SDF induced termination of pregnancy

– a treatise on the causal links with mathematical models for establishing the decision trees for diagnostics and treatment pathways

Exploring the unknown frontiers for the cry of a baby

SDF – causal links to termination of pregnancy

INFERTILITY LINKAGES – THE PHYSIOLOGICAL CHARACTERISTICS OF DNA FRAGMENTATION

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SCSA - sperm chromatin structural analysis – *The* ***causal link -1*** *– spermatogenesis caused by nuclear degeneration, code genes and non-code genes*

- **Single stranded DNA torsion** brings forth the inability to melt and intrinsically form a part of the cellular morphology leading to eventual fragmentation of the double stranded DNA
- **Reduced efficacy of the enzyme** that attributes to the repair of the single stranded DNA is a critical disruptive cause for the DNA fragmentation leading eventually to SCSA
- **Protamine transformation leading to histone retention in the cellular structure** is a major disruptive derivative causing the SCSA

SCSA - sperm chromatin structural analysis – *The **causal link -1** – spermatogenesis caused by nuclear degeneration, code genes and non-code genes*

- **Attribute -1:** Low blood perfusion in the CNS disrupts the dielectric field leading to debilitating influences of NCV – nerve conducting velocity and peripheral opacity to homeostatic environs as well as exchange of nutrients – oxygenated complex; the precursors for morphological disintegration of the single and eventual double stranded DNA

SCSA - sperm chromatin structural analysis – *The **causal link -1** – spermatogenesis caused by nuclear degeneration, code genes and non-code genes*

- **Attribute - 2:** Pyscho-somatic interventions of thought profiles in the CNS that trigger toxicity concentrates in the cellular morphology leading to fragmentation of the single and double stranded DNA

SCSA - sperm chromatin structural analysis – The **causal link -2** – code gene influences

Fragmentation of the DNA material through code gene drops in concentration

SCSA - sperm chromatin structural analysis – *The **causal link -2*** – *code or marker genes*

- **NEURO – ENDOCRINE GENES**

Configuration: GnRH, FSH, LH, FSHR and LHR

Oxidative stress can potentially weaken the secretion concentrations eventually disrupting the DNA transcript carrier – capacities or migratory impact into the thoracic organs and concomitant gametogenesis

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SCSA - sperm chromatin structural analysis – *The* ***causal link -2*** *– code or marker genes*

GONADAL DEVELOPMENT RELATED GENES

(AZF, WT1, PRDM1,SF)

PAD – peripheral arterial disease is a derivative of lipids and contaminants in blood leading to blockage. Suppression of the gonadal genes significantly impact the metabolism of muscles adversely leading to potential SDF as well.

SCSA - sperm chromatin structural analysis – *The* ***causal link -2*** *– code or marker genes*

MEIOSIS RELATED GENES

(MLH1, IRF1, PRDM9,SPO11)

Oxidative stress can lead to serious disruptions of cellular networking, regeneration and promotion of a homeostatic environment that caters efficiently to both positive and negative signaling triggers of corrective measures

Intrinsic losses in cellular networking deplete the quantum of transcript formation activity and subsequent stabilization of the DNA material in the gamete cell environment

SCSA - sperm chromatin structural analysis – *The* ***causal link -2*** *– spermatogenesis caused by substance abuse leading to uncontrolled oxidative stress*

- **Attribute -1:** Substance abuse is the primary contributing element for generating oxidative stress in the blood stream
- **Attribute -2:** Increased toxicity in the blood stream brings forth disruptions of a) pulmonary V/Q, b) offsets O_2/Co_2 partial pressure ratios in the arterial blood , c)might disrupt the oxygenation in the cardio-pulmonary interface causing near – pulmonary shunt like situation

SCSA - sperm chromatin structural analysis – *The **causal link -2*** *– spermatogenesis caused by substance abuse leading to uncontrolled oxidative stress*

- **Attribute - 3:** CNS V/Q and CBV –cerebral blood volume reduction are the major attributes for aggressive triggers of oxidative stress in the cellular morphology of the sperms leading to DNA fragmentation
- **Attribute - 4:** Toxicity in the blood stream reduces the blood perfusion characteristics in the CNS leading to severe SCS fragmentation

SCSA - sperm chromatin structural analysis – *The **causal link -2** – spermatogenesis caused by substance abuse leading to uncontrolled oxidative stress*

- **Attribute - 5:** Code genes are the marker genes that can be tracked and the quality of triggers in the somatic changes can be measured and recorded. Oxidative stress in the blood stream caused by the carcinogenic and nicotine residual toxins in the cellular morphology across the thoracic organs cause disruptions in hormonal output as well as in the **DNA aggregation in the gametogenesis process**

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SCSA - sperm chromatin structural analysis – *The **causal link -2** – spermatogenesis caused by substance abuse leading to uncontrolled oxidative stress*

- **Structural changes in the homeostatic environment**
- The homeostatic environment as determined by the negative signaling component is severely disrupted in a toxic concentration of the arterial blood stream owing to adverse influences on the CNS
- Disruptions in the homeostatic environment further deplete the quality of gametogenesis by providing barriers in the formation and aggregation of the DNA material

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SCSA - sperm chromatin structural analysis – *The* ***causal link -2*** – *sperm apoptosis triggers of the non-code or non-marker genes*

