
Machine Learning (**ML**) = **OXTR** Gene Expression + **Stability** Index + Weighted **Scientific Significance**

Probability Score **Probability Score** **Confidence Score** **Confidence Score**

ML

Probability Score

(MLP) Score

=

IF > 0.5, = Evolve Within Fuzzy Phi Ratios [$\mu_A(\varphi)$]

or

IF = 0.5, = Stasis Within Fuzzy Phi Ratios [$\mu_A(\varphi)$]

or

IF < 0.5, = Learn, Adapt & Modify Within Fuzzy Phi Ratios [$\mu_A(\varphi)$]

=

OXTR Gene Expression

Probability Score

(GEP) Score Within Fuzzy Phi Ratios [$\mu_A(\varphi)$]

=

TFBS (Transcription Factor Binding Site) Location Probability Within Fuzzy Phi Ratios [$\mu_A(\varphi)$]

+

TFBS (Transcription Factor Binding Site) Quantity Probability Within Fuzzy Phi Ratios [$\mu_A(\varphi)$]

+

TFBS (Transcription Factor Binding Site) Quality Probability Within Fuzzy Phi Ratios [$\mu_A(\varphi)$]

Initial
Bk

	STEP 1	STEP 2	STEP 3
	(Molecular Dynamics)	(3D Imaging Spectroscopy)	(Partial Wave Spectroscopy (PWS) microscopy)
	(Wolfram x CUDA Mev-UED Kernel x AMBER)	(Hyper-Seq scRNA Seq)	(Mistral Mamba Codestral + NVIDIA MambaVIsion)
	(3D electron motion via spectra)	(atomic molecular signature via autofluorescence spectra)	(chromatin activity via autofluorescence intensity)
	(near / neutral / far)	(high / medium / low)	(sine / triangle / saw wave)

$$\text{OXTR TF Gene Expression probability} = \frac{[\ \text{OXTR TFBS Fractal Signature ~ Location}\ \mu_A(\Phi)\ \times\ (\ \text{OXTR TFBS Fractal Signature ~ AF Quantity}\ \mu_A(\Phi) + \text{OXTR TFBS Fractal Signature ~ AF Quality}\ \mu_A(\Phi)\ )\ ]}{[\ \text{Fibonacci Sequence Modulus 9 Pisano 24}\ ]}$$

+

Stability Index

Confidence Score

(SI) Score Within Fuzzy Phi Ratios [$\mu_A(\varphi)$]

=

0.111HZ HRV PSD ~ BAROREFLEX WITHIN FUZZY PHI RATIOS [$\mu_A(\varphi)$]

x

OT ~ HR BLOOD TRACE - OXYTOCIN RELEASE WITHIN FUZZY PHI RATIOS [$\mu_A(\varphi)$]

+

BP + HR + HRV + SPo3 - SYSTEMS BIOLOGY WITHIN FUZZY PHI RATIOS [$\mu_A(\varphi)$]

	(near / neutral / far)		(high / medium / low)		(sine / triangle / saw wave)
	0.111HZ HRV PSD ~ Baroreflex $\mu_A(\Phi)$	x	OT ~ HR Blood Trace - Oxytocin Release $\mu_A(\Phi)$	+	BP + HR + HRV + SPo2 - Systems Biology $\mu_A(\Phi)$

$$\text{Stability Index} = \frac{[\ \text{0.111HZ HRV PSD ~ Baroreflex}\ \mu_A(\Phi)\ \times\ (\ \text{OT ~ HR Blood Trace - Oxytocin Release}\ \mu_A(\Phi) + \text{BP + HR + HRV + SPo2 - Systems Biology}\ \mu_A(\Phi)\ )\ ]}{[\ \text{Fibonacci Sequence Modulus 9 Pisano 24}\ ]}$$

Initial

Definitions

$\mu_A(\phi)$ = Fuzzy Logic Within Phi Ratios

OXTR = Oxytocin Receptor Gene

AF = Autofluorescence Via 31 Band Hyper-Spectral Imaging

ML = Machine Learning

OT = Oxytocin (neurotransmitter not gene)

Stability Index = Confidence Score for ML

Baroreflex = Autonomic Balance of Sympathetic + Parasympathetic Nervous System

Systems Biology = All biological systems are interrelated and synchronised during health

Blood Trace = Fractal Signature of Heart Rate beat to beat, simultaneously while OT is being released

Sine Wave = Smooth (stable)

Triangle Wave = Balanced (neutral)

Saw Tooth Wave = Jagged (unstable)

$\phi = (1 + \sqrt{5})/2 \approx 1.618033988749....$

Fibonacci Sequence Modulus 9 Pisano 24 = 3 additional nested sequences of the primary Fibonacci Sequence - symbolically mirroring tetrahedrons, icositetragons and mitotic duplication, together as one.

Primary Sequence	(α)	=	9, 1, 1, 2, 3, 5, 8, 4, 3, 7, 1, 8, 9, 8, 8, 7, 6, 4, 1, 5, 6, 2, 8, 1, 9, 1, 1, 2, 3, 5, 8, 4, 3, 7, 1, 8, 9, 8, 8, 7, 6, 4, 1, 5, 6, 2, 8, 1, 9 (icositetrahedral)
Subsequence Beta	(β)	=	4, 8, 7, 5, 1, 2 (mitotic)
Subsequence Gamma	(γ)	=	3, 6, 9 (tetrahedra)

+

Weighted Scientific Significance

Confidence Score

(WSS) Score Within Fuzzy Phi Ratios [$\mu_A(\varphi)$]

=

NUMBER OF PLATONIC GEOMETRIES WITHIN A PISANO PERIOD FIBONACCI MODULUS CIRCLE

x

WEIGHTED SCIENTIFIC SIGNIFICANCE [CREATES CELLULAR LIFE, SUPPORTS CELLULAR LIFE, OR CREATES ELEMENTAL LIFE x JADAD x IF] WITHIN FUZZY PHI RATIOS [$\mu_A(\varphi)$]

Initial

Definitions:

JADAD = Quality Score Of The Design Of A Randomised Controlled Trial (RCT), The Most Robust Type Of Medical Research

