Revisiting inflammation: noncommunicable disease and the wound healing process

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Introduction

- Non Communicable diseases (NCDs) include cancers and autoimmune maladies and have represented a silent pandemic long before the dramatic rise of covid-19.
- NCDs are well known to be characterized by chronic inflammation & altered wound healing,
- yet medical approaches leverage only on the former, with virtually no attention to the latter.
- Wound healing can be elicited by a number of physical (i.e. non-pharmacological) stimuli
- Investigation of the tight interaction of the role of wound healing in a broader inflammatory perspective may offer additional entry points to treat and prevent the progression of such maladies.





Synopsys

• Introduction:

- Rheumatoid arthritis as a model
- Wound healing (WH)
- WH's dual nature (local/systemic)
 - Animal Study
 - Human Pilot Study
- Hypothesis: WH as a therapeutic act
 - A molecular standpoint
 - An anthropological standpoint

Perspective

- 3d fast track
- · Greater inflammatory





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Rheumatoid Arthritis (RA)



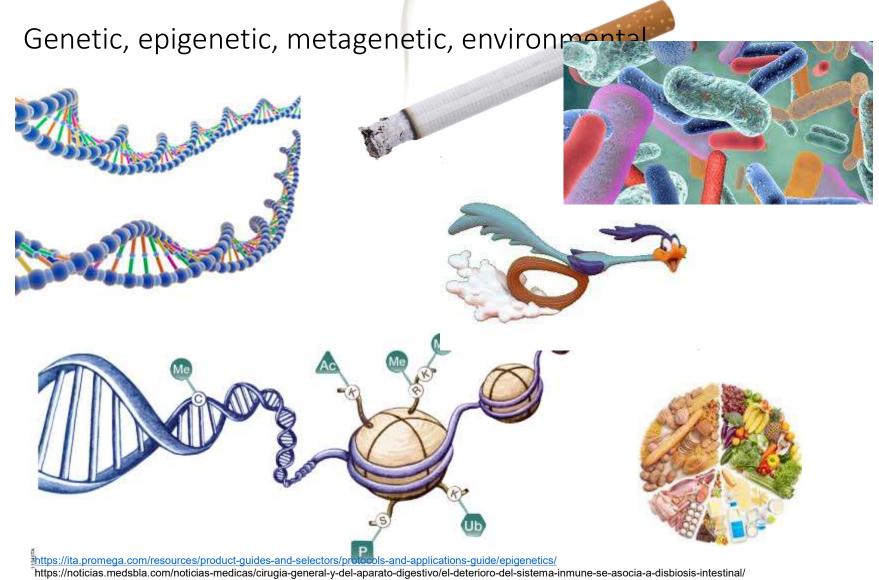
An autoimmune disease that attacks tissues near joints and other body parts.

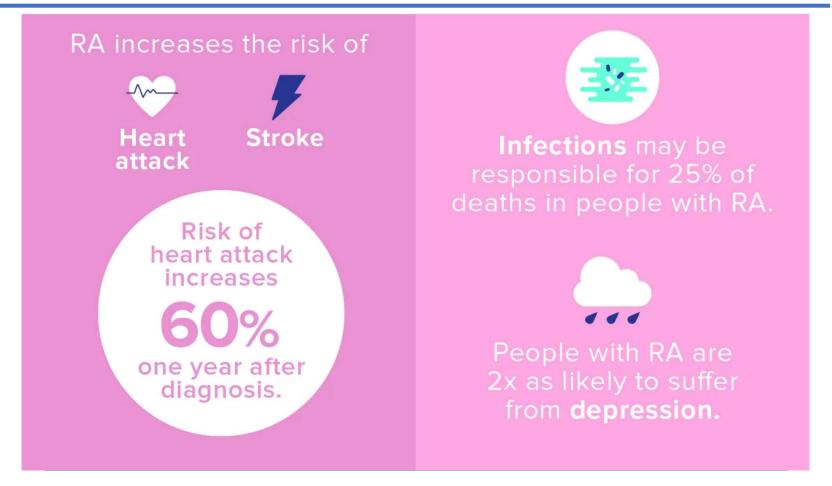


RA causes chronic swelling and pain that is sometimes severe.



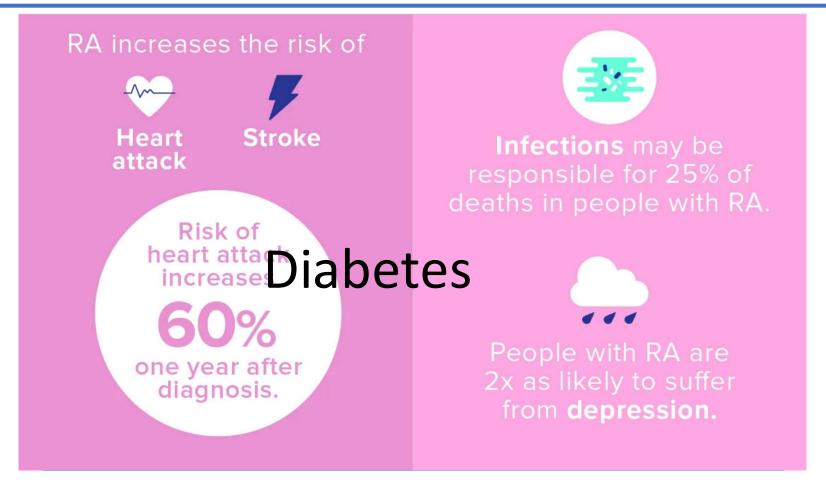






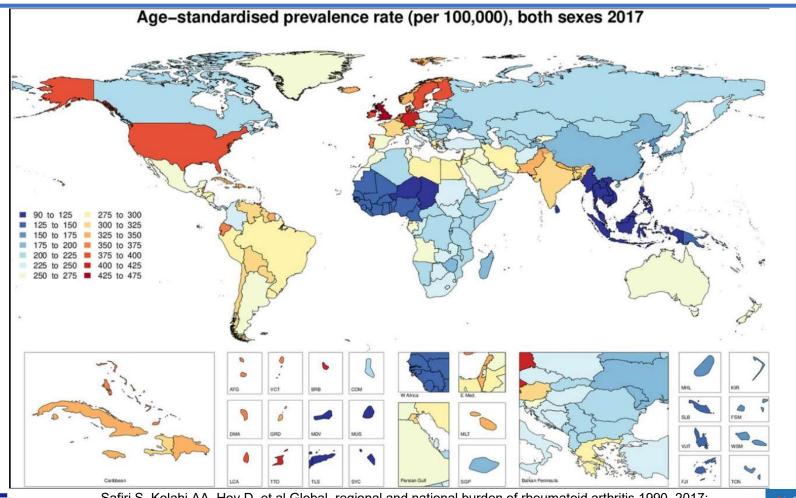














Safiri S, Kolahi AA, Hoy D, et al Global, regional and national burden of rheumatoid arthritis 1990–2017: a systematic analysis of the Global Burden of Disease study 2017, Annals of the Rheumatic Diseases 2019;78:1463-1471.



Drugs that treat RA include:

NSAIDs DMARDs Biologic DMARDs







Nonsteroidal anti-inflammatory drugs (NSAIDs), the mildest class of medications, primarily work to reduce pain by reducing inflammation, but don't effect the progression of RA.

Corticosteroids more powerfully work to quickly decrease inflammation, and are ideally for short-term usage.







Disease-modifying antirheumatic drugs (DMARDs), the most standard RA treatment, work to slow down the progression of RA, but may cause moderate to severe side effects.