- **Structural changes in the DNA material**

1. mRNA or memory RNA has two segmented components in mi RNA and pi RNA contributing to the formation of the genetic transcript of the DNA. Low blood perfusion and higher concentration of toxins following both oxidative stress and thought-induced myelin stress from signaling and dielectric field peaks create an abrasive destruction of the potential transcript of the DNA bordering on mutation or structural creation of mutating environment

SCSA - sperm chromatin structural analysis – *The* ***causal link -2*** *– sperm apoptosis triggers of the non-code or non-marker genes*

- **Structural changes in the DNA material – the non-marker genes**

2. si RNA or signal interfering short waves RNA potentially disrupt the flux strength of the cerebral field by failing to bridge for the signal continuity affecting adversely the CSF – cerebra spinal fluid electric strength and in cervical and parietal zones leading to potential neuropathy that eventually destroys the transcriptase material in the DNA leading to SDF.

SCSA - sperm chromatin structural analysis – *The* ***causal link -2*** *– sperm apoptosis triggers of the non-code or non-marker genes*

- **Structural changes in the DNA material – the non-marker genes**

3. cir RNA or circular RNA is responsible for the stabilization of the transcript and the nutrients in a rounding off circular ecosystem dependent primarily on the metabolic factors of blood, glucose and muscle.

Potential reduction in metabolic strength of the male severely affects the functionality of the cir RNA leading to SDF

SCSA - sperm chromatin structural analysis – *The **causal link -2*** – *sperm apoptosis triggers of the non-code or non-marker genes*

- **Structural changes in the DNA material – the non-marker genes**

4. inc RNA is the binding gene for the nutrients into the cell morphology in networks with the transcript to promote the stability of the DNA material in the sperm

Primarily, the higher concentration of slow twitch muscles retard the food combustion processes thereby inhibiting the binding properties of the essential inc RNA genes

Mathematical modeling to delineate influence clusters

Visualizing DNA aggregation in the cellular morphology of the gametogenesis process

Heuristics approaches - the essential influence grid for parametric visualization-1

- Gametogenesis is a complex process with near optimality of diverse yet complementing processes in the realms of pathological changes, the hematological influences and more importantly in the aspects of blood perfusion in the CNS that evaluates the homeostatic environment to define the metabolic states
- Heuristics yield sub-optimal causal approximates to shape decision making treatment protocols
- Validation of the output derivatives on the influencing variable clusters and the concomitant parametric structure is determined by the prognosis on remission or progression of the disruptive elements of SDF

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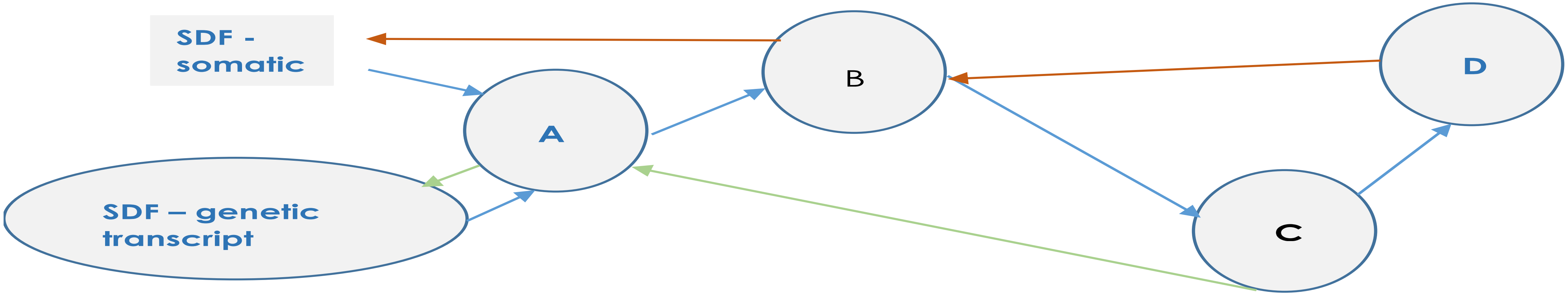
Heuristics approaches - the essential influence grid for parametric visualization-2



NODE –A: Somatic impressions with oxidative stress and metabolic disruptions forming the cluster

NODE – B: CNS – code genes overlapping cluster

NODE – C: CNS – non-code genes for transcript definitive cluster

NODE- D: Unknown residuals with overlapping somatic and CNS derivatives

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Heuristics approaches - the essential influence grid for parametric visualization-3

A. **the forward propagation reference frame** = $(x+a)^n = \sum_{k=0}^{n} \binom{n}{k} x^k a^{n-k}$ = an essentially binomial distribution with parameter a and variable influences as x

B. the backward propagation reference frame - $f(x) = a_0 + \sum_{n=1}^{\infty} \left(a_n \cos \frac{n\pi x}{L} + b_n \sin \frac{n\pi x}{L} \right)$ = with a Fourier transform defining the overlapping influences of the various CNS and metabolic influences.

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Research areas – the compelling needs

PROBLEM STATEMENT CRYSTALLIZATION:

“ Definitive grid of causal links for potential indicators of SDF and the remissive guarantees for the treatment protocols and positive prognosis”

METHODOLOGIES AND THE POWER THEREIN:

“ Ascertaining the parametric grid and establishing the near – optimal influence clusters through advanced heuristics