CENTREFOLD

Vaughan Jones and Knot Theory
A New Zealand Mathematician Unravels a New Invariant
which links Diverse Sciences in an Unforeseen Thread

What is so fascinating about Vaughan Jones's new polynomial invariant is not just that is has settled one of the most fundamental unresolved problems in topology—the development of a topological invariant which can distinguish left and right-handed simple knots—but that it also provides one of those rare instances where abstract pure mathematics provides an unforeseen relationship between diverse scientific disciplines.

Vaughan graduated from the University of Auckland in 1973 with an M.Sc. with first class honours in Mathematics. He had also taken Physics to stage III. He then moved overseas to take his Ph.D. at the Université de Génève, Switzerland, under the supervision of André Haefliger. He is now a Sloan Foundation Fellow and Professor of Mathematics at the University of California, Berkeley.

Vaughan Jones's work leading up to the discovery, was in Von Neumann algebras. This branch of quantum mechanics deals with the mathematical treatment of such observables as energy, position and momentum. In quantum mechanics, observables are represented by operators in Hilbert space. Commuting operators represent observables which can be measured simultaneously. The set of operators which commute with a given operator forms an algebra and provides a basis for the definition of Von Neumann algebras. A Von Neumann algebra on a Hilbert space is an algebra of bounded operators which is closed under the transpose-conjugacy of operators $(Ap,q) = (p,A^*p)$, where $(,)$ is the inner product.

A factor is a Von Neumann algebra whose centre is C^1. Any Von Neumann algebra can be built out of a collection of factors. Vaughan Jones's discovery arose from work he was doing on a class of factors called II_1 factors. These in addition possess a trace, a linear functional into C such that that $\mathrm{tr}(1) = 1$ and $\mathrm{tr}(ab) = \mathrm{tr}(ba)$. The trace, which in matrix notation corresponds to the sum of the diagonal entries, is all important in the development of the Jones polynomial. The most striking feature of the trace is that its range on projections $(e : e^2$

$= e$, $e = e*$) is the whole unit interval. By contrast, the normalized trace on projections of matrix algebras $M_n(C)$ are the $n + 1$ values $\{0, 1/n, 2/n, ..., 1)$. Projection operators correspond to choosing an axis with which to measure observables such as spin. The trace thus gives a measure of dimensionality which, in the case of a II_1 subfactor, provides for continuous dimensions. Another example of continuous dimensionality is provided by the fractal dimension of such structures as space-filling curves, where the dimensionality gives a measure between 1 and 2 for fractals whose length grows on a change of scale.

Vaughan was considering the relationship between a II_1 factor M and a subfactor N when the connection with knot theory emerged. Subfactors correspond to studying a subsystem of a quantum mechanical system. Trace theory (for operators) then leads to the definition of the index of N in M as

$$[M : N] = \dim_n(L^2(M)),$$

a real number $\geqslant 1$. In fact, though this index can take any value $\geqslant 4$, its only values < 4 are the numbers $4\cos^2(p/n)$, for integral $n \geqslant 3$.

The proof of this result threw up a set of relations which so resembled those of the braid group that it provoked a meeting between Vaughan Jones and knot theorist Joan Birman and the new polynomial emerged.
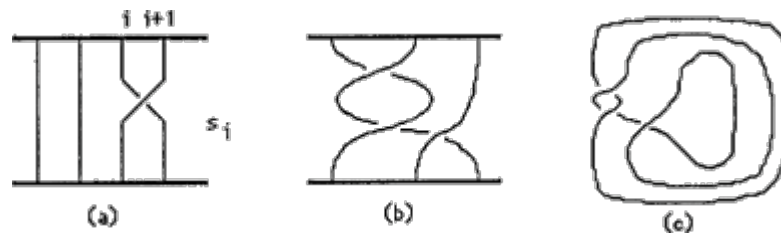

Fig 1

A braid differs from a knot in that it is a set of **descending** curves that begin and end at a corresponding set of points, as shown above (b). No curve can turn upwards at any point. Any two N-braids are concatenated by joining one above the other. The resulting group is easily generated by the elementary braids s_i as in (a), as in Artin's presentation:

$$\{s_1, s_2, ... , s_n : s_i s_{i+1} s_i = s_{i+1} s_i s_{i+1}, s_i s_j = s_j s_i \text{ if } ||i - j|| \geqslant 2\}$$

In the proof of the dimensionality theorem, Jones was led to study a tower of subfactors generated by the identity and N projections $e_1, e_2, ... , e_n$. The relations between the e_i were so similar to the braid presentation that the substitution

$$q_i = t^{1/2}(te_i - (1 - e_i))$$

has the correct relations and enables the definition of a representation r_t sending s_i to g_i .