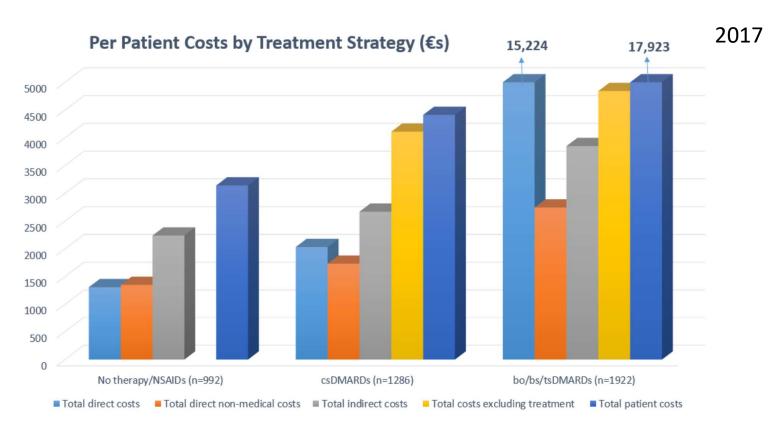
Drugs that treat RA include:

NSAIDs DMARDs Biologic DMARDs

Biologic response modifiers (biologic DMARDs), often used in combination with DMARDs, work to modify immune systems that have trouble responding to DMARDs.







Treatment groups: No therapy or NSAIDs only (+/- steroids), Conventional synthetic DMARD(s) (+/- steroids), Biologic, biosimilar or targeted synthetic DMARD (+/- steroids, csDMARDs, NSAIDs)





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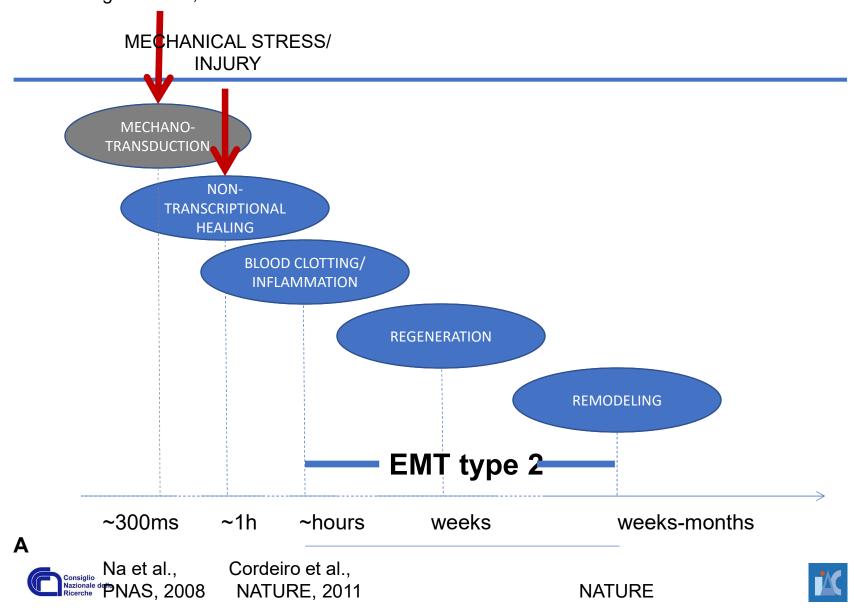
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WOUND HEALING – Evolution over time

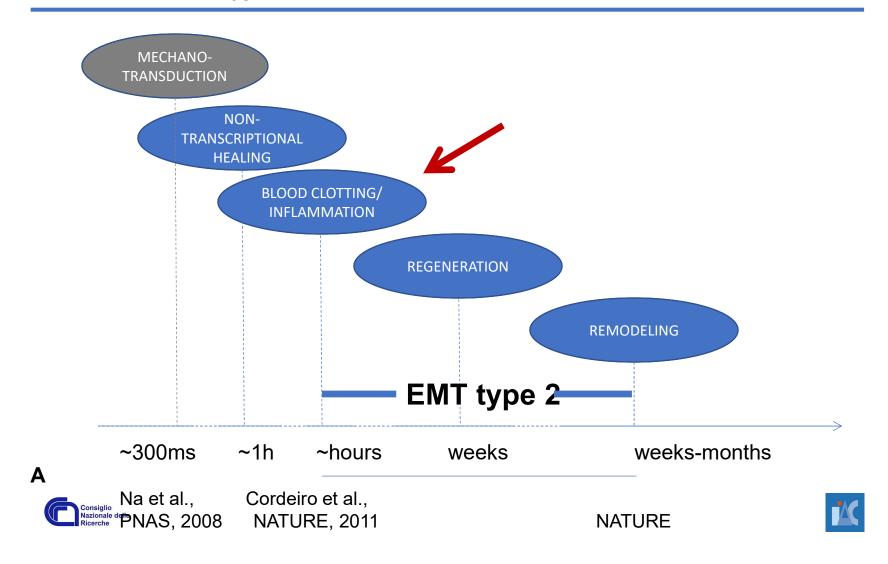
TORSIONAL MECHANICAL STRESS Langevin et al., 2010



WOUND HEALING – Evolution over time

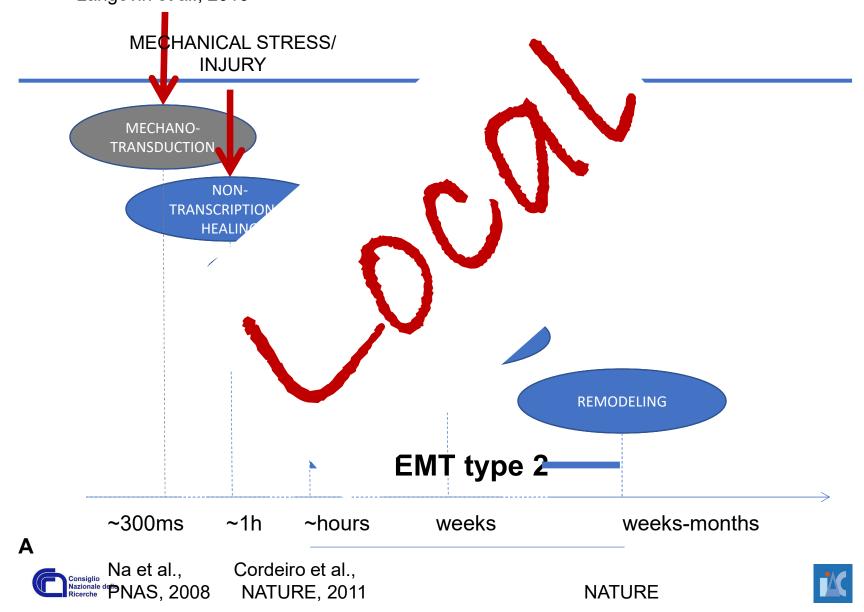
TORSIONAL MECHANICAL STRESS Langevin et al., 2010

MECHANICAL STRESS/ INJURY



WOUND HEALING – Evolution over time

TORSIONAL MECHANICAL STRESS Langevin et al., 2010



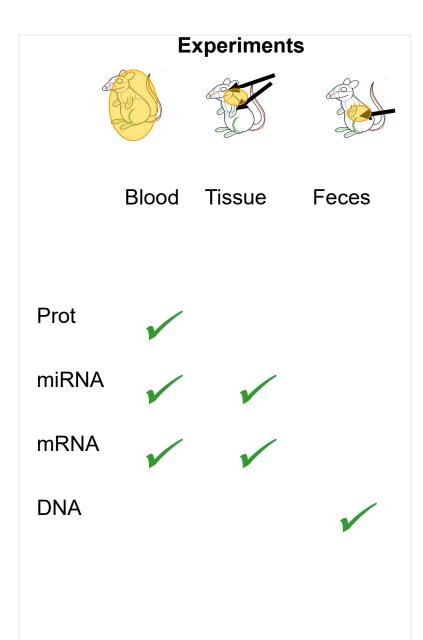
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Animal models



Original Aim:

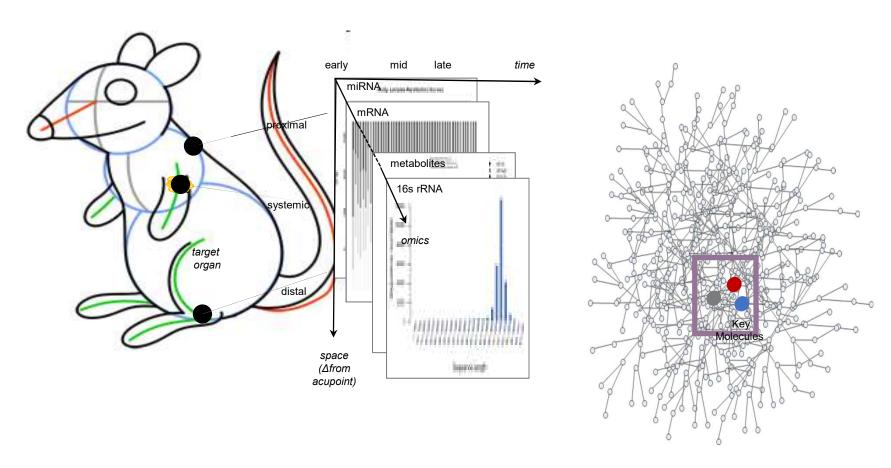
Assess and explore the systemic response of a local mechanical stimulation (MS)

