A Computational Study to Interrogate the Regulation of Hemostatic Systems in the Presence of SARS-CoV-2: Therapeutic Management of the Pathogenic Response through Interventions

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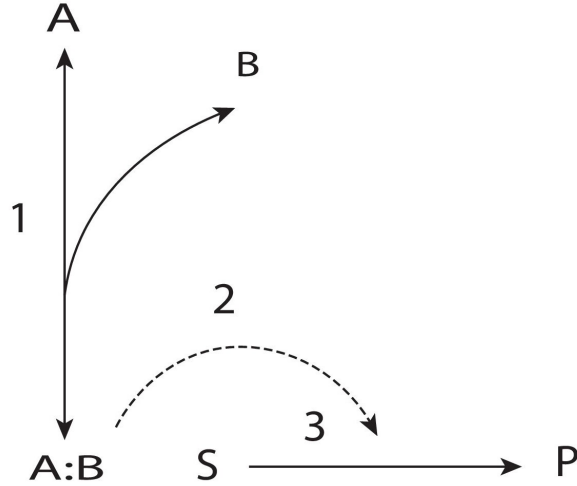## Dummy mathematical model

Fig 1. Reaction network diagram of dummy mathematical model.

$$\frac{d(A)}{dt} = -[k^+] * A * B + [k^-] * AB$$

$$\frac{d(B)}{dt} = -[k^+] * A * B + [k^-] * AB$$

$$\frac{d(AB)}{dt} = [k^+] * A * B - [k^-] * AB$$

$$\frac{d(S)}{dt} = -\frac{[k_{catS}^{AB}] * S * AB}{([k_{mS}^{AB}] + S)}$$

$$\frac{d(P)}{dt} = \frac{[k_{catS}^{AB}] * S * AB}{([k_{mS}^{AB}] + S)}$$

Assumed species A, B represent genes/proteins, and AB their complex. S and P indicate substrate and product. By kinetic law of mass action suppose association rate (k^+) and disassociation rate (k^-).

Assumed, AB cleaved substrate S, the cleavage rate is represented by $\frac{[k^{AB}_{catS}]*S*AB}{([k^{AB}_{mS}]+S)}$. Where k^{AB}_{catS} implies catalytic rate and k^{AB}_{mS} implies Michaelis constants such that $k^{AB}_{mS} = \frac{k^- + k^{AB}_{catS}}{k^+}$, disassociation constant $k_d = \frac{k^-}{k^+}$ [1].

References

1. Liu B, Zhang J, Tan PY, Hsu D, Blom AM, Leong B, Sethi S, Ho B, Ding JL, Thiagarajan PS. A computational and experimental study of the regulatory mechanisms of the complement system. PLoS Computational Biology. 2011 Jan 20;7(1):e1001059. https://doi.org/10.1371/journal.pcbi.1001059 PMID: 21283780