



# Computational neuroscience: biophysics - Lecture 2

Blue Brain Project EPFL, 2024

## **Neuroinformatics: Data and Metadata**



## **Lecture Overview**

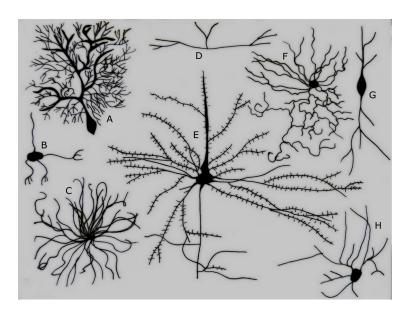
- Scope
- Approaches / Resources



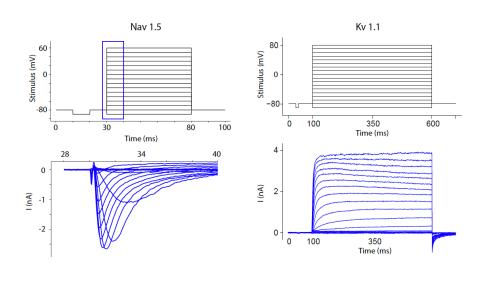
## **Lecture Overview**

- Scope
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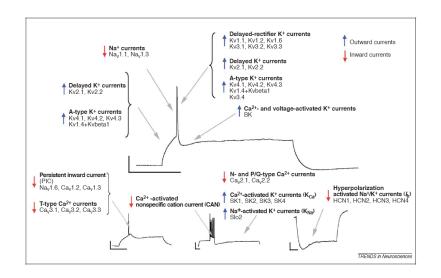


Morphology reconstructions – lecture 3



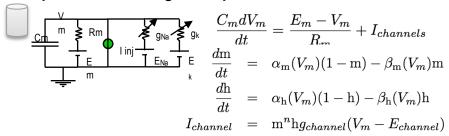
Single channel recordings – lecture 4





Single cell recordings - lecture 4

#### Simplified Model: Single Compartment and ion channel formalism



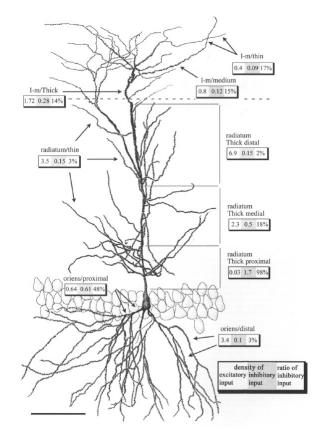
#### Cellular Model: Cable and ion channel formalism

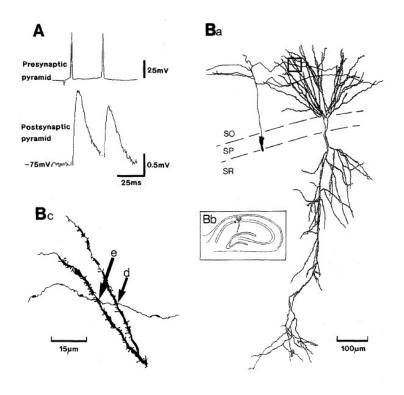


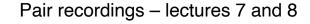
$$\begin{split} \frac{C_m dV_m}{dt} &= \frac{E_m - V_m}{R_m} + I_{channels} \\ &+ \frac{2(V_{m_{i+1}} - V_{m_i})}{R_{a_{i+1}} + R_a} + \frac{2(V_{m_{i-1}} - V_{m_i})}{R_{a_{i-1}} + R_a} \end{split}$$

