ALLEGATO 2

PROJECT DESCRIPTION[1]

TITLE: Artificial Intelligence-based Dengue virus infection predictor

ACRONYM: AI-DENInfect

PRESENTING ENTITY: Politecnico di Bari

ID CALL: COC-2-2024-UNIPV

Firmato digitalmente da:
CUPERTINO FRANCESCO
Firmato il 24/06/2024 10:39
Seriale Certificato: 1635484
Valido dal 19/07/2022 al 19/07/2025
InfoCamere Qualified Electronic Signature CA

[1] To be filled in English

1. GENERAL INFORMATION

Title:	**Artificial Intelligence-based Dengue virus infection predictor**
Acronym	AI-DENInfect
Project duration	14 months
Total Project Cost (Euro)	1.500.000,00
Cofinancing (if planned, Euro)	125.200,00
Financing requested (Euros)	1.374.800,00

Abstract

Artificial intelligence (AI) can play a prominent role in enhancing surveillance of viruses of the pandemic potential well behind the application of predictive models to analyze demographic, environmental, and pathogen-based data to track the spread of emerging microorganisms. AI may also be fundamental to unravel the intricacies of biology modifications during infection, that stem from the host-pathogen interactions and trickle down to modifications in the transcriptomic profiles and the protein post-translational patterns.

In this proposal, structured in line with the INF-ACT program, we propose a project to investigate pathogenicity through bioinformatic predictions and mathematical models to analyze patterns in viral molecular interactions. The viral model we will utilize for our study is the Dengue virus (DENV), a novel pandemic threat now reaching the South of Italy, becoming an emergency requiring a prompt response. Our initiative is not only aligned with the INF-ACT research program, but it also complements the GENESIS project, which aims to study the persistence of arboviral emerging viruses.

AI-DENInfect will investigate, through the development of several AI models, the genomic and structural adaptations mediating the molecular interaction between the viral proteins and the host protein targets. A particular focus will be on the initial stages of the infectious cycle of DENV.

Overall, the project will advance of the following scientific areas:

1. Development of the first comprehensive and effective predictor based on AI technologies to screen the infection pathogenesis of arboviral diseases
2. Application of bioinformatics and AI to combine genetic and structural data, deep learning algorithms, and advanced computational capabilities to solve important issues in infection biology, such as host-pathogen interactions which exert paramount effects on host species passage, cellular/host species tropism, replication dynamic, and viral fitness.

Keywords (up to 5): Artificial intelligence; Dengue virus; Viral entry and interference; Viral evolution; Predictive algorithm.

2. CONSORTIUM COMPOSITION

Consortium	Legal Entity Short Name	Public	Private	Country	Dept./ Division / Laboratory	Scientist-in-Charge
Presenting Entity						
1. Politecnico di Bari	POLIBA	X		Italy	Department of Electrical and Information Engineering	**Vitoantonio Bevilacqua**
Beneficiaries						
2. Università degli Studi della Campania "L. Vanvitelli"	UNIVAN	X		Italy	Department of Experimental Medicine	**Massimiliano Galdiero**
3. Mentotech	MENTOTECH		X	Italy	R&D Biotech	**Walter Sanseverino**
4. Negedia	NEGEDIA		X	Italy	R&D Biotech	**Beatrice Salvatori**