A tame link in 3-space is an embedding of one or more circles which can be represented as polygons (so that for example they do not have an infinite sequence of smaller knots). The above braid (b), denoted (b, 3) can be converted into the link (c) by joining corresponding points to form $b^{\wedge}$. Conversely, Alexander had proved that any tame link L can be represented

by some (b, n). This ultimately enables the definition of the Jones polynomial in terms of the trace:

$$V_L(t) = (-(t + 1)/t^{1/2})^{n-1} \mathrm{tr}(r_t(b))$$

where (b, n) is the braid corresponding to L.

The definition may also include a factor of $t^{e/2}$ (see the Notices article). The relation is so indirect that it is essential to find a more amenable relationship to use for calculation.

Alexander discovered his polynomial in 1928. Subsequently in 1970 Conway, elaborating on a theme of Alexander's original paper showed that the Alexander polynomials could be calculated inductively as follows: Consider a knot or set of links and concentrate on a single crossing point of a plane projection. Let L_+, L_0, L_- denote oriented links which agree except on a small disk, where they vary as shown below. The unoriented figure is eliminated in the oriented case, but will be discussed later.
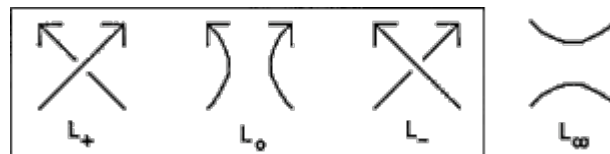

Fig 2

This sequence is very interesting, because it relates three knots rather than just the two which are involved in the usual process of 'passage' in which a strand is divided and passed over another before being rejoined (left versus right diagrams). The central diagram results from exchange of strands so that the sequencing order on the knot is changed. This has profound consequences in the case of DNA where the unknotting enzymes of such processes as supercoiling cause passage, but the second process of recombinational exchange is also possible. The two operations combined constitute the full repertoire of transformations under the new polynomial and the only transformations possible for DNA.

Conway showed that the normalized Alexander polynomial obeys the recurrence relation

$$AL_+(t) - AL_-(t) + (t^{1/2} - t^{-1/2})\, AL_0(t) = 0$$

Vaughan Jones's polynomial proved to obey a slightly different recurrence relation

$$tVL_+(t) - t^{-1}VL_-(t) + (t^{1/2} - t^{-1/2})\, VL_0(t) = 0.$$

The announcement of the Jones polynomial led to another astounding piece of mathematical serendipity when eight mathematicians in five different groups independently and simultaneously produced a two variable generalization of both the Jones and Alexander polynomials which could even more sensitively distinguish links up to the two shown below.

This can be represented most conveniently as a homogeneous three variable polynomial, P with all terms having zero net power in x, y, and z. In particular P obeys the recurrence relation

$$xPL_+(x,y,z) + yPL_-(x,y,z) + zPL_0(x,y,z) = 0.$$

The other polynomials can be expressed in terms of P as follows

$$AL(t) = PL(1, -1, t^{1/2} - t^{-1/2}), \qquad VL(t) = PL(t, t^{-1}, t^{1/2} - t^{-1/2}).$$