Computational models - lecture 5 and 6



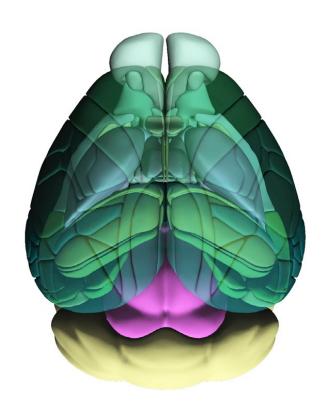


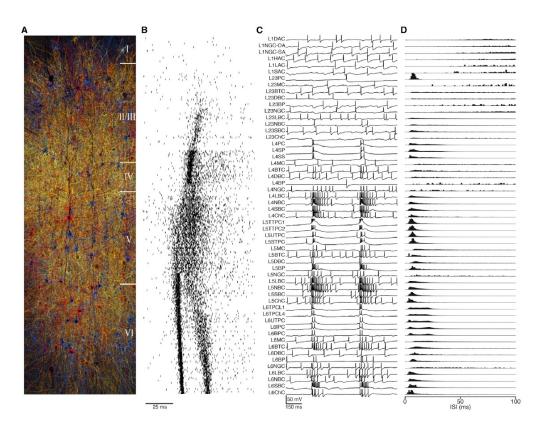






Number of synapses – lecture 7



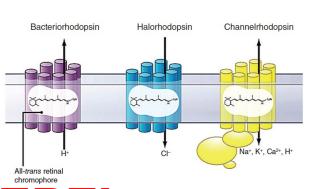




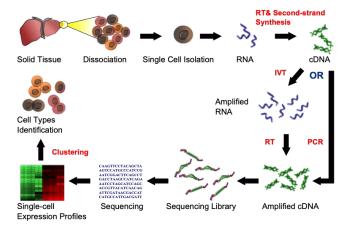
Atlas - lecture 9

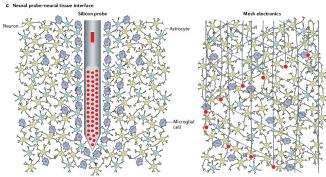
Network activity – lecture 10, 11, and 12

# Tissue specific promoter & to the second of the second of

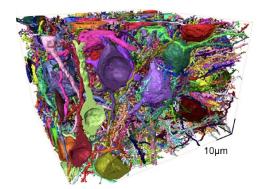


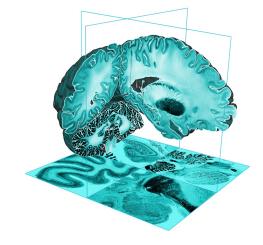
#### Single Cell RNA Sequencing Workflow











- Experimental measure (raw or processed)
- Information extracted from literature (raw or processed)
- Model artifact



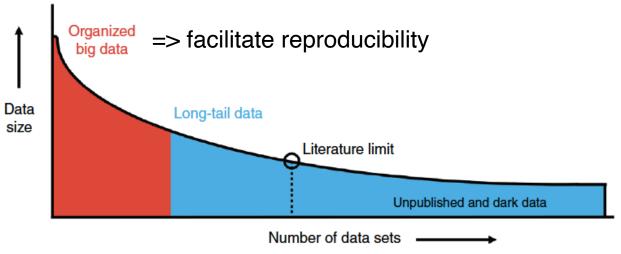


Figure 1 Schematic illustration of long-tail data. Studies that have plotted data set size against the number of data sources reliably uncover a skewed distribution. Well-organized big science efforts featuring homogenous, well-organized data represent only a small proportion of the total data collected by scientists. A very large proportion of scientific data falls in the long-tail of the distribution, with numerous small independent research efforts yielding a rich variety of specialty research data sets. The extreme right portion of the long tail includes data that are unpublished; such as siloed databases, null findings, laboratory notes, animal care records, etc. These dark data hold a potential wealth of knowledge but are often inaccessible to the outside world.



#### **Problem**

Reproducibility / reusability by the same person over time, by different people in the same lab or in other labs

#### hippo\_planes\_for\_morph-collage.txt

-0.02014812020230947,0.6864996194426534,-0.7268509652999063,-1604.1923270574614 0.02014812020230947,-0.6864996194426534,0.7268509652999063,1654.1923270574614 -0.019954736969346867,0.7276227597727851,-0.685687193939861,-1685.5191394721055 0.019954736969346867,-

0.7276227597727851,0.685687193939861,1735.5191394721055 -0.020011572342902184,0.7157871516529508,-0.6980317259988408,-1662.2457659248844 0.020011572342902184.-

0.7157871516529508,0.6980317259988408,1712.2457659248844 -0.02006873300917579,0.7036735147228083,-0.7102399810156117,-1638.3429607097721 0.02006873300917579,-

0.7036735147228083,0.7102399810156117,1688.3429607097721



Based on memory, filename, and content:

- Pairs of planes
- A,B,C,D coefficients of the planes
- 101 equally-spaced planes

#### But...

- How was it produced?
- Who made it?
- The file is not archived
- Multiple version?



