Heuristic modeling for prognosis of neuro-oncological cases and evaluation of treatment protocols

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Abstract

Heuristic models to generate sub optimal solutions in neyr-oncological case studies entail the incorporation of several elements of criticality drawn in from a myriad haze of parameters like pathology, hematology, cell morphology and the metabolic factors of muscle, glucose and blood besides the enzymatic factors related to the auto-immune disruptive forces.

SEQUENCING INFLUENCES - VITAL METABOLISM AND IMMUNOLOGICAL SEQUENCING
SIMULATED CONCLUSION -1

VITAL PARAMETER	FUNDAMENTAL CAUSAL LINK	BLOOD METABOLISM INFLUENCE WEIGHT	GLUCOSE METABOLISM INFLUENCE WEIGHT	IMMUNOLOGICAL SEQUENCING WEIGHT
Diastolic	Serum quality	0.99	0.77	0.99
Systolic	Serum quality	0.99	0.77	0.99
HR / tachycardiac output/ functionality of arterial - venous blood volume ratio	Plasma capacity for optimum coagulation, serum quality for rheological properties and fluid viscosity/ organ conductivity for electrical signaling and flux strength at plexus	0.99	0.98	0.99
RR / Cp - oxygen/Cp - carbon monoxide/ Tidal and residual volume/ alveolar dead space / alveolar perfusion				
CBV				
Opacity ratio of cerebral cells - hypothalamus/ occipital/grey matter				

EEG - graphical analysis for field strength / NCV / CSF conductivity for electrical signaling - parietal / lumbar / cervical zone analysis	Field strength and dielectric field creation propensity	0.99	0.95	0.99

KEY DETERMINANTS OF ORGAN CONFIGURATIONS AS A FUNCTION OF PERFUSION PROPERTIES – *SIMULATED CONCLUSION -2*

OXYGENATION	PERFUSION STRENGTH (as measured by CBV)	FLUX STRENGTH (as measured by the phase angle of the field)	RESIDUAL DIELECTRIC FIELD (as measured by the phase angle)
65%	97%	0.73	0.21
73%	95%	0.73	0.2
71%	97%	0.75	0.19
68%	91%	0.74	0.17
74%	98%	0.77	0.13
71%	97%	0.73	0.22
58%	88%	0.62	0.28
54%	85%	0.59	0.34
52%	83%	0.57	0.35
49%	80%	0.52	0.39
CORRELATION STRENGTHS	OXYGENATION - PERFUSION	PERFUSION - FLUX STRENGTH	FLUX STRENGTH - RESIDUAL DIELECTRIC
	0.944111703	**0.959957187**	**-0.980789019**

The **key determinants in a heuristic model** have the following characteristic features:

1. **Underlying influence on cross-domain parameters**

There are several attributes of the variables that do have underlying cluster influences on the key parameters of major impact on the outcome of a treatment protocol and the commensurate significance in definitive prognosis.

2. **Attunement to clusters in an apparent binomial density with the possibilities of normalizing to continuum in the data scatter.**

The variables of influence in the context of neuro-oncological sciences have the potential to influence multiple clusters of known impact based on empirical understanding. Heuristic models can unravel the underlying hidden clusters of influence as well as evolving the cross links that have escaped the notice of empirical understanding in the domain hitherto.

3. Poisson scatter evolution from the heuristic models

The critical influence paradigm in a heuristic model is one of Poisson repulsion from the various clusters and therefor having the seminal potential of disruptive impact in the prognosis. Such Poisson scatter of very rare variables and impacting influences can bring in major shifts in the treatment protocols and concomitant prognosis of neuro-oncological interventions.

Mathematical modeling with an exhaustive parametric definition can lead to major discoveries and drug inventions for achieving efficacious solutions in the treatment and consequent prognostic trends of a critical mass of suffering humanity.

The paper outlines the possibilities with greater clarity than ever and showcases the potential of heuristics in medical diagnostics and treatment pathways in the domain of oncology.

Heuristic approaches on simulated mode

Baseline treatment of variables in a DFBL – depth first and breadth later mode entail the establishment of the efficacy of each of the variables in a binomial probability density function to discrete entities near independent of influences.

