A Multilayered Assessment of Neural Interface Materials via IN3-BIO

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The development of implantable neural interfaces relies on identifying biomaterials that seamlessly integrate with biological tissues without triggering adverse immune responses. Biocompatibility assessment has traditionally been an experimental process, but the increasing complexity of material science demands more scalable, data-driven approaches.
Current evaluations often struggle with fragmentated data across scientific literature and the high variability in cellular responses at the molecular level.
The lack of centralized, structured repositories for material-induced biological effects limits the ability to predict biocompatibility before moving to costly and intensive *in vitro* and *in vivo* trials.
In this study, we introduce IN3-BIO, a comprehensive and scalable platform for evaluating material biocompatibility through harmonized *in silico*, *in vitro*, and *in vivo* pipelines. Our *in silico* framework combines Natural Language Processing (NLP) for automated knowledge extraction with transcriptomic profiling to characterize material-cell interactions, bridging the gap between unstructured scientific knowledge and biological data.
Utilizing the DEBBIE tool and custom R-based scripts, we automated the retrieval of 7,453 abstracts which were refined through meta–analysis to 1,516 key studies. Through biomedical concept recognition (genes, chemicals, cell lines) and through manual curation, we transformed fragmented literature into a unified knowledge base that informs and optimizes subsequent *in vitro* and *in vivo* experiments. Furthermore, by analyzing 17 transcriptomic datasets from the cBiT database, we provide a molecular-level validation of findings reported in the literature, addressing the gap between high-level observations and gene-level regulation. Although data heterogeneity presents challenges for predictive modeling, our approach ensures data integrity by validating published findings and aligning them with experimental observations.
This two-tier computational approach effectively overcomes the challenges of data heterogeneity, providing a standardized and reproducible framework for preliminary biocompatibility screening.
By synthesizing AI-driven text mining with bioinformatics, this workflow accelerates the discovery of safe biomaterials, offering a blueprint for more efficient medical device development. Ultimately, these computational methodologies reduce dependence on trial-and-error experimentation, paving the way for the next generation of precision neural implants.

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