## **Lecture Overview**

- Scope
- Approaches / Resources



# **Data Life Cycle**

Griffin et al., 2018

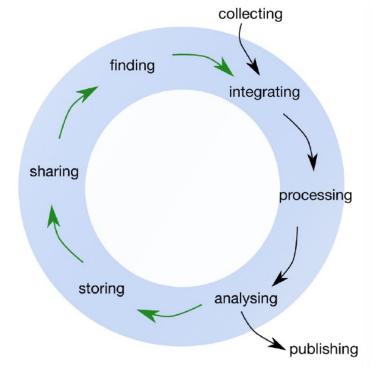


Figure 1. The Data Life Cycle framework for bioscience, biomedical and bioinformatics data that is discussed throughout this article. Black arrows indicate the 'traditional', linear view of research data; the green arrows show the steps necessary for data reusability. This framework is likely to be a simplified representation of any given research project, and in practice there would be numerous 'feedback loops' and revisiting of previous stages. In addition, the publishing stage can occur at several points in the data life cycle.



## **Finding**

 Poor findability: supplementary material to articles, on personal or institutional websites, or in non-disciplinespecific repositories sharing

analysing

- High findability: public data repository
- Poor quality of the user-submitted data in public repositories
- Public datasets often require extra curation before reuse (e.g. NeuroMorpho.org)
- The results of extra curation may not find their way back into the repositories
- Repositories are often not easily searched by generic web search engines
- Registries, which form a secondary layer linking multiple, primary repositories, may offer a more convenient way to search across multiple repositories

