

## An Extension of Classical Mathematical Derangements

Any collection of objects can be arranged or ordered in several ways. Each such arrangement is called a permutation of the collection of objects. Take some permutation of a collection of objects as an initial permutation. A derangement (from the initial permutation) is defined to be a distinct permutation such that no object is placed in the same position as it was in the initial permutation. For example, with the collection of the numbers  $\{1, 2, 3\}$ , taking  $1\ 2\ 3$  as the initial permutation, the derangements from  $1\ 2\ 3$  are  $2\ 3\ 1$  and  $3\ 1\ 2$ . This is the classical derangement case that was studied extensively by de Montfort in the early 18th century. De Montfort was able to provide a formula to compute the number of derangements from any permutation of a collection of any given size. This concept has roots in statistical analysis and calculations of outcomes of chance.

Using an appropriate recasting of the problem as a question of forbidden positions on chessboards, this research extends the classical derangement question by disallowing certain positions for certain objects in the collection. In the above example, one may disallow 1 to be in the 3rd position, for instance, so that the only derangement from  $1\ 2\ 3$  is  $3\ 1\ 2$ . This disallowing of certain positions for certain objects is made precise in the language of Ferrers boards, or (square) chessboards with a missing section in the lower right corner. Although the enumeration of these derangements is certainly not equivalent to the classical case, and not necessarily independent of the initial permutation, it will be shown that in particular cases (in particular, when the missing section of the Ferrers board is rectangular) the derangements do satisfy some properties that also hold in the classical case.

This research is theoretically interesting as a particular case of the mathematical theory of matchings and set partitions. It has direct applications to computer science and computational mathematical biology, for example in the elucidation of the pseudoknot structure of RNA.