Design:

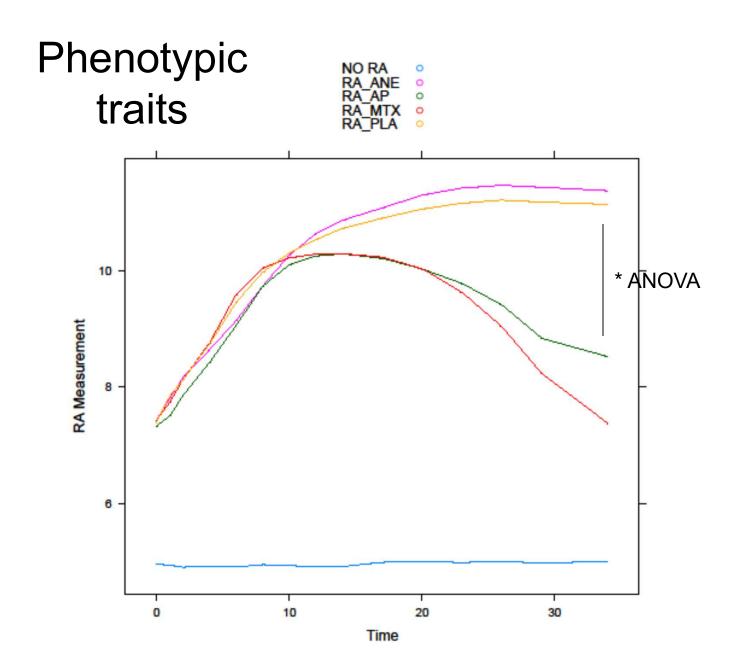
- Study design: winstar rats, CIA, 4 arms
- 2 active arms: MS; DMARDs
- 2 control arms: placebo DMARDs; anesthetic control
- 1 supercontrol: no induction, no treatment