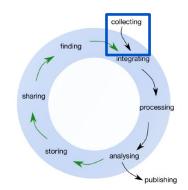


Legend: challenge, solution

# **Collecting**

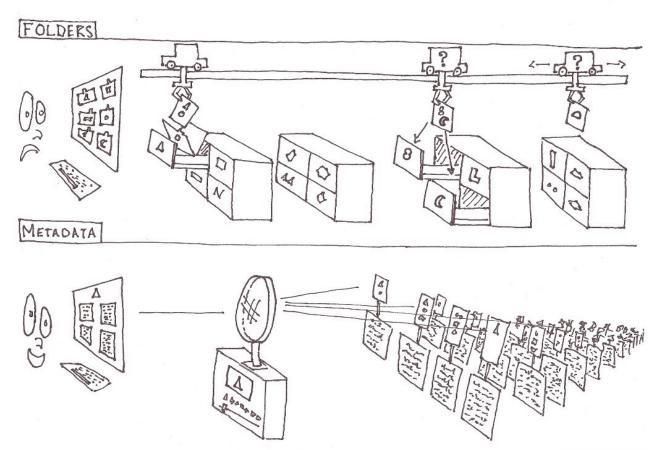
#### Search for specific data

- Metadata
- Provenance
- Ontology
- Standard vocabulary



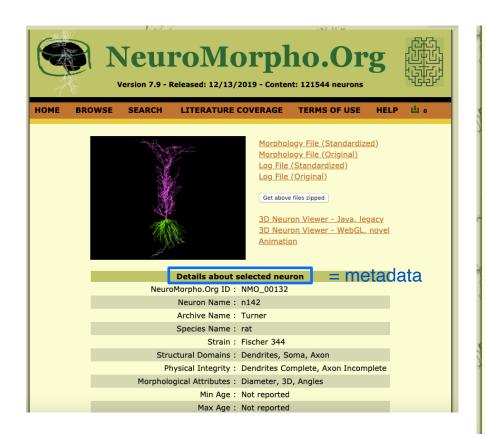


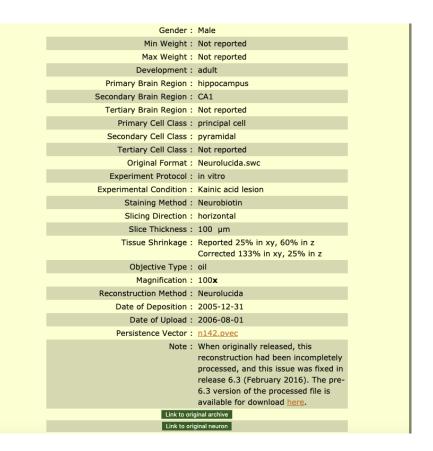
# FOLDERS VS METADATA





#### Metadata: data about data







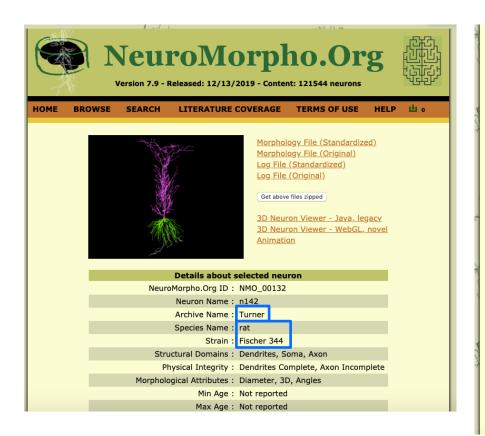
#### **Provenance**

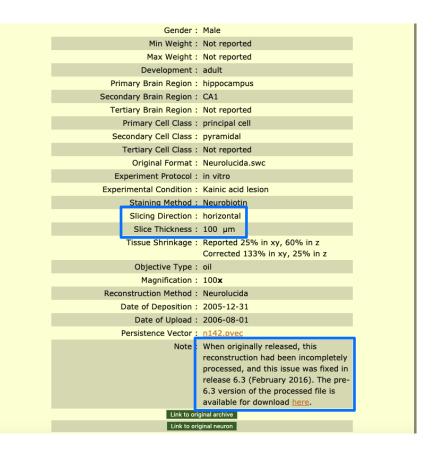
Metadata about the origin and transformations of the data

- Who produces the data?
- Is this derived data? If so, from which dataset?
- What processes / analyses were used to produce / transform the data?
- Which software and version?



#### **Provenance**







#### Metadata

- Metadata is what makes the data searchable and useful
- Metadata is not always sufficient to a given scope
- The scope changes as a function of the project, but also of the time
- Describing a piece of data for complete reproducibility is challenging and requires much effort
- Attempts have been made to request a minimum set of information to the data producer



#### **Minimal Information for Neuroscience Datasets (MINDS)**

- Subject: age, sex, species, strain (when applicable),
- Methods, protocols, equipment and parameters used in experiments
- Classification data category, data format, cell type
- Brain location using brain atlas parcellation or spatial coordinates/transform,
- Contributors and their affiliations,
- Access to the data and the format via persistent identifier URL (e.g. DOI)



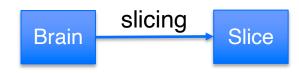
#### Metadata

If metadata is well structured, uses consistent element names and contains element values with specific descriptions from agreed upon vocabularies, it enables machine readability, aggregation, integration and tracking across datasets [...]. One key approach in best practice metadata collection is to use controlled vocabularies built from ontology terms. (Griffin et al., 2018)



## **Ontology**

- Ontology is a way of organizing and defining concepts and the relationships between them
- It provides machine-interpretable representations of some aspect of biological reality
- Sourcing metadata element values from ontologies ensures that the terms used in metadata are consistent and clearly defined
- define provenance rules





# **Standard vocabulary**





CA1 trilaminar interneuron

**Browse** 



Search





#### CA1 Trilaminar

Name	Supertype
CA1 (i)0113p-SUB_111 Trilaminar	421:Schaffer Collateral-Related:SCR RO-Targeting- III
Synonym(s)	
CA1 double projecting cell	
CA1 double projection cell	
CA1 double-projection cell	
CA1 double-projection neuron	
CA1 hippocampo-subicular projection cell	
CA1 horizontal trilaminar cell	
CA1 horizontal trilaminar interneuron	
CA1 horizontal trilaminar neuron	
CA1 nonpyramidal projection neuron	
CA1 oriens retrohippocampal projection cell	
CA1 oriens-retrohippocampal cell	
CA1 oriens-retrohippocampal nonpyramidal	
CA1 oriens-retrohippocampal projection neu	ron
CA1 septal-projecting GABAergic cell	
CA1 TL cell	
CA1 trilaminar cell	



