

BUILDING AN ATLAS OF TANGLES

KENNETH L BAKER, DROR BAR-NATAN, NEIL HOFFMAN,
AND ANASTASIIA TSVIETKOVA

1 The fields of topology and geometry have been greatly advanced by a wealth of
2 simple examples to analyze. In the study of 3-manifolds from topological, geometric,
3 combinatorial and quantum points of view, the first examples that allow to check
4 intuitive ideas are often knots and links. The purpose of this research project is to
5 extend the classification of knots and links to a classification of tangles, which one
6 can consider as building blocks for knots and links.

7 While *tangle* can describe a variety of objects, we will consider tangles comprised
8 of a arcs and b circles properly embedded in the 3-ball up to isotopy fixing the
9 boundary of a in the boundary of the ball. First, we seek to enumerate all tangles
10 such that $a = 2$ of small complexity, namely that the tangle admits a planar
11 diagram having m or fewer crossings. (The actual m will be determined later by
12 the computation time of our algorithms.) Second, we will classify these tangles up
13 to isotopy type. In future work, we would seek to develop and apply techniques to
14 higher values for a .

15 The results of this project should be of interest to (at least) two audiences.
16 First, 3-manifold topologists, especially knot theorists, will benefit from having
17 this “infrastructure project” addressed. By providing a concise and defined table
18 to test ideas against, topologists will be able to understand their relevance and to
19 gauge their computability of any new tangle invariant. There are numerous papers
20 where this analysis has been applied to the tabulations of knots and links (see
21 papers citing [7] and Rolfsen’s table [8]). Tangles themselves form the building
22 blocks for knots and links, and so a deeper understanding of tangles would lead to
23 advances in the field. A second audience for this project is applied mathematicians,
24 such as, for example, DNA topologists. The double helix backbone of DNA may
25 be modeled with tangles and its topology effects its various functions, replication
26 among others (see e.g. [2]). The action of certain proteins upon DNA may be
27 studied in this model through *subtangle replacements* [5], i.e. removing a rational
28 tangle from a link or tangle and closing that tangle with a second rational tangle.

29 Our research program is straightforward, however we will now provide greater
30 detail to what is mentioned above. First, we seek to extend and implement the
31 enumeration of knots and links as performed in the tables of [1] to our setting in

32 order to enumerate all possible tangles with small crossing number comprised of
33 two arcs and n circles. Second, we hope to classify all such tangles up to isotopy.

34 Initially, there are two techniques we hope to use to distinguish these tangles.
35 In recent work (see [9, §4.2]), the fourth investigator applies the idea of *encircled*
36 *tangles*, namely adding an extra embedded circle to a tangle diagram such this
37 embedded circle alternates between over and under crossings with the two arcs of
38 the tangle that connect to the boundary. Excluding a few pathological cases, the
39 tangle inside the circle has a canonical hyperbolic structure independent of the
40 link containing it by [9, Theorem 7.5]. Therefore, this structure can be used as
41 an invariant to distinguish tangles. Additionally, to any tangle in the ball we can
42 associate a 3-manifold that is a double cover of the ball branched over the arcs and
43 circles of the tangle. In particular, when the tangle has only two arcs, this manifold
44 will have torus boundary. A wealth of 3-manifold invariants may then be deployed
45 for distinguishing non-homeomorphic tangles. While some ideas along these lines
46 have been implemented as part of the software ORB [6], that piece of software is
47 no longer being updated. In addition to the updates for compatibility with current
48 computer architectures, this software would also need to be tweaked to include a
49 scriptable interface.

50 The SQuaREs model is well suited for building such an atlas of tangles. This
51 project will require a considerable use of computational tools. Having a number of
52 people working in collaboration to first build and then later maintain and grow the
53 atlas seems ideal for the work that needs to be done. In addition, the final product
54 will be freely available software that would include a sortable repository similar
55 to [1]. The third and fourth authors will take responsibility for the large scale
56 computational tasks and maintenance of the atlas, while the second author, based
57 on his experience with [1], and the first author drawing on his experiences with
58 both 3-manifold topology and DNA topology [2, 3], will guide the project ensuring
59 the resulting atlas and its interface are flexible and user-friendly. In addition, our
60 team meets the criterion of the SQuaREs model. This collaboration would bring
61 together not only four people at different stages of their careers, namely two post
62 doctoral researchers and two professors, but also four people that are well suited to
63 solve this specific problem because their variety of expertise.

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85 KENNETH L BAKER, ASSISTANT PROFESSOR, DEPARTMENT OF MATHEMATICS, UNIVERISTY OF
 86 MIAMI, MIAMI, FL

87 *E-mail address:* kenken@math.miami.edu

88 DROR BAR-NATAN, PROFESSOR, DEPARTMENT OF MATHEMATICS, UNIVERSITY OF TORONTO,
 89 TORONTO, ONTARIO, CANADA

90 *E-mail address:* drorbn@math.toronto.edu

91 NEIL HOFFMAN, POST DOCTORAL RESEARCHER, DEPARTMENT OF MATHEMATICS AND STATIS-
 92 TICS, UNIVERSITY OF MELBOURNE, MELBOURNE, AUSTRALIA

93 *E-mail address:* nhoffman@ms.unimelb.edu.au

94 ANASTASIIA TSVIETKOVA, POST DOCTORAL RESEARCHER, ICERM, BROWN UNIVERSITY, PROV-
 95 IDENCE, RI

96 *E-mail address:* n.tsvet@gmail.com