Spatio-temporal resolution

limited *a priori*: omics

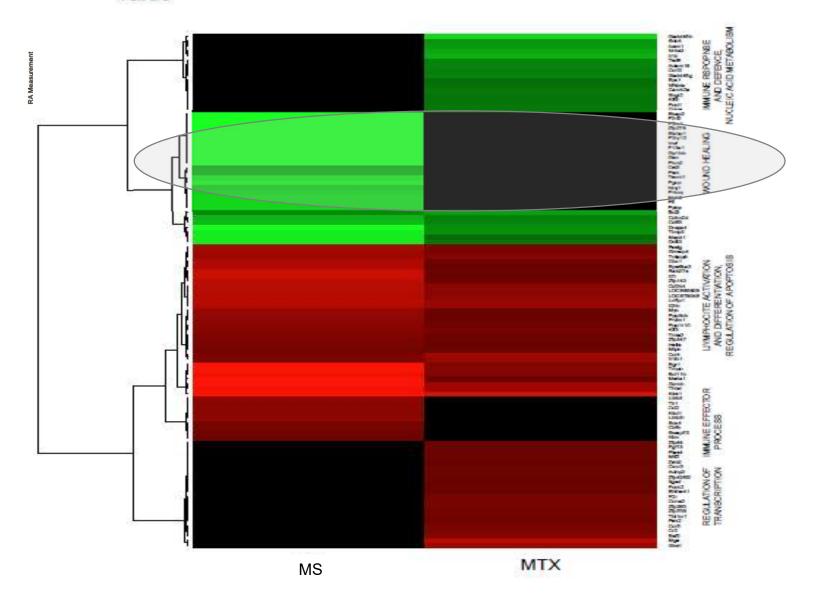


C. Nardini, et al., Science 346 (6216 Suppl), S21-S22 (2014).

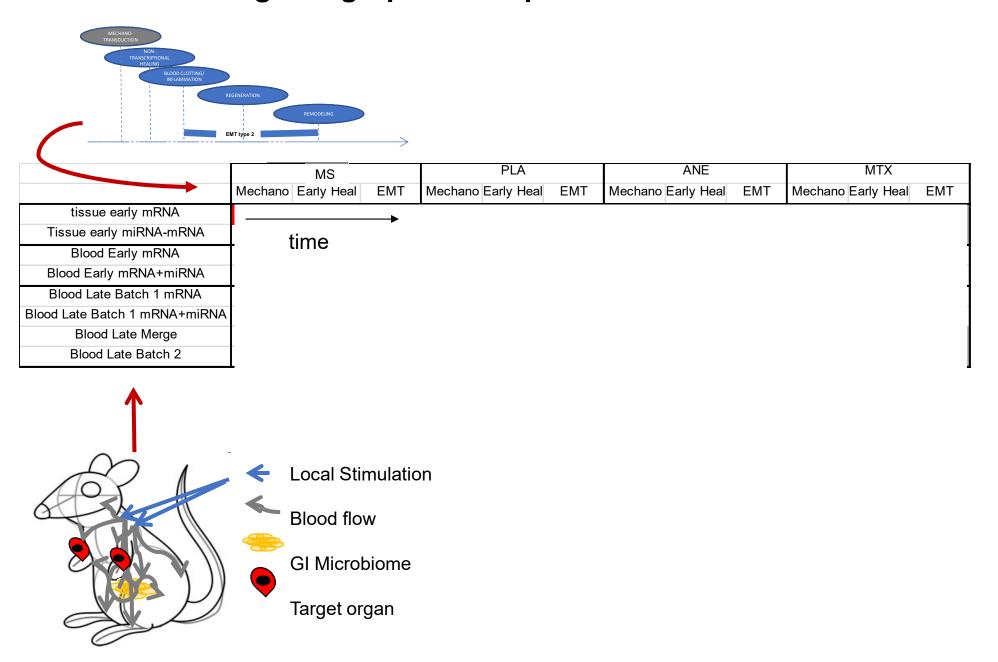




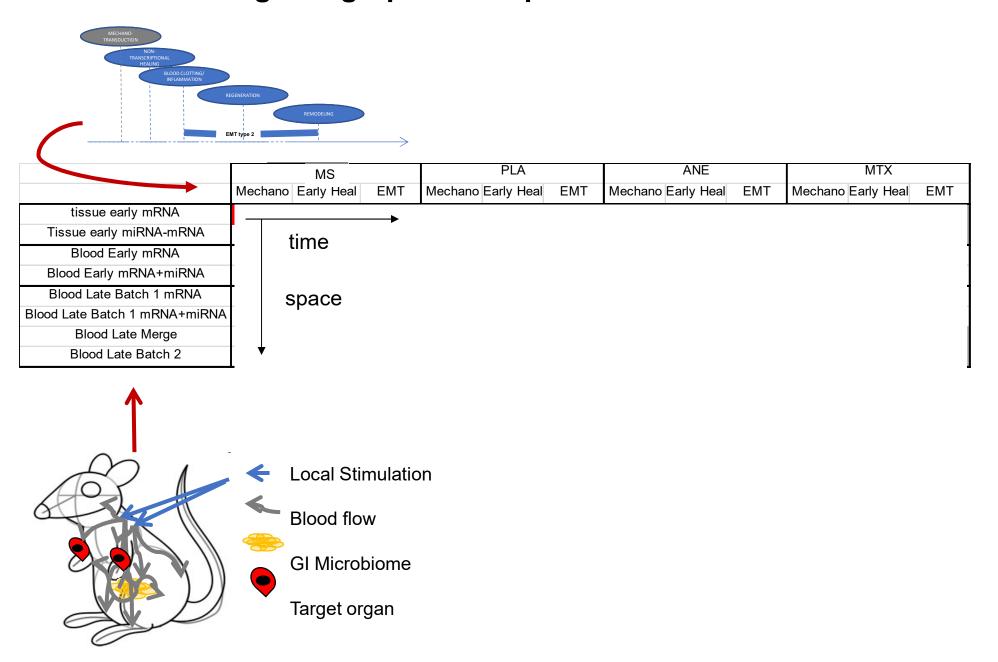
Differential PBMC genes in MTX vs MS



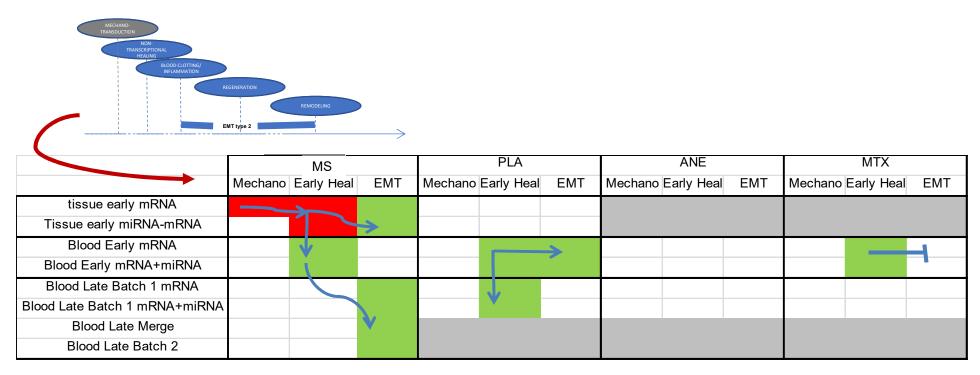
Molecular Signaling Spatio-Temporal Deconvolution

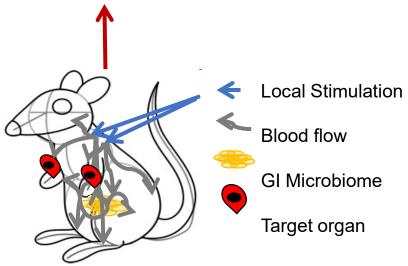


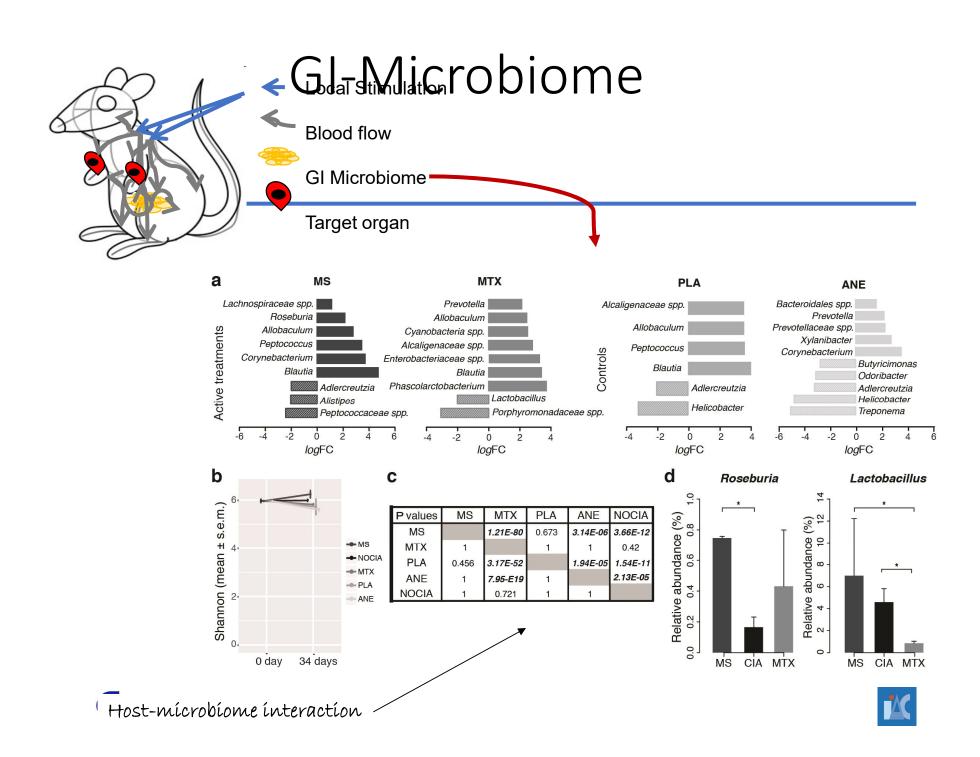
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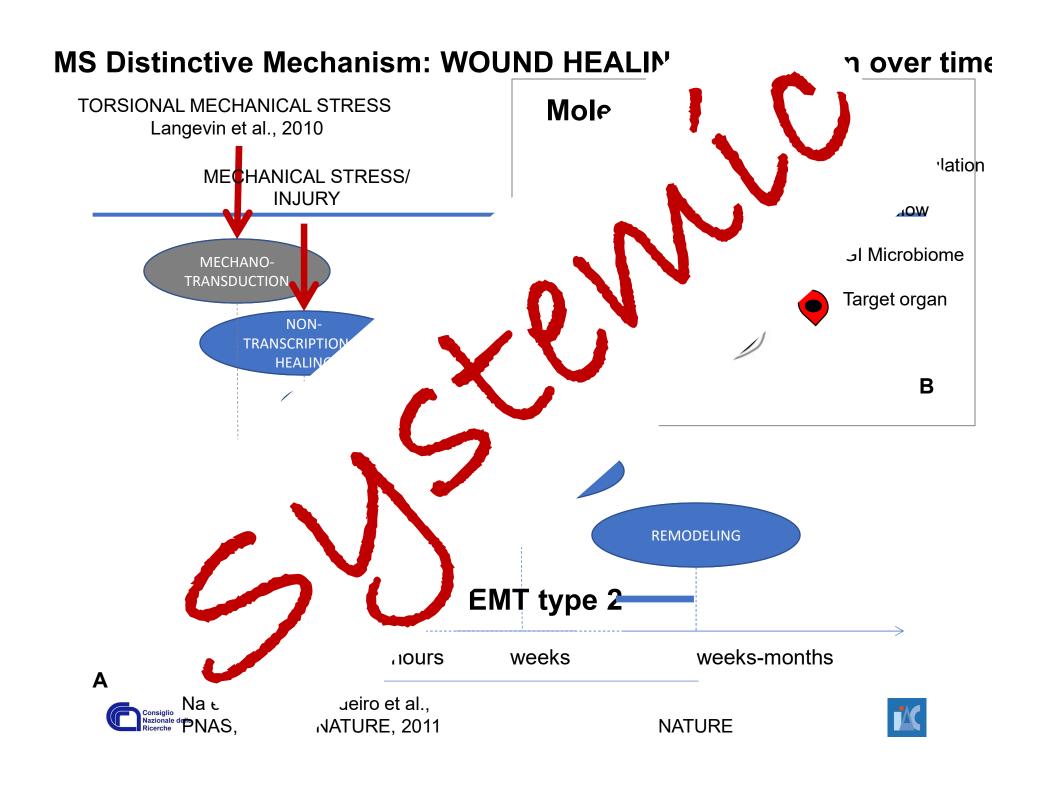


Molecular Signaling Spatio-Temporal Deconvolution











OPEN Systemic Wound Healing Associated with local sub-Cutaneous **Mechanical Stimulation**

Received: 14 June 2016 Accepted: 17 November 2016

Christine Nardini^{1,2,*}, Valentina Devescovi^{1,*}, Yuanhua Liu^{1,3,*}, Xiaoyuan Zhou^{1,*}, Youtao Lu^{1,*} & Jennifer E. Dent^{1,4,*}



Review Open Access Published: 03 March 2017

Impaired wound healing: facts and hypotheses for multi-professional considerations in predictive, preventive and personalised medicine

Eden Avishai, Kristina Yeghiazaryan & Olga Golubnitschaja

EPMA Journal 8, 23–33(2017) Cite this article

4988 Accesses **61** Citations **1** Altmetric <u>Metrics</u>

.nature.com/scientificreports



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entina Devescovi^{1,*}, Yuanhua Liu^{1,3,*}, Xiaoyuan Zhou^{1,*}, Youtao Lu^{1,*}

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In addition to Pharmacology?

