Research Results

María de los Angeles Guevara Hernández

1.- Adams et al. in 1992 introduced the concept of dealternating number for a link. The dealternating number of a link diagram D is the minimum number of crossing changes necessary to transform D into an alternating diagram. The dealternating number of a link L, denoted $dalt(L)$, is the minimum dealternating number of any diagram of L. Further, they proved that if a prime knot K has dealternating number one then K is either a hyperbolic knot or a torus knot. On the other hand, Kawauchi in 2010 introduced the concept of alternation number. The alternation number of a link diagram D is the minimum number of crossing changes necessary to transform D into some (possibly non-alternating) diagram of an alternating link. The alternation number of a link L, denoted by $alt(L)$, is the minimum alternation number of any diagram of L.

It is immediate by definition that dealternating number is greater than or equal to the alternation number for any link L; however, in general, it is not easy to show an arbitrary gap between them. In this sense, I have investigated the alternation number and the dealternating number of knots and I have constructed for each positive integer n a family of infinitely many hyperbolic prime knots with alternation number 1 and dealternating number equal to n. Besides, these knots have braid index equal to $n+3$ and Turaev genus equal to n.

2.-We have given formulae to obtain the HOMFLY polynomial of certain oriented 3-tangles and links formed by the closure of them. In particular, we have non-recursive formulae for the Conway-Alexander polynomial. Furthermore, by using the Alexander polynomial, we give a family of knots, which consisting infinitely many non-alternating prime knots, which have alternation number equal to one. This family contains the first non-alternating knots: *8-19, 8-20, 8-21,* and *9-42*.

1.-Changes in the DNA molecules topology can be produced by the action of certain enzyme. In order to characterize topologically the action of several site-specific recombination Ernst and Sumners in 1990 introduced the tangle model, which is a useful topological tool in the study of the mechanism of action of certain enzymes on DNA molecules. In particular, the model proves helpful to determine the topological structure of the DNA molecules resulting from those reactions.

Roughly speaking, the tangle model consists in solving a system of three equations in which the *unknowns* on the left-hand side of each equation are tangles, whereas the *known* data on the right-hand sides are 2-bridge knots in many cases. Under the assumption that the 3-tangles involved were in fact 3-braids, a particular class of 3-tangles, we prove that, while a system of two equations always admits a solution for any selection of 2-bridge knots, adding a third equation reduces the number of possible knots to only 6, 9 or 18, the exact value depending on the relationships satisfied by the knots in the first two equations. If a fourth equation is adjoined, however, exactly one 2-bridge knot may appear in the right-hand side for the system to admit a solution. Furthermore, a new simple method that exploits an unexpected cyclic behavior of the solutions was presented and used to construct the proofs. The method relies on the continued fractions associated with 2-bridge knots and their behavior under the concatenation of 3-braids.