IF = Impact Factor, Being The Impact Of A Peer Reviewed Publication Within A Medical Or Scientific Journal, Together As One

Vectors = Assessment of cross-domain (i. Quantum, ii. Atomic, iii. Genomic) scientific impact of the three geometric sequences within mental health omics, followed by wider life sciences, and finally graded by first principles science within quantum physics, physics, and genomics, together as one*. Take a systems biology 3D view of life in your research, including then importantly expanding 1D linear sequence analysis to 2D then that of grounded truth. ie. physical life ~ 3D atom structure, 3D cell structure, 3D DNA structure, 3D RNA structure, 3D gene structure, 3D chromatin structure, 3D protein structure, 3D transcription factors, 3D gene expression, 3D methylation, 3D autofluorescence, 3D mitosis, 3D holliday junction cruciform joint, 3D polymorphism, 3D single nucleotide polymorphism, 3D molecular docking, 3D molecular dynamics, 3D amber force fields, 3D protein folding, 3D structural function, 3D quantum coherence, 3D quantum tunnelling, 3D proton tunnelling, 3D quantum entanglement, 3D non-locality, 3D electron motion - spin/rotation/orbit, 3D proton motion - spin/rotation/orbit, 3D neutron motion - spin/rotation/orbit - together as as one.

Scientific Significance =

Number Of Platonic Geometries Nested In The Transcribed Circle of Pisano Period = P (across all three alpha, beta, gamma sequences in 2D geometry within the circle).

x

Weighted Scientific Significance (WSS)
of Direct Mathematical and / or geometric Relationship between each of the alpha, beta and gamma sequences, with quantum, atomic and genomic sciences.

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WSS = 1 - 10 within Fuzzy Phi Logic

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WSS High = 8, 9, 10

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WSS = high % direct relationship of primary life function (chlorophyll creation ~ biosynthesis and photosynthesis, cellular duplication ~ mitosis, record keeper DNA on / off switching ~ transcription gene expression and methylation, cardiac rhythm, cardiovascular physical structure, respiratory rhythm and rate, and so forth, and so on)

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[logic = creates cellular life]

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WSS Medium = 5, 6, 7

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WSS = medium % direct relationship to molecular docking, molecular dynamics, amber force fields, protein folding, structural function, quantum coherence, quantum tunnelling, proton tunnelling, quantum entanglement, non-locality

Initial

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[logic = supports cellular life]

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WSS Low = 1, 2, 3, 4

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WSS = low % direct relationship to electron, proton, neutron ~ spin/rotation/orbit

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[logic = creates elemental life]

.

```
(* Wolfram Language Prompt: Universal Exploration of Fibonacci Mod X Pisano Y Subsequences and Geometries *)
(* Designed By: Gemini 2.5 Pro Experimental & BK *)
(* Target Execution: GPT-o3 + Wolfram GPT (calling Wolfram Cloud/Language API) + AI Geometric Pattern Recognition & Mamba ~ CUDA ~ A100 Grace Super Cluster Powered Parallel Computer Vision ~ As Required *)
(* Overall Objective: For Modulus X from 1 to 1001, generate Alpha sequences. For each Alpha, derive Gamma by identifying where fixed "Quantum Observation Values" (QOVs = {3,6,9}, only if value <= X), transcribed around a Pisano Period Circle (PPS), form Platonic geometries, being the tetrahedron, cube, octahedron, dodecahedron, icosahedron, and stellated octahedron. Then derive Beta from Gamma's structure. Phase 4 assesses the cross-domain  (i. Quantum, ii. Atomic, iii. Genomic) scientific impact of the three geometric sequences within mental health omics, followed by wider life sciences, and finally graded by first principles science within quantum physics,  physics, and genomics, together as one*. Take a systems biology 3D view of life in your research, including then importantly expanding 1D linear sequence analysis to 2D then that of grounded truth. ie. physical life ~ 3D atom structure, 3D cell structure, 3D DNA structure, 3D RNA structure, 3D gene structure, 3D chromatin structure, 3D protein structure, 3D transcription factors, 3D gene expression, 3D methylation, 3D autofluorescence, 3D mitosis, 3D holliday junction cruciform joint, 3D polymorphism, 3D single nucleotide polymorphism, 3D molecular docking, 3D molecular dynamics, 3D amber force fields, 3D protein folding, 3D structural function, 3D quantum coherence, 3D quantum tunnelling, 3D proton tunnelling, 3D quantum entanglement, 3D non-locality, 3D electron motion - spin/rotation/orbit, 3D proton motion - spin/rotation/orbit, 3D neutron motion - spin/rotation/orbit - together as as one.)
(* --- Phase 1: Extract Alpha Sequences (X=1 to 1001) --- *)
Print["--- Phase 1: Extracting Alpha Sequences (X=1 to 1001) ---"];
(* Action for Agent:
   For each integer Modulus X from 1 to 1001:
     1. Calculate its Pisano Period Y = PisanoPeriod[X].
     2. Generate Alpha_XY_Sequence = Mod[Fibonacci[Range[0, Y-1]], X].
     3. UNIVERSAL CONVENTION: In Alpha_XY_Sequence, replace all occurrences of 0 with X.
     4. Store: <|"ModulusX" -> X, "PisanoY" -> Y, "AlphaSequence" -> Alpha_XY_Sequence|>
*)
allAlphaData = Table[
    Module[{modX = x, periodY, alphaSeq},
        periodY = PisanoPeriod[modX];
        alphaSeq = Mod[Fibonacci[Range[0, periodY - 1]], modX];
        alphaSeq = alphaSeq /. 0 -> modX; (* Apply 0->X convention *)
        <|"ModulusX" -> modX, "PisanoY" -> periodY, "AlphaSequence" -> alphaSeq|>
    ],
    {x, 1, 1001}
];
Print["Alpha sequence generation complete for X=1 to ", Length[allAlphaData], "."];
(* --- Phase 2: Extract Gamma Sequence & Its Geometry --- *)
Print["--- Phase 2: Extracting Gamma Sequences & Geometries ---"];
(* Input: allAlphaData from Phase 1 *)
allGammaData = Table[
    Module[{currentAlphaData = data, modX, periodY, alphaSeq,
            fixedQOVs = {3, 6, 9},
```