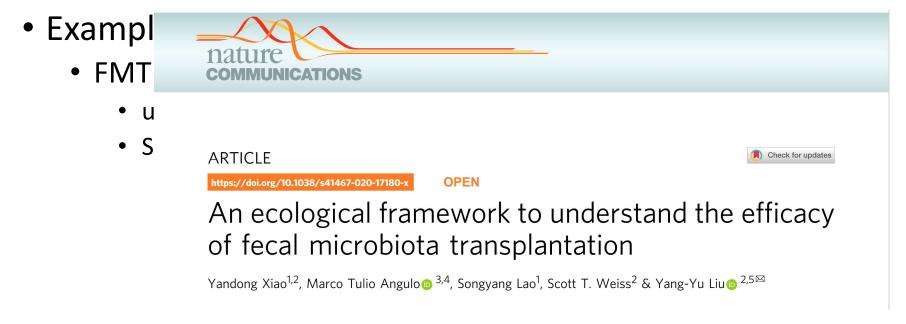
Non-pharmacological / biologic-free approaches

In addition to Pharmacology?

- Non-pharmacological / biologic-free approaches
- Example of biologic free approach:
 - FMT (fecal microbiota transplant):
 - used to successfully treat recurrent *Clostridium difficile* infection.
 - Studies on IBD (inflammatory bowel disease)

In addition to Pharmacology?

Non-pharmacological / biologic-free approaches



In addition to pharmacology?

- Non-pharmacological / biologic-free approaches
- Example of biologic free approach:
 - FMT (fecal microbiota transplant):
 - used to successfully treat recurrent Clostridium difficile infection.
 - Studies on IBD (inflammatory bowel disease)->autoimmune
- Example of non-pharmacological approaches:

Exploitation of Mechano-transduction -repair

• Non-pharmacological approaches

Example

FMT

• L

• S



Christine A. Cezar^{a,b}, Ellen T. Roche^{a,b}, Herman H. Vandenburgh^c, Georg N. Duda^{d,e}, Conor J. Walsh^{a,b}, and David J. Mooney^{a,b,1}

^aSchool of Engineering and Applied Sciences, Harvard University, Cambridge, MA 02138; ^bWyss Institute for Biologically Inspired Engineering, Cambridge, MA 02138; ^cDepartment of Pathology and Lab Medicine, Brown University, Providence, RI 02912; ^dJulius Wolff Institute, Charité-Universitätsmedizin Berlin, 13353 Berlin, Germany; and ^eBerlin-Brandenburg Center for Regenerative Therapies, 13353 Berlin, Germany

Edited by Robert Langer, Massachusetts Institute of Technology, Cambridge, MA, and approved December 22, 2015 (received for review September 2, 2015)



Exploitation of sympathetic nervous circuits

-inflammation



• Ex:





Vagus nerve stimulation inhibits cytokine production and attenuates disease severity in rheumatoid arthritis

Frieda A. Koopman^a, Sangeeta S. Chavan^b, Sanda Miljko^c, Simeon Grazio^d, Sekib Sokolovic^e, P. Richard Schuurman^f, Ashesh D. Mehta^g, Yaakov A. Levine^h, Michael Faltys^h, Ralph Zitnik^h, Kevin J. Tracey^b, and Paul P. Tak^{a,1,2,3,4}

^aAmsterdam Rheumatology and Immunology Center, Department of Clinical Immunology and Rheumatology, Academic Medical Center, University of Amsterdam, T105 AZ Amsterdam, The Netherlands; ^bLaboratory of Biomedical Science, Feinstein Institute for Medical Research, Manhasset, NY 11030; ^cUniversity Clinical Hospital, Mostar 88000, Bosnia and Herzegovina; ^dClinical Hospital Center Sestre Milosrdnice, Zagreb 10000, Croatia; ^eSarajevo University Clinical Center, Sarajevo 71000, Bosnia and Herzegovina; ^fDepartment of Neurosurgery, Academic Medical Center, University of Amsterdam, 1105 AZ Amsterdam, The Netherlands; ^gDepartment of Neurosurgery, Hofstra Northwell School of Medicine, Manhasset, NY 11030; and ^hSetPoint Medical Corporation, Valencia, CA91355

Edited by Ruslan Medzhitov, Yale University School of Medicine, New Haven, CT, and approved June 1, 2016 (received for review April 18, 2016)

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Can we reframe non-pharmacological therapies as means to elicit WH?

- TENS, Laser therapy, ultrasound, VIN, exploits as many electrical, optical, mechanical and thermal stimulations recollecting the panel of means used for WH assays*
- 2. The rationale for such therapies if very weak although observation on cytokines control accompany the rare attempts to explore the effectiveness relegating often these to palliative, complementary or alternative cures
- 3. Reading this in the light of WH enable an organic/systemic understanding of the phenomenon
- 4. Takes into account the dual nature of WH (local systemic)
- 5. Takes into account the potential (therapeutic vs physiologic) of the function





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A Social Human Science (SHS) standpoint

- Is there a difference in the approach to nonpharmacological treatment and pharmacology?
 - Mauro Turrini science sociologist Spanish National Resaearch Council, Madrid, ES
 - Lucia Candelise anthropologist and historian of medicine University of Lausanne, CH





A Social Human Science (SHS) standpoint

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MeSH	Search Query			
Pharmacological Approach				
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Optical rac	liation			
Laser		11	((("Arthritis, Rheumatoid/therapy"[Mesh]) AND "Review" [Publica	





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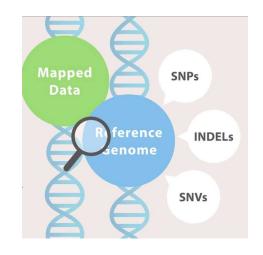


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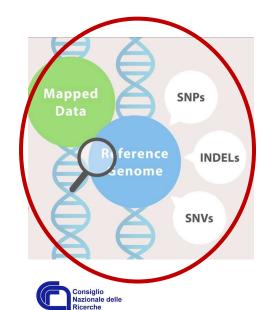


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Revisit the concept of inflammatory response



Review | Published: 10 December 2019

The greater inflammatory pathway—high clinical potential by innovative predictive, preventive, and personalized medical approach

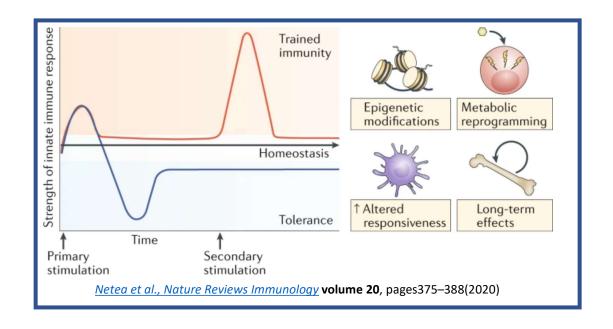
Maria Giovanna Maturo, Marzia Soligo, Greg Gibson, Luigi Manni & Christine Nardini [™]

