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BIODIVERSITY BIOTECHNOLOGICAL POTENTIAL ASSESSMENT USING ALGORITHMS FOR AUTOMATIC WEB SURVEY

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Marine biotechnology studies are mainly species-approach, and regarding to its genetics, biochemical process and natural or industrial products. Studies with a biodiversity-approach are very scarce or even absent. This project aimed to advance the technology to improve the biodiversity assessment regarding to its biotechnological potential. The biotechnological potential of determined species is here defined as the amount and the relevance (as citation numbers) of the studies regarding biotechnology issues. In an attempt to test this innovative approach, the algorithms 'Scholar.py' and 'Sci-stat', both available on Github repository, were used to reach an automatic search on 'Google Scholar' and to the metrics of the results regarding scientific names associated with the term 'biotechnology'. The lists of species used was obtained from the SISBio database, from the reported sampling data of the Marine Extractive Reserve of Arraial do Cabo/RJ (ResexMar-AC) and the Marine National Park of Fernando de Noronha/PE (ParnaMar-FN), the two Federal Marine Conservation Units with the largest tourist flow in Brazil. Three formulas, based on number of results, mean citation of the studies, and the range of year of them, were tested to rank the species. For the ones that repeatedly appeared in the top positions, the abstract of the first ten studies were read to check the results quality and to identify the potential of that species regarding to biotechnology. As main results, the data draws attention that ResexMar-AC has a richer marine environment (corroborating with the literature), and the available literature suggests that the species listed in the ResexMar-AC have a greater biotechnological potential. ResexMar-AC held all the best-ranked species, and most of them are considered exotic or are native but considered exotic in other parts of the world. In other hand, some of the best ranked species was considered as false positives, because the studies abstract evidenced that it is not regarding that specie, or it is quite generalist. As for example, ten of ten abstracts read of *Amphibalanus trigonus* were actually studies about *A. amphitrite*, enhancing a bias in the developed approach. Although this bias enhance the need of algorithm improvement, this innovative approach evidence its applicability to biodiversity assessments, to secondary data survey, and to species potentially good indicators and, in this case, with biotechnological potential for further investigations.