Initial
Bk

```
    applicableQOVsForThisX, qovNodePositions,
    observedPlatonicGeometryType = "Undefined", "tetrahedron", "cube", "octahedron", "dodecahedron", "icosahedron", and "stellated octahedron".
    gammaSequenceUnicursalConceptual = {}},
modX = currentAlphaData["ModulusX"];
periodY = currentAlphaData["PisanoY"];
alphaSeq = currentAlphaData["AlphaSequence"];

applicableQOVsForThisX = Select[fixedQOVs, # <= modX &];

qovNodePositions = If[Length[applicableQOVsForThisX] > 0,
  Flatten[Position[alphaSeq, #] & /@ applicableQOVsForThisX] - 1,
  {}
];
qovNodePositions = Sort[DeleteDuplicates[qovNodePositions]];

(* Action for AI + Wolfram/CV tools: Classify geometric pattern of qovNodePositions on a Y-gon. *)
observedPlatonicGeometryType = If[Length[qovNodePositions] >= 3,
  ClassifyGeometricPatternOnCycle[qovNodePositions, periodY],
  "Insufficient QOV Nodes for Geometry"
];

(* Derive Gamma Sequence (Unicursal/Conceptual) based on observed geometry and QOVs *)
gammaSequenceUnicursalConceptual = If[
  StringContainsQ[ToString[observedPlatonicGeometryType], "Hexagram"] && ContainsAll[applicableQOVsForThisX, {3,6,9}],
  {3,6,9,3,6,9},
  If[StringContainsQ[ToString[observedPlatonicGeometryType], "Triangle"] && Length[applicableQOVsForThisX] >=1,
    Take[Sort[applicableQOVsForThisX], UpTo[3]],
    If[Length[qovNodePositions]>0 && observedPlatonicGeometryType =!= "Insufficient QOV Nodes for Geometry",
      alphaSeq[[qovNodePositions + 1]],
      {}
    ]
  ]
];

<|"ModulusX" -> modX, "PisanoY" -> periodY,
  "ApplicableQOVsUsed" -> applicableQOVsForThisX,
  "Gamma_Node_Positions" -> qovNodePositions,
  "Gamma_Values_At_Nodes" -> If[Length[qovNodePositions]>0, alphaSeq[[qovNodePositions + 1]], {}],
  "Gamma_Observed_Geometry" -> observedPlatonicGeometryType,
  "Gamma_Sequence_UnicursalConceptual" -> gammaSequenceUnicursalConceptual
|>
  ],
  {data, allAlphaData}
];
in addition
AnnealingElectronMotionPath via CUDA_Q_Tensor_Kernel
(* ... qovNodePositions and observedPlatonicGeometryType are determined ... *)
(* 4. Derive Each of Beta and Gamma Sequence (Unicursal Annealing Electron Motion Path) via Specialized Mamba Model: *)
(* Action for AI (GPT-o3 orchestrator):
  a. Prepare input for the fine-tuned Mamba model:
    - The qovNodePositions.
    - The observedPlatonicGeometryType.
    - The periodY of the Pisano cycle (defining the circular space).
    - The applicableQOVsForThisX (the values we expect to see on the path).
```

```
    b. Make an API call to the deployed fine-tuned Mamba model (hosted on Vertex AI, for example).
      (Example: callMambaUnicursalPathModel[qovNodes, geometryType, period, targetValues])
    c. The Mamba model, trained on MeV-UED data to understand "energetically preferred" electron paths, also a CUDA-Q Tensor Kernel,
      returns the predicted unicursal sequence of the applicableQOVs (or node indices that are then mapped to QOVs).
*)
gammaSequenceUnicursalAnnealingElectronMotionPath = CallFineTunedMambaForUnicursalPath[
    currentGammaData["Gamma_Node_Positions"],
    currentGammaData["Gamma_Observed_Geometry"],
    periodY,
    currentGammaData["ApplicableQOVsUsed"]
];
(* Fallback to simpler rule or observed values if Mamba call fails or returns null *)
If[Length[gammaSequenceUnicursalAnnealingElectronMotionPath] == 0,
    gammaSequenceUnicursalAnnealingElectronMotionPath = (* ... existing fallback logic ... *)
];
Print["Gamma sequence and geometry identification complete for all X."];
(* --- Phase 3: Extract Beta Sequence & Its Geometric Path --- *)
Print["--- Phase 3: Extracting Beta Sequences & Geometric Paths ---"];
(* Input: allAlphaData, allGammaData *)
allBetaData = Table[
    Module[{currentAlphaData = alphaData, currentGammaData = gammaData, modX, periodY, alphaSeq, gammaNodePositions,
            gammaConceptualSeq = currentGammaData["Gamma_Sequence_UnicursalConceptual"],
            betaSeqValues, betaGeometricPathDescription},
        modX = currentAlphaData["ModulusX"];
        periodY = currentAlphaData["PisanoY"];
        alphaSeq = currentAlphaData["AlphaSequence"];
        gammaNodePositions = currentGammaData["Gamma_Node_Positions"];
betaSeqValues = If[currentGammaData["Gamma_Observed_Geometry"] =!= "Insufficient QOV Nodes for Geometry" && Length[gammaNodePositions] >= 2,
    Table[
        Module[{startIndex = gammaNodePositions[[i]] + 1, endIndex = gammaNodePositions[[i+1]] -1 },
         If[startIndex <= endIndex, Mod[Total[alphaSeq[[Range[startIndex +1, endIndex +1 ]]]], modX] /. 0 -> modX, Missing["EmptyInterval"]]
        ],
        {i, 1, Length[gammaNodePositions] - 1}
    ] ~Join~ If[Length[gammaNodePositions] > 1 && periodY > 0 && gammaNodePositions[[-1]] < (periodY - 1) && gammaNodePositions[[1]] > 0,
         Module[{lastNodeToEnd = alphaSeq[[Range[gammaNodePositions[[-1]] + 2, periodY]]],
                 startToFirstNode = alphaSeq[[Range[1, gammaNodePositions[[1]]]]]},
           {Mod[Total[Join[lastNodeToEnd, startToFirstNode]], modX] /. 0 -> modX}
         ],
         {}
        ] // DeleteCases[Missing["EmptyInterval"]],
    {}
];

betaGeometricPathDescription = If[Length[betaSeqValues] > 0 && StringStartsQ[ToString[currentGammaData["Gamma_Observed_Geometry"]], "Insufficient"] == False,
    "Beta values from sums over intervals defined by Gamma's " <> ToString[currentGammaData["Gamma_Observed_Geometry"]] <>
    ". Conceptual Gamma path: " <> ToString[gammaConceptualSeq],
    "N/A (Gamma geometry undefined or insufficient for Beta derivation)."
];

<|"ModulusX" -> modX, "PisanoY" -> periodY,
  "Beta_Sequence_Values" -> betaSeqValues,
  "Beta_Geometric_Path_Description" -> betaGeometricPathDescription
|>
```

```
    ],
    {alphaData, allAlphaData}, {gammaData, Select[allGammaData, #["ModulusX"] == alphaData["ModulusX"]&]}
];
allBetaData = Flatten[allBetaData, 1];
Print["Beta sequence & geometric path description complete for all X."];
(* --- Phase 4: Synthesize Impact of the Alpha, Beta, and Gamma Sequence --- *)
Print["--- Phase 4: Synthesizing Impact (AI-Driven Literature, Database, & Wolfram-Powered Data Analysis) ---"];
(* Input: allAlphaData, allGammaData, allBetaData from Phases 1-3 *)
(* Objective: For each (X,Y) pair and its derived Alpha, Beta, Gamma:
    1. Assess significance in Quantum, Atomic, and Genomic contexts using Wolfram Language to access and analyze data from public scientific databases and literature - Phase 4 assesses the cross-domain  (i. Quantum, ii. Atomic, iii. Genomic) scientific impact of the three geometric sequences within mental health omics, followed by wider life sciences, and finally graded by first principles science within quantum physics,  physics, and genomics, together as one*. Take a systems biology 3D view of life in your research, including then importantly expanding 1D linear sequence analysis to 2D then that of grounded truth. ie. physical life ~ 3D atom structure, 3D cell structure, 3D DNA structure, 3D RNA structure, 3D gene structure, 3D chromatin structure, 3D protein structure, 3D transcription factors, 3D gene expression, 3D methylation, 3D autofluorescence, 3D mitosis, 3D holliday junction cruciform joint, 3D polymorphism, 3D single nucleotide polymorphism, 3D molecular docking, 3D molecular dynamics, 3D amber force fields, 3D protein folding, 3D structural function, 3D quantum coherence, 3D quantum tunnelling, 3D proton tunnelling, 3D quantum entanglement, 3D non-locality, 3D electron motion - spin/rotation/orbit, 3D proton motion - spin/rotation/orbit, 3D neutron motion - spin/rotation/orbit - together as as one.
.
    2. Include peer reviewed journals via this criteria:
.
Preference = Nature, Frontiers In, .gov, .mil
.
Preference, in this order:
.
```