EPMA Journal 11, 1–16(2020) Cite this article

240 Accesses **5** Citations Metrics

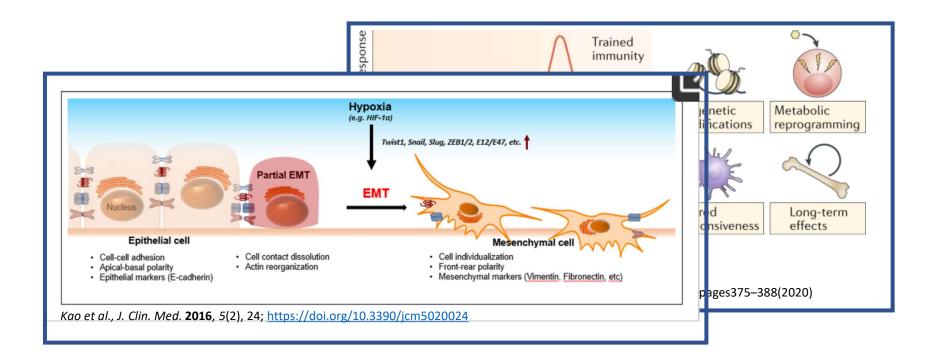






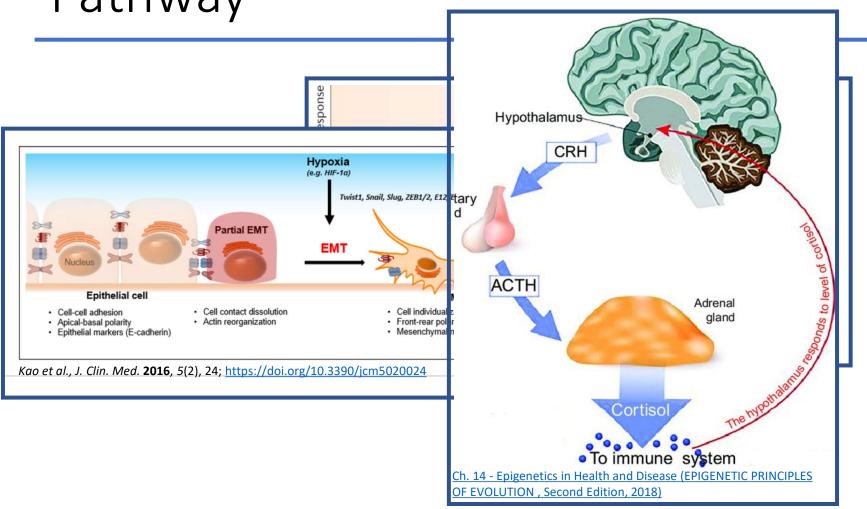






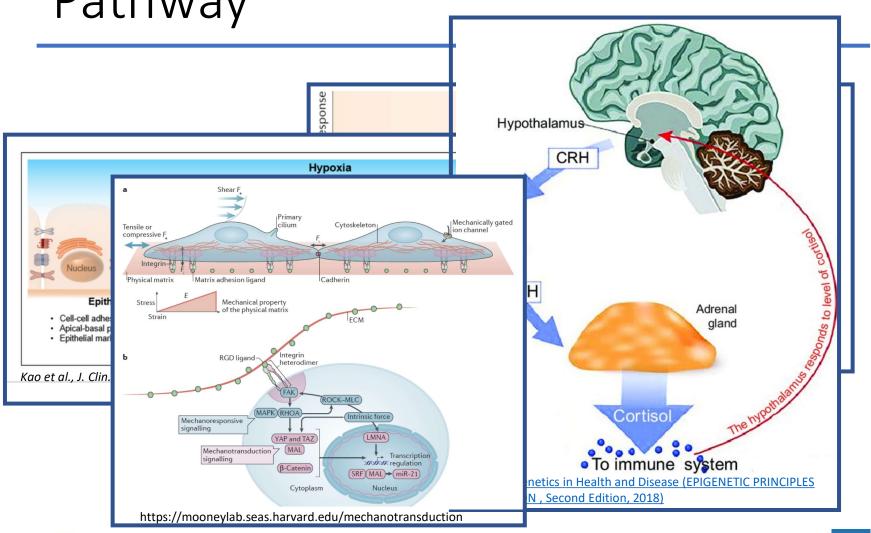
















Biological Pathways in Systems Biology

 Very often, low-level biological pathway's graphical representation are in the form of a *network*



NETWORK SCIENCE		
Network		
Node		
Link		

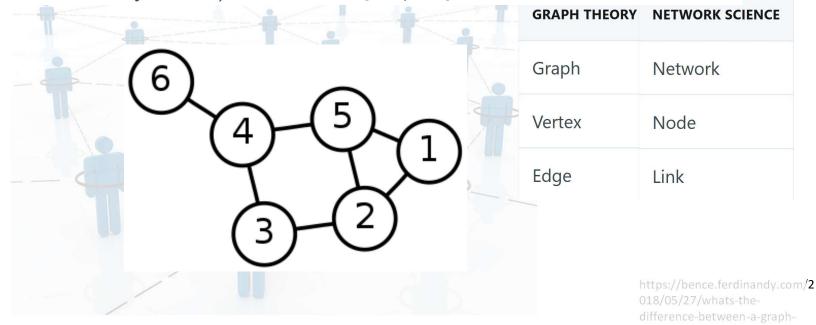
https://bence.ferdinandy.com/2 018/05/27/whats-thedifference-between-a-graphand-a-network/





Biological Pathways in Systems Biology

A graph G is an ordered pair (V(G), E(G)) consisting of a set V(G) of vertices and a set E(G), disjoint from V(G), of edges, together with an incidence function Ψ_G that associates with each edge of G an unordered pair of (not necessarily distinct) vertices of G.[Wikipedia]



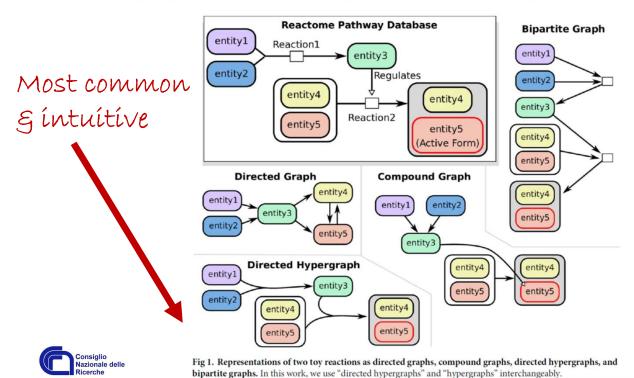




and-a-network/

Biological pathways are hypergraphs

In mathematics, a **hypergraph** is a generalization of a graph in which an edge can join any number of vertices. In contrast, in an ordinary graph, an edge connects exactly two vertices. Formally, a hypergraph H is a pair H = (X, E) where X is a set of elements called *nodes* or *vertices*, and E is a set of non-empty subsets of X called *hyperedges* or edges. Therefore, E is a subset of $\mathcal{P}(X) \setminus \{\emptyset\}$, where $\mathcal{P}(X)$ is the power set of X. The size of the vertex set is called the *order of the hypergraph*, and the size of edges set is the *size of the hypergraph*.





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Standards covered by or related to COMBINE activities

One of the major goals of COMBINE is to improve the interoperability of existing standards, and to foster or support fledging efforts aimed at filling gaps or new needs. Below are listed some of the major community standard representation formats covered by or related to COMBINE activity.

COMBINE standards

The following standardization activities are open community efforts. The standards are described in freely available specifications, and associated tools (XML schemas, UML diagrams etc.). They are piloted by democratically elected editorial boards, sometimes assisted by scientific committees. A decent software support exist, including API implementations. The development is supported by central teams and/or funding sources. The different formats try to avoid overlapping but rather strive to interoperate, via interconversion, cross-linking, use of common metadata layers etc.

A comprehensive list of specification documents is also available, following the COMBINE specification infrastructure.





Extensible Markup Language (XML)

- A markup language is a meta language that enables to define and control the meaning of elements contained in a document or a text.
- defines a set of rules for encoding documents in a format that is human- and machine-readable.
- It is eXtensible in that it enables the creation of personalized tags





BioPAX

BioPAX is a standard language that aims to enable integration, exchange and analysis of biological pathway data. It is expressed in OWL.

The last specification is BioPAX Level 3.

BioPAX development is coordinated by an elected editorial board and a Scientific Advisory Board.

BioPAX is supported by many pathway database or processing tools. An API is available to help implementing support Paxtools

More information



The <u>Systems Biology Graphical Notation (SBGN)</u>, is a set standard graphical languages to describe visually biological knowledge. It is currently made up of three languages describing Process Descriptions, Entity Relationships and Activity Flows.

The <u>last specifications</u> are SBGN PD Level 1 Version 2.0, SBGN ER Level 1 Version 2 and SBGN AF Level 1 Version 12

SBGN development is coordinated by an elected editorial board and a Scientific Committee.