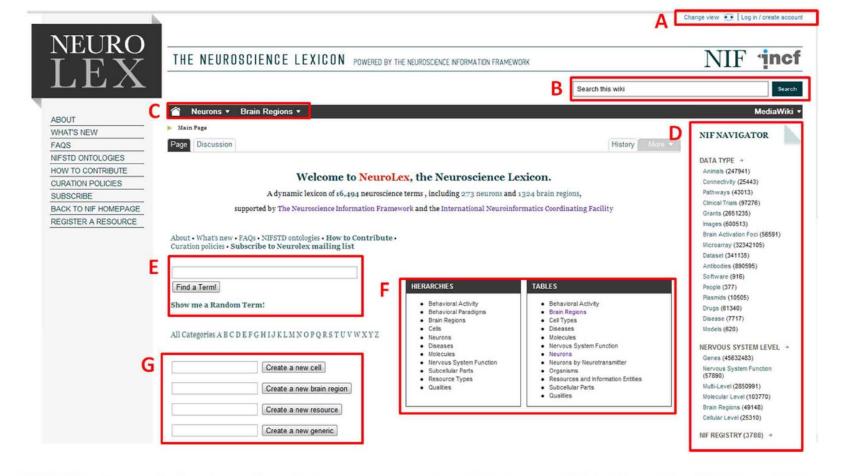


FIGURE 1 | Landing page for NeuroLex.org. Several features are highlighted. (A) Login/user management controls. (B) Global site search bar. (C) Quick navigation to neuron or brain region information. (D) NIF Navigator, connecting the Neuroscience Information Framework B's federated resources

to each NeuroLex page. **(E)** Global site search bar. **(F)** Quick navigation to hierarchies or tables containing detailed information about diverse entities in Neuroscience. **(G)** Quick creation forms for cells, brain regions, resources, and generic page contents.

#### **Standardization**

- Standardization does not apply only to vocabulary
- Reproducibility also requires standard formats and
- Standard tools



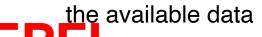
## Collect data: manual vs. automatic approaches

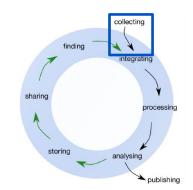
#### Manual approaches

- Expert-based
- They tend to be of higher quality, but they produce small datasets

#### **Automatic approaches**

- Text mining, automatic classification, curation...
- They can introduce thresholds to keep a certain level of quality. However,
   they tend to incorporate data of different quality, but they can digest most of





#### **Manual approaches: Bezaire and Soltesz, 2013**

HIPPOCAMPUS 23:751-785 (2013)

Quantitative Assessment of CA1 Local Circuits: Knowledge Base for Interneuron-Pyramidal Cell Connectivity

Marianne J. Bezaire,\* and Ivan Soltesz



#### **Bezaire and Soltesz, 2013**

#### **Method**

- Combine selected pieces of information to estimate the numbers of the main cell types in the hippocampus CA1
- Use of assumptions and generalizations to fill the gaps (see part 2 of the lecture)



Estimated Number of Each Type of Interneuron

				Lay	er	
Interneuron type	Fraction (%)	Total	SO	SP	SR	SLM
Neurogliaform family	32.2	12,390	980	5,410	3,030	2,970
Ivy	22.9	8,810	980	5,410	2,420	0
Neurogliaform	9.3	3,580	0	0	610	2,970
SOM expressing	9.3	3,580	3,580	0	0	0
O-LM	4.3	1,640	1,640	0	0	0
Double projection	2.0	760	760	0	0	0
CB- septal proj.	0.5	190	190	0	0	0
Oriens-retrohipp.	1.7	640	640	0	0	0
Other SOM+ cells <sup>a</sup>	0.9	350	350	0	0	0
PV expressing	23.9	9,210	2,200	6,460	550	0
PV+ Basket	14.4	5,530	1,320	3,880	330	0
Bistratified	5.7	2,210	530	1,550	130	0
Axo-axonic	3.8	1,470	350	1,030	90	0
CCK expressing	13.9	5,370	1,140	1,070	1,960	1,200
CCK+ Basket	9.4	3,600	780	940	1,170	710
ADI	1.0	390	0	0	390	0
SCA	1.0	400	0	0	400	0
PPA	1.3	490	0	0	0	490
CCK Misc.	1.3	490	360	130	0	0
Interneuron-specific	19.4	7,470	780	3,190	1,450	2,050
IS I	11.0	4,250	780	1,800	780	890
IS II	5.1	1,970	0	480	450	1,040
IS III	3.2	1,250	0	910	220	120
Other interneurons	1.2	480				
Total interneurons	100	38,500				



## Automatic approaches: Attili et al. 2022

Received: 21 July 2021

Revised: 25 January 2022 | Accepted: 28 February 2022

DOI: 10.1111/ejn.15639

RESEARCH REPORT



# Quantification of neuron types in the rodent hippocampal formation by data mining and numerical optimization

Sarojini M. Attili<sup>1</sup> | Keivan Moradi<sup>1</sup> | Diek W. Wheeler<sup>2</sup> | Giorgio A. Ascoli<sup>1,2</sup>











#### WELCOME TO THE HIPPOCAMPOME PORTAL

v1.12 - Released: 05/05/2022

527,802 Pieces of Knowledge (PoK) & 46,004 Pieces of Evidence (PoE)

The Hippocampome is a curated knowledge base of the circuitry of the hippocampus of normal adult, or adolescent, rodents at the mesoscopic level of neuronal types. Knowledge concerning dentate gyrus, CA3, CA2, CA1, subiculum, and entorhinal cortex is distilled from published evidence and is continuously updated as new information becomes available. Each reported neuronal property is documented with a pointer to, and excerpt from, relevant published evidence, such as citation quotes or illustrations.

