1135-92-1188   **Ricardo Sanchez*** (`rsanchezh70@hotmail.com`) and **Lucia Barrera Arenas**. *Key concepts on mathematics for bioinformatics.*

The mathematical community and the non-mathematical community working on Bioinformatics have the benefit of numerous algorithms available for the analysis of the genomes and associated concepts. Concepts such as the Manhattan Tourist Problem, Euclidean Distance, Hamming Distance use equations such as $d(P,Q)+d(Q,R) \geq d(P,R)$, known as the triangle inequality may use the BLAST program on the NIH website. Other Graph Theory algorithms are available for the construction of phylogeny trees inside BLAST and others such as MEGA that includes multiple alignment, EMBOSS for Global and Local Alignments. There are more concepts applied here from Combinatorics, String Theory to analyze insertions and deletions on the sequences (v,w); $d(v,w)=n+m-2s(v,w)$, with s, the length of the string. Many of these algorithms are available for researchers and students. (Received September 20, 2017)