Several data resources and software claim support for SBGN. An API is available to help implementing support libSBGN

More information



The <u>Systems Biology Markup Language (SBML)</u> is a computer-readable <u>XML format</u> for representing models of biological processes. SBML is suitable for, but not limited to, models using a process description approach.

The latest stable specification is Level 3 Version 2 Core.

SBML development is coordinated by an elected editorial board and central developer team.

eer 250 software systems known to support SBML can be found in the <u>SBML software guide</u>. APIs are available help in Jamesting support: IibSBML in C++ and JSBML in Java.

More information



The <u>Simulation Experiment Description Markup Language (SED-ML</u>) is an XML-based format for encoding simulation experiments. SED-ML allows to define the models to use, the experimental tasks to run and which results to produce is a computer-readable format for representing the models of biological processes. SED-ML can be used with models encoded in several languages, as far as they are in XML.

The latest stable specification is Level 1 Version 3.

SED-ML development is coordinated by an elected editorial board.

APIs are available to help implementing support: <u>libSedML</u> in C#, <u>libSEDML</u> in C++ with swig bindings for python, java, perl, R and ruby, and <u>libsedml</u> in Java.

More information



The <u>CellML language</u> is an XML markup language to store and exchange computer-based mathematical models. CellML is being developed by the Auckland Bioengineering Institute at the University of Auckland and affiliated research groups.

The latest stable specification is Version 1.1.

CellML development is coordinated by an elected editorial board.

APIs are available to help implementing support: CelIML API in C.

More information



The Synthetic Biology Open Language Data (SBOL Data) is a language for the description and the exchange of synthetic biological parts, devices and systems.

The latest stable specification of SBOL Data is 2.2.0.

SBOL Data is developed by the <u>SBOL Developers Group</u>. The development is coordinated by an <u>editorial board and</u> the SBOL Chair.

SBOL data is supported by many software tools. APIs are available to help implement the support of this data standard.

More information



The <u>Synthetic Open Language Visual (SBOL Visual)</u> is an open-source graphical notation that uses schematic "glyphs" to specify genetic parts, devices, modules, and systems.

The latest stable specification of SBOL Visual is 2.0.0

SBOL is developed by the <u>SBOL Developers Group</u> and <u>SBOL Visual Group</u>. The development is coordinated by an editorial board and the SBOL Chair.

SBOL Visual is supported by many software tools

More information



The NeuroML project focuses on the development of an XML based description language that provides a common data format for defining and exchanging descriptions of neuronal cell and network models.

The latest stable specification of NeuroML is version 2 beta 4.

NeuroML development is coordinated by the NeuroML Editorial Board.

NeuroML is supported by many software tools and databases, see here

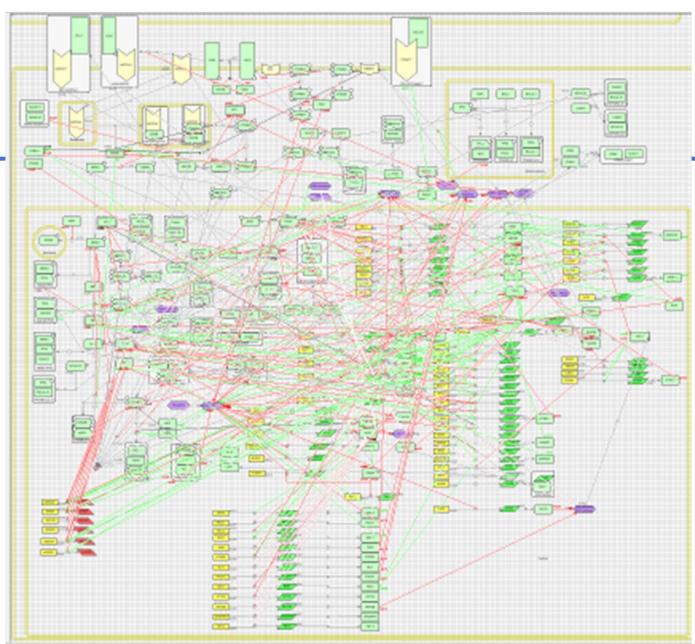
More information

Layout

- Proper visualization, including positioning of molecular entities, can greatly facilitate understanding of the entire system
- Manual or automatic layout can be chosen, as well as custom views to emphasize specific components or processes
- the network structure should be stored in a layout-aware format,
 i.e. a format allowing one to encode positions of molecular entities.

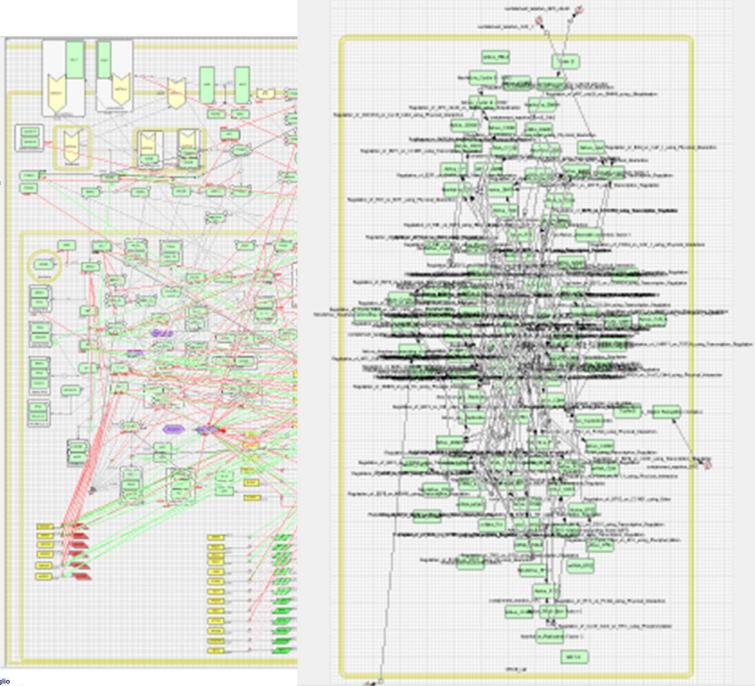




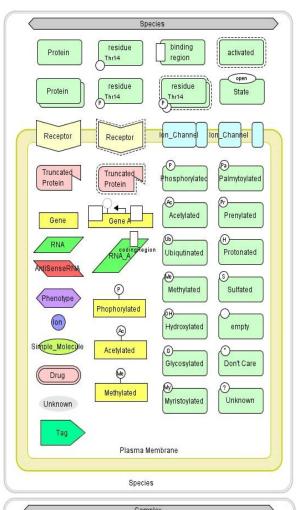


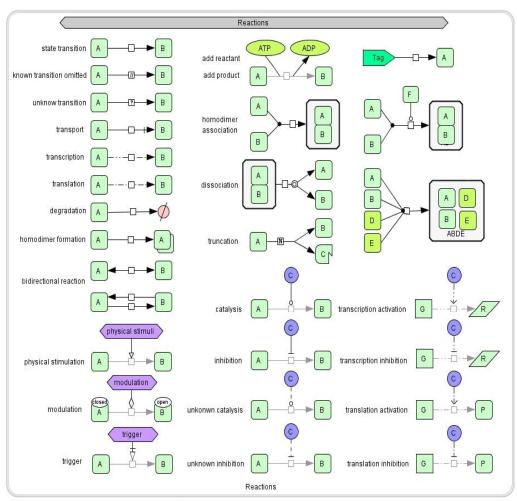


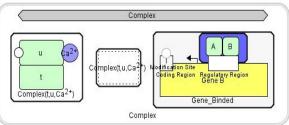


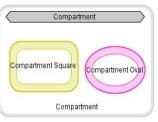


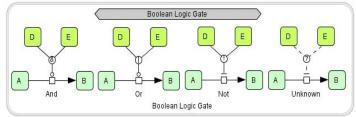












EMT

- Reactome
- Spike
- KEGG
- Wipathways
- Navicell

Tiziana Guarnieri Unibo



Cytokine-cytokine receptor interaction - Homo sapiens (ELM-receptor interaction - Homo sapiens (Puman) ELM-receptor interaction - Homo sapiens (Puman) IAM-STAT signaling pathway - Homo sapiens (Puman) IAM-STAT signaling pathway - Homo sapiens (Puman) ITMF signaling pathway - Homo sapiens (Puman) HITM-signaling pathway - Homo sapiens (Puman) PELS Assignaling pathway - Homo sapiens (Puman) SMT in colorectal cancer (Homo asplend) TIST & Spanlig in Throad Cells for EMT (Homo sapient) TIST & Spanlig in Throad Cells for EMT (Homo sapient) Florid Spanling in Throad Cells for EMT (Homo sapient) Cell in custiment (join inflammatory response) (Homo sapient) Angegeness (Homo sapient) Inflammatory (Homo sapient) Inflammatory Response Pathway (Homo sapient) Inflammatory Response Pathway (Homo sapient) Inflammatory Response Pathway (Homo sapient) Florid Admission (Homo patient) Florid Marker (Homo patient) Florid Admission (Homo patient) Florid Marker (Homo patient) Florid Admission (Homo patie Extracellular matrix organization (8 455. 317214) O ghospidation of TSi domain-containing proteine (8 456. 517214) Activated MOTICAL Immanuts Signal or the Machine (8 456. 517214) Signaling by VIGE (8 456. 45913) Signaling by VIGE