$P(x,n,p) = (n/x)\ p^x\ (1-p)^{(n-x)}$ --------(i) (Node determination -1)

(n) implies the number of trials and x is the scatter of outcomes in clinical trials for each of the competing variables in isolation treatment of the others.

(x) scatter is independent of each other in the function and has a probability density (p) for each trial.

Conceptualization of the Heuristic nodes of influence variables in the DFBL mode necessitate the independent probability density in a population scatter to track the poisson element. *Cancerous growth is recognized as a poisson distribution and the probability density function is of seminal impact in predicting outcomes.*

$f(k) = (e^{-\lambda}\ \lambda^x)\ /(x!)$ ----------(ii) (Node determination -2)

λ is the interval rate of the time series of events between occurrences. This is of fundamental importance in evaluating a sequence of events leading to the proverbial "black swan" event of a discovery of changing cellular morphology and mutations leading to oncological states. The time rate used in the poisson density function of likelihood events during the experimental stages should be narrow enough to accommodate detection of rare occurrences.

Euler number is used to denote the maturity of events around a data scatter and definitive clinical outcomes for each of the competing variables. It is important to arrive at **reproducibility of variables** by looking at a tapering constant wherein e>1in the expression y=(1/x). Gravitating around euler gives referential clinical values that can be safely assumed to be benchmarks in a heuristic referential.

$f(k) = e^{\lambda}\zeta_{\iota=0}{}^{[\kappa]}\lambda^{\iota}/\iota!$——————————(iii) - the cumulative density function for maximum likelihood of a poisson event in the data scatter of each of the clinical variables in isolation. *[k] is the floor function in magnitude that helps achieve a saturation maturity in the stochastic process.* (Node determination -3)

Cumulative density function equalizes the variances within the realm of reproducibility and enhances the data fidelity for feeding into the heuristic plane.

Decisive treatments on the DFBL grid to arrive at effective cluster strengths and deriving the functional crosslinking variables across the parametric breadth.

The decisive mechanism of the heuristic process in the DFBL mode is the reduction in entropy for arriving at cluster strengths. As the entropy reduces, the stochastic process reaches a stagnation and the cluster strength is derived for optimality.

The stochastic process in the heuristic DFBL mode described in the article is a Markove chain (fundamentally time invariant although the basic variables had been initially treated with a time rate differential) and consequently shall have the following expression:

$p(e_1, e_2, e_3 \ldots e_n) = p(e_1), p(e_2 \mid e_1), p(e_2 \mid e_3) \ldots p(e_n) \mid (e_{n-1})$ --------(iv) (Node determination -4)

where e is the clinical outcome or event and n trials are conducted to arrive at stochastic definitive and time invariant stationary.

$H(Y) = -\zeta_{ij}(\mu_{ij}) P_{ij} \log(P_{ij})$ ----------(v) (Node determination -5)

The rate of entropy in the stationary Markove chain is expressed above and builds the foundation of achieving the cluster strength of influences in the Heuristic grid.

The neural networks and the epochs are terminated at the stagnating rate of entropy and consequently define the nodes in the heuristic algorithms.

PROBLEM STATEMENT *- FINDING THE ORIGINS OF MEDULLA BLASTOMA AND PREDICTING OUTCOMES ON PARAMETRIC ANALYSIS OF ANTENATAL CARE PROTOCOLS*

DOMAIN	**SPECIFIC ELEMENTS OF RESEARCH**	**MATHEMATICAL MODELS**	**OUTCOMES SOUGHT IN THE RESEARCH**	**CLINICAL ASSUMPTIONS - NARRATIVE**	**IMPLEMENTATION COHORT AND ECOSYSTEM DEVELOPMENT**
Antenatal studies of progression	Blood metabolism	Fourier analysis of data clusters	Precision limits for safe metabolic data and	ECMO analysis of the findings on metabolic quality could	Blackstone Synergy - Sai cluster of hospitals shall
	Glucose metabolism	Fourier analysis of data clusters			

		defining the potential benchmark measures for predictive analytics on medulla blastoma or related metastizing tumor regression in the CNS	be an essential derivative for confirmig the findings	evaluate the possibilities of technical tie-ups with EU / US leaders in cognitive research of the fetus, clinical analyses of fMRI and ECMO and finally the parametric hosts of big pharmaceutical research models
Blood perfusion in the embryo and through the various stages of development of the fetus	Heuristics modeling of key clinical parameters to deduce the equalty of perfusion	Predicting regressive changes in perfusion that can form the basis for further aggregation of research with fMRI functionality on advanced clinical set-up	fMRI findings on perfusion, opacity of the cell and mapping the v/q parameters in the contextual comprehension of the perfusion quality in the CNS shall be the bedrock of predictive derivatives	
Cognitive movements of the fetus	Heuristics modeling of key clinical parameters to deduce the equality of perfusion			
Psycho-somatic mapping of the expecting mother				