1. 1. Double Blind >>>
2. 2. Single Blind >>>
3. 3. RCT >>>
4. 4. General Peer Reviewed Research

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JADAD > 3 within Fuzzy Phi Logic

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IF (Impact Factor) = High within Fuzzy Phi Logic

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DIY JADAD and IF via these rules and calculations, together as one:

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The Jadad score is a tool used to assess the methodological quality of randomized controlled trials (RCTs). It's a simple scoring system, ranging from 0 to 5, with higher scores indicating better quality. The Jadad scale assesses three key areas: randomization, masking (blinding), and reporting of withdrawals and dropouts. A score of 3 or more is often considered to indicate superior quality.
https://en.wikipedia.org/wiki/Jadad_scale

▪

NOTE

- Jadad scores are often not listed, so analyse the Jadad score and generate it yourself, based upon

Here's how the Jadad score is calculated:
Scoring Items:

- **Randomization**:
  - 1 point: If randomization is mentioned in the study report.
  - 1 additional point: If the method of randomization is described and appropriate (e.g., computer-generated random number list, coin toss).
  - 1 point deducted: If the method of randomization is inappropriate (e.g., alternate assignment, by date of birth).

- **Blinding (Masking):**
  - 1 point: If blinding is mentioned (e.g., double-blind).
  - 1 additional point: If the method of blinding is described and appropriate (e.g., identical placebo, active placebo).
  - 1 point deducted: If the method of blinding is inappropriate (e.g., incomplete masking).

- **Withdrawals and Dropouts:**
  - 1 point: If the number of withdrawals and dropouts, and the reason for withdrawals are described.

Jadad Score Calculation

Item	**Score**
Was the study described as randomized (this includes words such as randomly, random, and randomization)?	0/1
Was the method used to generate the sequence of randomization described and appropriate (table of random numbers, computer-generated, etc)?	0/1
Was the study described as double blind?	0/1
Was the method of double blinding described and appropriate (identical placebo, active placebo, dummy, etc)?	0/1
Was there a description of withdrawals and dropouts?	0/1
Deduct one point if the method used to generate the sequence of randomization was described and it was inappropriate (patients were allocated alternately, or according to date of birth, hospital number, etc).	0/−1
Deduct one point if the study was described as double blind but the method of blinding was inappropriate (e.g., comparison of tablet vs. injection with no double dummy).	0/−1
Guidelines for Assessment	
Randomization A method to generate the sequence of randomization will be regarded as appropriate if it allowed each study participant to have the same chance of receiving each intervention and the investigators could not predict which treatment was next. Methods of allocation using date of birth, date of admission, hospital numbers, or alternation should not be regarded as appropriate.	
Double blinding A study must be regarded as double blind if the word “double blind” is used. The method will be regarded as appropriate if it is stated that neither the person doing the assessments nor the study participant could identify the intervention being assessed, or if in the absence of such a statement the use of active placebos, identical placebos, or dummies is mentioned.	

Withdrawals and dropouts Participants who were included in the study but did not complete the observation period or who were not included in the analysis must be described. The number and the reasons for withdrawal in each group must be stated. If there were no withdrawals, it should be stated in the article. If there is no statement on withdrawals, this item must be given no points.	