The two variable form, P' can be constructed in various ways but a convenient form is $P'L(x,z) = PL(x,x^{-1},z)$ which then obeys the recurrence relation

$$xP'L_+(x,z) + x^{-1}P'L_-(x,z) + zP'L_0(x,z) = 0.$$

$$P'L(x,z) = (-x^{-4} - x^{-2} + 2 + x^2) + (x^{-4} + 2x^{-2} - 2 - x^2) \cdot z^2 + (-x^{-2} + 1) \cdot z^4.$$
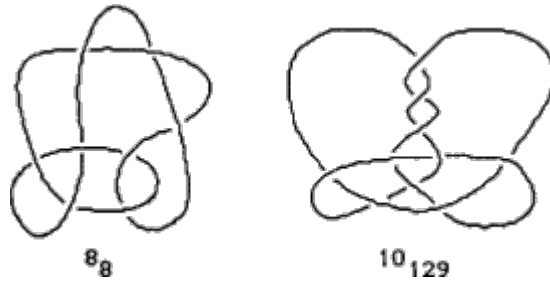
8_8 10_{129}

Fig 3

The traditional methods for computing the Alexander polynomial via the group of the knot enable a knot with many crossing overs to have A calculated in one step via determinants associated with the overpasses or through the homotopy group. By contrast, the algorithms above grow exponentially with the complexity of the knot and become excessively complex for more elaborate knots, however they have an intrinsic intuitive appeal in that the polynomial of any knot can be calculated by building it up successively from the above triplet relation beginning with the trivial polynomial 1 for a single unknotted circle. The first such step is shown below:
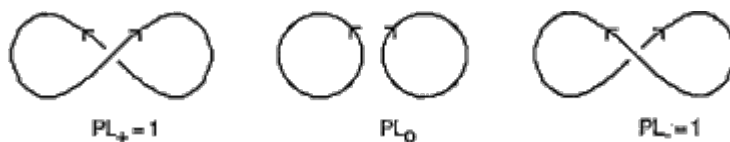
$PL_+ = 1$ PL_0 $PL_- = 1$

Fig 4

hence by the recurrence relation we have

$$x \cdot 1 + y \cdot 1 + z \cdot PL_0 = 0 \ \text{ or } \ PL_0 = (x + y)/z.$$

A further development of the polynomial saga has been the discovery of an independent polynomial on unoriented links which involves all four diagrams of Fig. 2. In particular, $QL(x)$ is defined by

$$QL_+ + QL_- = x \cdot (QL_0 + QL_{00})$$

whence

$$Q8_8(x) = 1 + 4x + 6x^2 - 10x^3 - 14x^4 + 4x^5 + 8x^6 + 2x^7$$

$$Q10_{129}(x) = 1 - 12x - 2x^2 + 26x^3 + 4x^4 - 20x^5 - 4x^6 + 6x^7 + 2x^8$$

As is shown above, this invariant can distinguish the knots of Fig. 3, but it cannot tell links from their mirror images. Kaufmann has refined Q to include orientation by a clever route which can also enable a computation of the Jones polynomial without having to consider the order of the decompositions of individual nodes. Because the Q polynomial relationship involved two uncrossed types, it is possible to use it to reduce the projection of a link to unknotted components. Study of the writhe of the resulting graph enables orientation to be included in the new polynomial R. In fact it has been shown that

$$VL(t) = (t^{-3/4}, -(t^{-1/14} + t^{1/4}))$$

so the Jones polynomial is a special case of both P and R.

The connection with molecular biology is every bit as interesting as the connection with quantum mechanics. The double helix of DNA and RNA has one complete turn for every ten base pairs. The human haploid genome contains 3×10^9 base pairs, and hence approximately 10^8 twists per cell. In addition supercoiling, linking and recombination between strands gives nucleic acid dynamics an exceedingly complex knotting behaviour. Single nucleic acid strands are oriented by their sugar-phosphate polarity. Over the last few years several types of topoisomerase enzyme have been discovered which permit a variety of knotting and linking operations. Type 1 topoisomerases cut a single DNA strand and permit the passage of another strand. They can relax supercoiling by allowing a double helix to unwind around one strand and can link and knot single stranded loops. Type 2 gyrases can perform similar operations on double-stranded loops. Resolvase by contrast can extrude a specific portion of a twisted loop to form two linked loops. In addition, recombinational processes such as occur in sexual crossing-over in meiosis relate PL_0 to PL_+ and PL_-.