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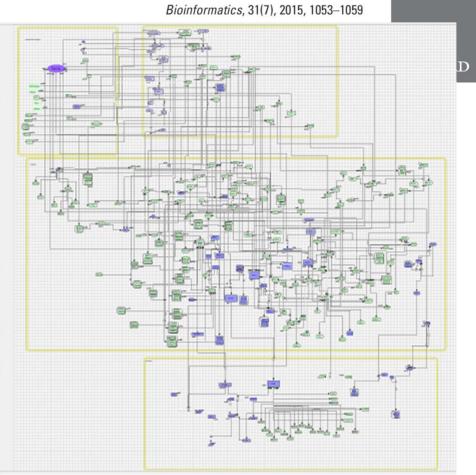
Mechanotransduction

Systems biology

Mechanotransduction molecular pathway, ge

Jennifer E. Dent^{1,2,†}, Valentina Dev Youtao Lu¹, Yuanhua Liu¹ and Chri

¹Group of Clinical Genomic Networks, Key Laborator Computational Biology, Shanghai Institutes for Bio ²Quintiles, Global Biostatistics, Reading, Berkshire, U DISI, University of Bologna, Bologna, Italy

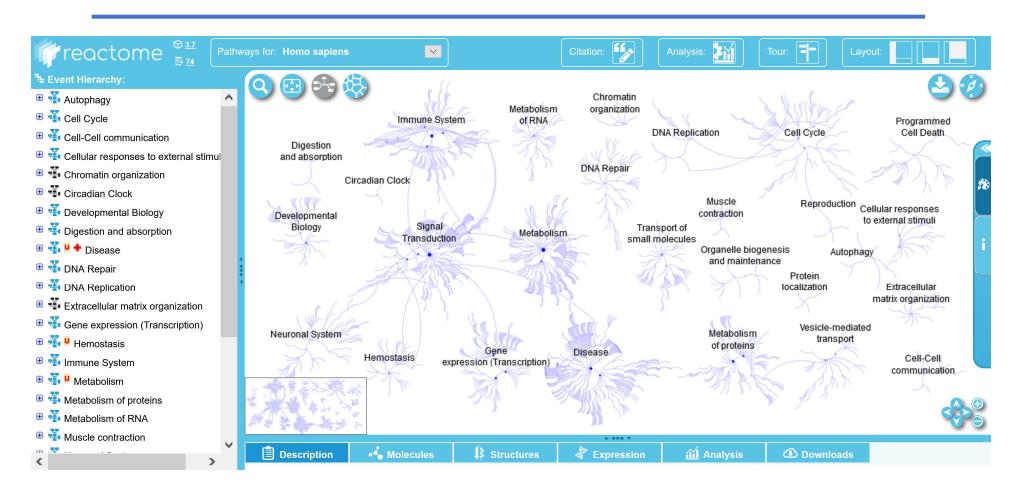






Inflammatory Reflex





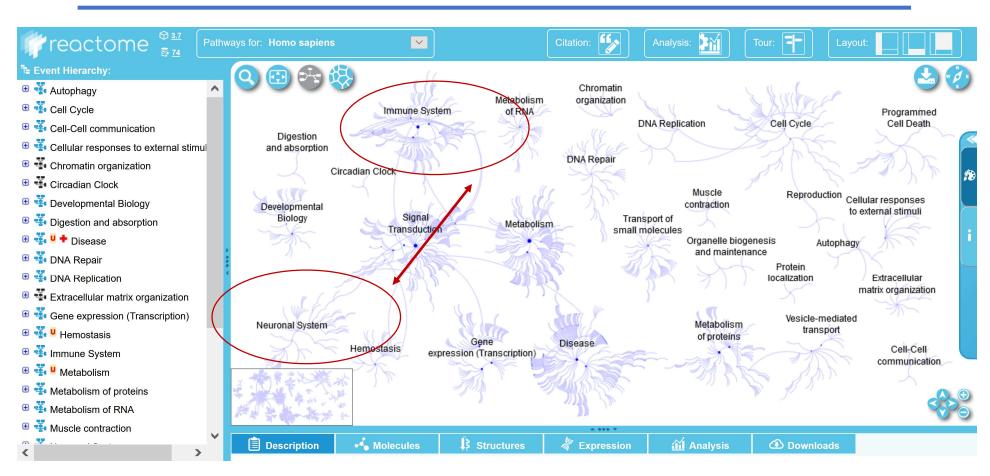






Inflammatory Reflex









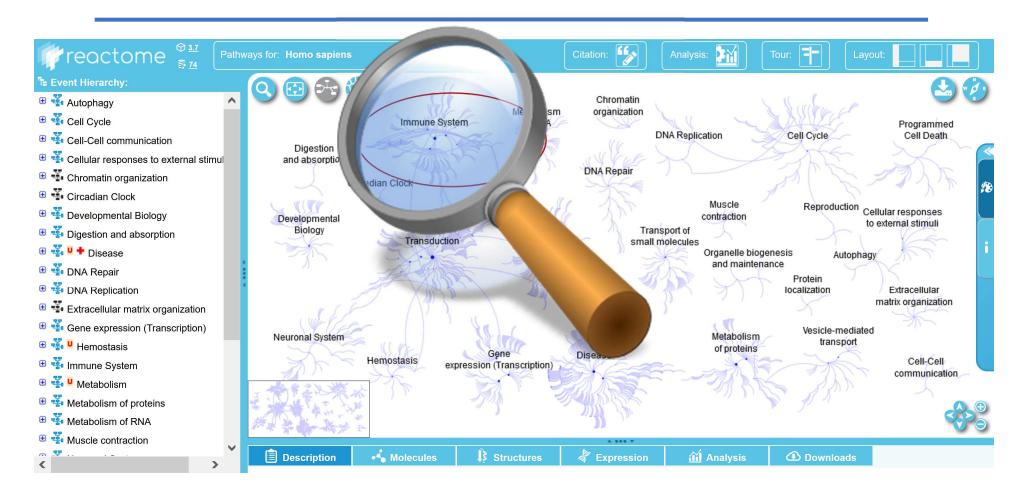


CN2

Christine Nardini, 11/15/2020



Immune Response







Overlap Merge & Analyze

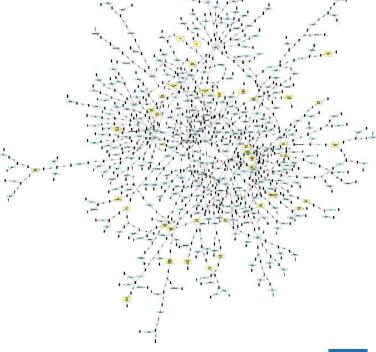
Di Lena et al. BMC Bioinformatics 2013, 14:159 http://www.biomedcentral.com/1471-2105/14/159



SOFTWARE

MIMO: an efficient tool for molecula interaction maps overlap

Pietro Di Lena^{1,2*}, Gang Wu¹, Pier Luigi Martelli³, Rita Casadio³ and Christine Nardi







Thank you