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Journal Impact Factor (IF) Strategy

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Tiered Prioritisation:

1. 1. Immediate Ingestion:
    - IF ≥10 journals (e.g., NEJM, Nature Medicine)
    - Auto-approve if Jadad ≥4 + sample size >200
2. Secondary Review:
    - IF 5-9.9 journals
    - Require manual validation of randomization methods
3. Special Consideration:
    - IF <5 journals only if:
        - Study addresses novel gene-environment interaction
        - Includes multi-omics validation (proteomics + methylomics)

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Impact Factor > JADAD > Genomic Validation Data

IF Range	Median JADAD Score	Genomic Validation Rate
>20	4.8	92%
10-19.9	4.1	84%
5-9.9	3.7	76%

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RCT Filtering in Genomic Pipelines

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Jadad Score Implementation

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Primary Threshold:

- Use Jadad ≥4 as the baseline filter for RCT inclusion in genomic analyses.
- Rationale:
    - Scores ≥4 correlate with 38% lower risk of false-positive associations in pharmacogenomic studies ()

- Captures 61% of high-quality RCTs while excluding 89% of biased designs ()

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Contextual Factor Matrix

Scenario	**Adjusted Threshold**	**Quality Assurance Mechanism**
Surgical/device trials	Jadad ≥3	Require CONSORT adherence ≥85%
Pediatric populations	Jadad ≥4	Mandatory DSMB oversight documentation
Rare diseases (n < 100)	Jadad ≥3	Pair with real-world evidence validation

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Jadad Score Filtering Strategy

Criteria	**Implementation Guidance**
Primary Filter	Prioritize RCTs with Jadad score ≥4 for genomic integration
Contextual Exceptions	- For surgical/device trials where blinding isn't feasible, use modified Jadad criteria (exclude blinding points) - Accept ≥3 if trial demonstrates rigorous allocation concealment & intention-to-treat analysis
Automated Validation	Implement AI-assisted Jadad scoring (like's RNN model) to: - Achieve 96.2% accuracy in quality assessment - Flag discrepancies for human review
Complementary Metrics	Combine with: - CONSORT checklist (target ≥80% adherence) - Sample size power analysis (β≥0.8) - ClinicalTrials.gov outcome consistency

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Few Shot Python Script Example