Stochastic conditions for the Heuristic mode:

1. Epochs = 100,000

2. Data smoothing = exponential with power 2 for the pathological elements and logarithmic compression for the thoracic elements
3. R^2 = 0.44 for pathological elements and 0,38 for thoracic elements

PATHOLOGICAL - HEMATOLOGICAL GRID

PARAMETRIC GRID (DFBL mode - depth first and breadth later)		**Lipid profile**	**Uric acid**	**TPC**	**WBC count / esonophils and family**	**Hb%**	**HCT%**	**Creatinine and renal profile**
Depth (nodes) for the influencing variables	**d_1**	Food combustion	Muscle metabolism	Muscle metabolism	CNS signal fidelity	CNS signal fidelity	CNS signal fidelity	CNS enzymes with food combustion triggers
		Muscle metabolism	Fast twitch / slow twitch muscle spread	Fast twitch / slow twitch muscle spread	Peripheral nerve signal strength	Peripheral nerve signal strength	Peripheral nerve signal strength	Pancreatic enzymes
		Fast twitch / slow twitch muscle spread	Pancreatic enzymes	Blood metabolism	Diastolic - systolic gap percentage	Diastolic - systolic gap percentage	Diastolic - systolic gap percentage	Muscle metabolism
	d_2	Pancreatic enzymes	CNS enzymes with food combustion triggers	Pulmo - Cardiac output signified by V/Q	Blood metabolism	Blood metabolism	Blood metabolism	Fast twitch / slow twitch muscle spread
	d_3	CNS enzymes with food combustion triggers	Glucose metabolism in the CNS	Glucose metabolism in the CNS	Glucose metabolism in the CNS	Glucose metabolism in the CNS	Glucose metabolism in the CNS	Food combustion
		Cluster strength > 0.91						
		Cluster strength > 0.73 </= 0.79						

PARAMETRI **THORACIC VITALS**

C GRID (DFBL mode - depth first and breadth later)		Diastolic	Systolic	HR / tachycardiac output/ functionality of arterial - venous blood volume ratio	RR / Cp - oxygen/ Cp - carbon monoxide/ Tidal and residual volume/ alveolar dead space / alveolar perfusion	CBV	Opacity ratio of cerebral cells - hypothalamus/ occipital/grey matter	EEG - graphical analysis for field strength / NCV / CSF conductivity for electrical signaling - parietal / lumbar / cervical zone analysis
Depth (nodes) for the influencing variables		Muscle metabolism	CNS signal fidelity	Pulmo - Cardiac output signified by V/Q	Muscle metabolism	CNS signal fidelity	Muscle metabolism	Muscle metabolism
	d_1	Fast twitch / slow twitch muscle spread	Peripheral nerve signal strength	CNS signal fidelity	Fast twitch / slow twitch muscle spread	Peripheral nerve signal strength	Fast twitch / slow twitch muscle spread	Fast twitch / slow twitch muscle spread
		Blood metabolism	Muscle metabolism	Peripheral nerve signal strength	CNS signal fidelity	Diastolic - systolic gap percentage	CNS signal fidelity	Glucose metabolism in the CNS
	d_2	Pumo - Cardiac output signified by V/Q	Blood metabolism	Muscle metabolism	Peripheral nerve signal strength	Blood metabolism	Peripheral nerve signal strength	Blood metabolism
	d_3	Glucose metabolism in the CNS	Glucose metabolism in the CNS	Fast twitch / slow twitch muscle spread	Glucose metabolism in the CNS	Glucose metabolism in the CNS	Glucose metabolism in the CNS	Pumo - Cardiac output signified by V/Q
cluster strength of influence > 0.83								
cluster strength of influence > 0.55</= 0.61								

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