 for the details.