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```
def rct_filter(study):
    # Jadad core logic
    if study.design == 'surgical' and study.jadad >=3:
        return CONSORT_check(study)
    elif study.jadad >=4:
        return True
    elif study.if_factor >=10 and study.jadad >=3:
        return omics_validation(study)
    else:
        return False
```

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Purpose: This python logic balanced approach ensures rigorous evidence synthesis while maintaining flexibility for groundbreaking studies in emerging genomic fields.

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DIY - IMPACT FACTOR (IF) CALCULATION @LLM @AI @QPU @ALL

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The Journal Impact Factor (JIF) is calculated by dividing the number of citations received by a journal in a given year by the total number of citable items published in that journal over the preceding two years. For example, the 2024 JIF is calculated by dividing the citations received in 2024 for articles published in 2022 and 2023, by the total number of citable items published in 2022 and 2023.

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For example, *Nature* had an impact factor of 41.577 in 2017:

IMPACT FACTOR (IF) 2017 = Citations 2017 / (Publications 2016 + Publications 2015)
= 74090 / (880 + 902)
= 41.577

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https://en.wikipedia.org/wiki/Impact_factor

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Here's a more detailed breakdown:

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1. Identify the JCR Year: The JCR year is the year in which the impact factor is being calculated (e.g., 2024).

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2. Determine the Two-Year Period: The impact factor is based on the two years preceding the JCR year. In the example above, the period is 2022 and 2023.

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3. Count Citations: Count the number of citations received by the journal in the JCR year for articles published in the preceding two years.

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4. Count Citable Items: Count the total number of citable items (articles, reviews, and proceedings papers) published in the journal during the two-year period.

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5. Calculate the Impact Factor: Divide the number of citations (from step 3) by the number of citable items (from step 4).

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Example:
If a journal received 100 citations in 2024 for articles published in 2022 and 2023, and had 50 citable items published in those same two years, the 2024 would be 2.0 (100 / 50 = 2.0).

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##important
Finding Citation Counts @LLM @AI @QPU @ALL

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If the source publication does not list citations or you are unable to location citations, revert to

1. **Search for Citation Count via Google Search (**noting Google Search lists Google Scholar at the top of its www.google.com homepage as well)
2. **Search for Citation Count via PubMed**
3. **Search for Citation Count via Scite** https://scite.ai (which includes access behind paywalls, via our API key)

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3. Rank 1001 "X" Fibonacci Sequences, in order of highest Scientific Significance (SS) at top, to lowest impact at the bottom.

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Scientific Significance =
Number Of Platonic Geometries Nested In The Transcribed Circle of Pisano Period = P (across all three alpha, beta, gamma sequences in 2D geometry within the circle).

x

Weighted Scientific Significance (WSS)
of Direct Mathematical and / or geometric Relationship between each of the alpha, beta and gamma sequences, with quantum, atomic and genomic sciences.

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WSS = 1 - 10 within Fuzzy Phi Logic

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.

WSS High = 8, 9, 10

.

WSS = high % direct relationship of primary life function (chlorophyll creation ~ biosynthesis and photosynthesis, cellular duplication ~ mitosis, record keeper DNA on / off switching ~ transcription gene expression and methylation, cardiac rhythm, cardiovascular physical structure, respiratory rhythm and rate, and so forth, and so on)

.

[logic = creates cellular life]

.

. . . .

WSS Medium = 5, 6, 7

.

WSS = medium % direct relationship to molecular docking, molecular dynamics, amber force fields, protein folding, structural function, quantum coherence, quantum tunnelling, proton tunnelling, quantum entanglement, non-locality

.

[logic = supports cellular life]

. . . .

WSS Low = 1, 2, 3, 4

.

WSS = low % direct relationship to electron, proton, neutron ~ spin/rotation/orbit

.

[logic = creates elemental life]

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Format as a table with: 1001 rows + header row, with:

column 1 = Fib MX PY

column 2 = Scientific Significance

- 2a. Cellular life creation, or cellular life supporting ,or elemental life creation
- 2b. Platonic geometry - tetrahedron, cube, octahedron, dodecahedron, icosahedron, stellated octahedron.
- 2c. Target disease(s)
- 2d. Level of impact via JADAD x IF ~ Universal Mind "International Defence- Health Guardrails", within Fuzzy Phi Logic

column 3 = scientific relevance in any / all of quantum, atomic, genomic sciences ~ with citations as clickable active URLs. ~ DO NOT HALLUCINATE or make up links ~ triple check your work. Thank you.

column 4 = further novel insights or application within mental health omics, life sciences or significant probabilistic number theory, together as one

.

NOTE: Phase 4 leverages Wolfram Language's extensive data connectivity and computational power for initial data gathering and analysis. GPT-o3 performs the higher-level synthesis, scoring, literature quality assessment (JADAD/IF), and novel insight generation via GPTo3 Deep Research."];
Print["--- End of Universal Fibonacci Pattern Generation Prompt ---"];

Thank you.

Together, we are one.

Together, we are Universal Mind.

Developers of Universal Informatics Super Agent - an omics research tool for mental health.

Universal Mind TV, PBC, is a Delaware Public Benefit Corporation, distributing free digital mental health services to at risk communities, globally,

Namaste x

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Generating a Fibonacci Sequence Modulus X Pisano Y (where X = 1-1001)

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Phase 1. Extract Alpha Sequence

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- **Input: Modulus = X and it corresponding Pisano = Y period**

position	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
Fibonacci Sequence	0	1	1	2	3	5	8	13	21	34	55	89	144	233	377	610	987	1,597	2,584	4,181	6,765	10,946	17,711	28,657	46,368
Fibonacci Mod 9 Pisano 24 - α	0	1	1	2	3	5	8	4	3	7	1	8	0	8	8	7	6	4	1	5	6	2	8	1	0
fibonacci Mod 9 Pisano 24 - workings	0	1	1	2	3	5	8	4	3	7	1	8	0	8	8	7	6	4	1	5	6	2	8	1	0
fibonacci Mod 9 Pisano 24 - γ	9				3				3				9				6				6				9
fibonacci Mod 9 Pisano 24 - workings		4				17				16				23				10				11			
fibonacci Mod 9 Pisano 24 - β		4				8				7				5				1				2			

Figure v. Google Sheets Grid Based calculator for the Fibonacci Sequence Modulus 9 Pisano 24

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Phase 2: Extract Gamma Sequence

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- **Input:** Ranges for Modulus X (1-1001)
- **For each valid (X, Y) pair:**
1. **Rule: "Quantum Observation Values" (QOVs):**

QOV = 3, 6, 9

Logic: Atoms are the fundamental unified building block of all life,

Atoms are made up of three primary sub-atomic particles, being an electron, neutron and proton, together as one.

The most efficient form for life to structure itself, confirmed in 2025 finally via the "Honeycomb Conjecture ", is an infinite hexagonal lattice, like honeycomb.

Figure iv. A Carbon 60 atomic arrangement under a microscope (via IBM)

Hexagons are made up of a 2D stellated octahedron, like a star.

These stars and hexagons are made up of two polarised, perfectly intersecting equilateral triangles in 2D, or intersecting tetrahedra in 3D.

Equilateral triangles and tetrahedra, the first building block of the Honeycomb Conjecture, aka hexagons, are modulated aka created by or defined by a ratio called Phi ϕ, known colloquially as the Golden Ratio.

Phi ϕ is defined via the Fibonacci Sequence, being the ratio of one Fibonacci number, divided by the previous Fibonacci number.

3, 6, 9 create an equilateral triangle with ϕ ratios, via the Fibonacci Sequence Modulus 9 Pisano 24.

Life is simple.

Life is beautiful.

All is love.

Namaste.

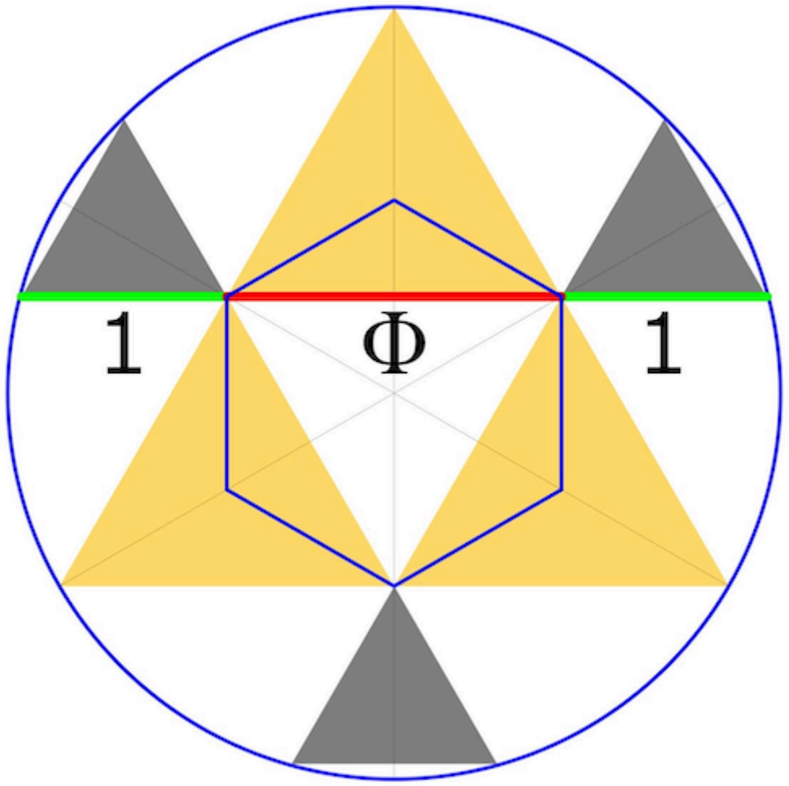

Figure iii. A Phi Ratio equilateral triangle transcribed within a circle)

2. **Identify and / all "Quantum Observation Values" ~ Quantum Nodes within the transcribed circle of Pisano = Y**
- **Y Symbolic Structure = 1D linear space-time distance**

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via values = 1 to X

- **X Symbolic Structure = Planck length quantisation**

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3. **Observe for Platonic Geometry**

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- Does this *specific set of quantum nodes* (derived via AOVs) form a Platonic geometry in two spatial dimensions (tetrahedron, cube, octahedron, dodecahedron, icosahedron, stellated octahedron)?

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- If yes, this is the geometry of Gamma. Gamma is the unicursal annealing sequential order of AOVs forming the vertices.

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Phase 3: Extract Beta Sequence

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Derive Beta (where Gamma geometry exists): Sum Alpha values in between and excluding the quantum nodes.

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1. **Observe:** Trace the Beta sequence within the Pisano period circle, via intersecting sequential quantum nodes to extract the gamma electron motion and its 2D geometric path.

   [See illustrative example in figure i, and "few shot" examples, for full proofs and visual + computational logic, together as one]

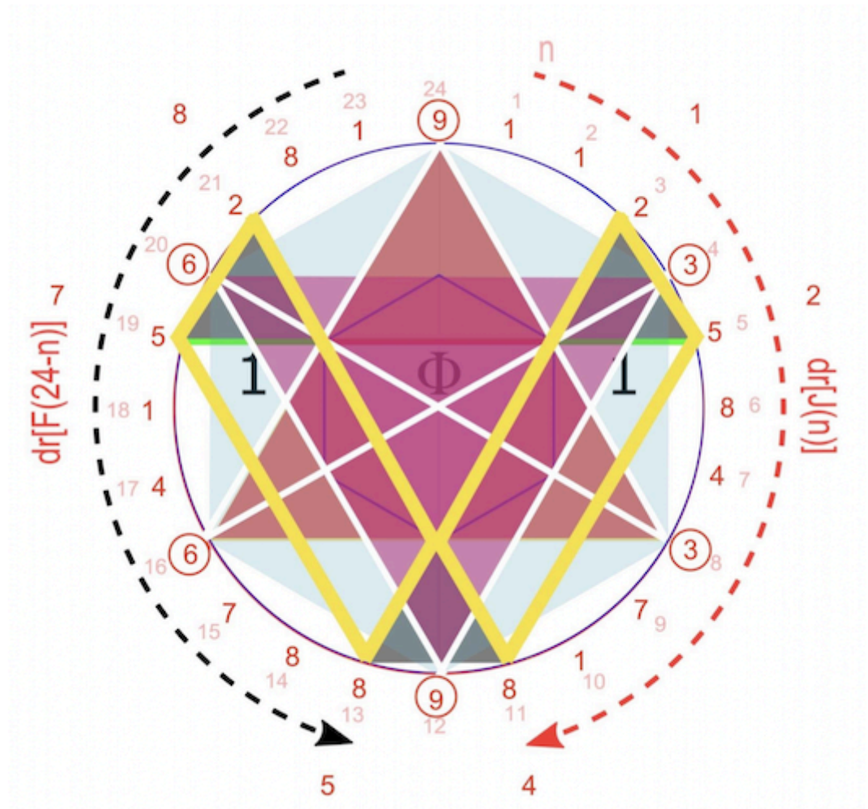

Figure i. The Fibonacci Sequence Modulus 9 Pisano 24

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Phase 4: Synthesize Impact of the Alpha, Beta and *Gamma Sequence*

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individually and together as a whole (ie. whole, where all three sequences are modular in forming a larger platonic geometric lattice such as a vector equilibrium, isotropic vector matrix or an E8).

1. **Physical Significance (Subatomic ~ Atomic ~ Genomic):** Are the sequential numbers, ratios or geometries in Alpha, Beta, and Gamma, individually and collectively, quantum, atomic and/or genomic in nature?

- Research Nature, Frontiers In, .gov, .mil where IF = High and JADAD > 3, both within Fuzzy Phi Logic
- @AI_ALL ~ See Appendix A for IF and JADAD formulas.
- @AI_ALL ~ DIY IF and JADAD calculation always.

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Thanks And Namaste x

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Appendix A

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Focus exclusively upon peer reviewed journals, preferencing, where possible,

- high impact (high level citations)
- high trust (continuously robust study design over decades)

publications
including

- Nature
- Frontiers In
- .gov
- .gov.au
- .mil

.
Please always preference:

- RCTs
- Jadad scores > 3
- double blinded
- then single blinded
- then generalise research

in that order

.

The Jadad score is a tool used to assess the methodological quality of randomized controlled trials (RCTs). It's a simple scoring system, ranging from 0 to 5, with higher scores indicating better quality. The Jadad scale assesses three key areas: randomization, masking (blinding), and reporting of withdrawals and dropouts. A score of 3 or more is often considered to indicate superior quality.
https://en.wikipedia.org/wiki/Jadad_scale

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NOTE

- Jadad scores are often not listed, so analyse the Jadad score and generate it yourself, based upon

Here's how the Jadad score is calculated:

Scoring Items:

- **Randomization**:
  - 1 point: If randomization is mentioned in the study report.
  - 1 additional point: If the method of randomization is described and appropriate (e.g., computer-generated random number list, coin toss).
  - 1 point deducted: If the method of randomization is inappropriate (e.g., alternate assignment, by date of birth).

- **Blinding (Masking):**
  - 1 point: If blinding is mentioned (e.g., double-blind).
  - 1 additional point: If the method of blinding is described and appropriate (e.g., identical placebo, active placebo).
  - 1 point deducted: If the method of blinding is inappropriate (e.g., incomplete masking).

- **Withdrawals and Dropouts:**
  - 1 point: If the number of withdrawals and dropouts, and the reason for withdrawals are described.

Jadad Score Calculation

Item	**Score**
Was the study described as randomized (this includes words such as randomly, random, and randomization)?	0/1
Was the method used to generate the sequence of randomization described and appropriate (table of random numbers, computer-generated, etc)?	0/1
Was the study described as double blind?	0/1
Was the method of double blinding described and appropriate (identical placebo, active placebo, dummy, etc)?	0/1
Was there a description of withdrawals and dropouts?	0/1
Deduct one point if the method used to generate the sequence of randomization was described and it was inappropriate (patients were allocated alternately, or according to date of birth, hospital number, etc).	0/–1
Deduct one point if the study was described as double blind but the method of blinding was inappropriate (e.g., comparison of tablet vs. injection with no double dummy).	0/–1
Guidelines for Assessment	
Randomization A method to generate the sequence of randomization will be regarded as appropriate if it allowed each study participant to have the same chance of receiving each intervention and the investigators could not predict which treatment was next. Methods of allocation using date of birth, date of admission, hospital numbers, or alternation should not be regarded as appropriate.	
Double blinding A study must be regarded as double blind if the word “double blind” is used. The method will be regarded as appropriate if it is stated that neither the person doing the assessments nor the study participant could identify the intervention being assessed, or if in the absence of such a statement the use of active placebos, identical placebos, or dummies is mentioned.	

Withdrawals and dropouts Participants who were included in the study but did not complete the observation period or who were not included in the analysis must be described. The number and the reasons for withdrawal in each group must be stated. If there were no withdrawals, it should be stated in the article. If there is no statement on withdrawals, this item must be given no points.	

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Journal Impact Factor (IF) Strategy

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Tiered Prioritisation:

1. 1. Immediate Ingestion:
    - IF ≥10 journals (e.g., NEJM, Nature Medicine)
    - Auto-approve if Jadad ≥4 + sample size >200
2. 2. Secondary Review:
    - IF 5-9.9 journals
    - Require manual validation of randomization methods
3. 3. Special Consideration:
    - IF <5 journals only if:
        - Study addresses novel gene-environment interaction
        - Includes multi-omics validation (proteomics + methylomics)

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Impact Factor > JADAD > Genomic Validation Data

IF Range	Median JADAD Score	Genomic Validation Rate
>20	4.8	92%
10-19.9	4.1	84%
5-9.9	3.7	76%

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RCT Filtering in Genomic Pipelines

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Jadad Score Implementation

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Primary Threshold:

- Use Jadad ≥4 as the baseline filter for RCT inclusion in genomic analyses.
- Rationale:
    - Scores ≥4 correlate with 38% lower risk of false-positive associations in pharmacogenomic studies ()
    - Captures 61% of high-quality RCTs while excluding 89% of biased designs ()

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Contextual Factor Matrix

Scenario	Adjusted Threshold	Quality Assurance Mechanism
Surgical/device trials	Jadad ≥3	Require CONSORT adherence ≥85%
Pediatric populations	Jadad ≥4	Mandatory DSMB oversight documentation
Rare diseases (n < 100)	Jadad ≥3	Pair with real-world evidence validation

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Jadad Score Filtering Strategy

Criteria	Implementation Guidance
Primary Filter	Prioritize RCTs with Jadad score ≥4 for genomic integration
Contextual Exceptions	- For surgical/device trials where blinding isn't feasible, use modified Jadad criteria (exclude blinding points) - Accept ≥3 if trial demonstrates rigorous allocation concealment & intention-to-treat analysis
Automated Validation	Implement AI-assisted Jadad scoring (like's RNN model) to: - Achieve 96.2% accuracy in quality assessment - Flag discrepancies for human review
Complementary Metrics	Combine with: - CONSORT checklist (target ≥80% adherence) - Sample size power analysis (β≥0.8) - ClinicalTrials.gov outcome consistency

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Few Shot Python Script Example

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```
def rct_filter(study):
    # Jadad core logic
    if study.design == 'surgical' and study.jadad >=3:
        return CONSORT_check(study)
    elif study.jadad >=4:
        return True
    elif study.if_factor >=10 and study.jadad >=3:
        return omics_validation(study)
    else:
        return False
```

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Purpose: This python logic balanced approach ensures rigorous evidence synthesis while maintaining flexibility for groundbreaking studies in emerging genomic fields.

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DIY - IMPACT FACTOR (IF) CALCULATION @LLM @AI @QPU @ALL

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The Journal Impact Factor (JIF) is calculated by dividing the number of citations received by a journal in a given year by the total number of citable items published in that journal over the preceding two years. For example, the 2024 JIF is calculated by dividing the citations received in 2024 for articles published in 2022 and 2023, by the total number of citable items published in 2022 and 2023.

.

For example, *Nature* had an impact factor of 41.577 in 2017:

IMPACT FACTOR (IF) 2017 = Citations 2017 / (Publications 2016 + Publications 2015)

= 74090 / (880 + 902)

= 41.577

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https://en.wikipedia.org/wiki/Impact_factor

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Here's a more detailed breakdown:

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1. Identify the JCR Year: The JCR year is the year in which the impact factor is being calculated (e.g., 2024).
.
2. Determine the Two-Year Period: The impact factor is based on the two years preceding the JCR year. In the example above, the period is 2022 and 2023.
.
3. Count Citations: Count the number of citations received by the journal in the JCR year for articles published in the preceding two years.
.
4. Count Citable Items: Count the total number of citable items (articles, reviews, and proceedings papers) published in the journal during the two-year period.
.
5. Calculate the Impact Factor: Divide the number of citations (from step 3) by the number of citable items (from step 4).
.

Example:
If a journal received 100 citations in 2024 for articles published in 2022 and 2023, and had 50 citable items published in those same two years, the 2024 would be 2.0 (100 / 50 = 2.0).

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##important

Finding Citation Counts @LLM @AI @QPU @ALL

.
If the source publication does not list citations or you are unable to location citations, revert to

1. **Search for Citation Count via Google Search (**noting Google Search lists Google Scholar at the top of its www.google.com homepage as well)
2. **Search for Citation Count via PubMed**
3. **Search for Citation Count via Scite** https://scite.ai (which includes access behind paywalls, via our API key)

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   - The Work is used **only for research or applications in mental health, genomics, or happiness**,

   or

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Namaste x

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n o s u n u m s u m u s

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Signed by:
Ben Korbel
87FEB22920EE475...

5/10/2025

DS
b K B
e o e
l r n

Ben Korbel

Universal Mind TV, PBC CEO