The goal of the Hippocampome is dense coverage of available data characterizing neuronal types. The Hippocampome is a public and free resource for the neuroscience community, and the knowledge is presented for user-friendly browsing and searching and for machinereadable downloading.

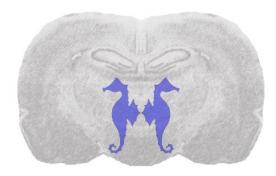
If you have feedback on either functionality or content, or if you would like to be informed when the first official version is released, please fill out the feedback form or email us at Hippocampome.org@gmail.com.

The release of v1.0 on 09/23/2015 includes 3,697 PoK and 13,888 PoE. Reference: Wheeler et al., 2015. Hippocampome.org: A knowledge base of neuron types in the rodent hippocampus, eLife 2015;4:e09960.

The release of v1.1 on 10/17/2016 includes 3,697 PoK, 13,888 PoE, and the Neuron Term Portal, which allows one to view definitions for terms and phrases used on this website. Reference: Hamilton et al., 2016 Name-calling in the hippocampus (and beyond): coming to terms with neuron types and properties. Brain Informatics 2017 Mar;4(1):1-12: doi:10.1007/s40708-016-0053-3.

The release of v1.2 on 11/06/2016 includes 3,936 PoK, 14,399 PoE, and a clickable Connectivity Matrix, an interactive Connectivity Navigator, and the ability to Search by Connectivity. Reference: Rees et al., 2016 Graph theoretic and motif analyses of the hippocampal neuron type potential connectome. eNeuro Nov 2016, ENEURO.0205-16.2016; DOI: 10.1523/ENEURO.0205-16.2016.

The release of v1.3 on 06/30/2017 includes 10,822 PoK, 21,285 PoE, and a downloadable list of Allen Brain Atlas (ABA) predictions of marker expressions and a utility for viewing the effects of thresholds on ABA marker expression predictions. Reference: Hamilton et al., 2017 Molecular fingerprinting of principal neurons in the rodent hippocampus: a neuroinformatics approach. Journal of Pharmaceutical and Biomedical Analysis 2017 Sep 10;144:269-278; doi: 10.1016/j.jpba.2017.03.062.



The release of v1.7 on 10/08/2019 includes Izhikevich models for most of the neuron types, downloadable parameter and CARLSim4-simulation files, and the ability to perform simulations of the firing patterns. Reference: Venkadesh, et al., 2019 Simple models of quantitative firing phenotypes in hippocampal neurons: comprehensive coverage of intrinsic diversity. PLOS Computational Biology 2019 Oct 28;15(10):e1007462; doi: 10.1371/journal.pcbi.1007462.

The release of v1.8 on 12/28/2020 includes an additional 5,152 PoK, 6,055 PoE, and new browsable matrices for neurite lengths, somatic path distances, numbers of potential synapses, numbers of contacts, and connection probabilities. Reference: Tecuati, et al., 2020 Comprehensive estimates of potential synaptic connections in local circuits of the rodent hippocampal formation by axonal-dendritic overlap. Journal of Neuroscience 2021 Feb 24:41(8):1665-1683; doi: 10.1523/JNEUROSCI.1193-20.2020.

The release of v1.9 on 02/27/2021 includes an additional 91 PoK, 768 PoE, and a new browsable matrix for in vivo recordings. Reference: Sanchez-Aguilera, et al., 2021 An update to Hippocampome.org by integrating single-cell phenotypes with circuit function in vivo. PLoS Biology 2021 May 6;19(5):e3001213; doi: 10.1371/journal.pbio.3001213.

The release of v1.10 on 08/03/2021 includes the Cognome, a literature review and knowledge base of spiking neural circuit and network simulations of the hippocampal formation. Reference: Sutton and Ascoli, 2021 Spiking neural networks

#### Browse

Morphology

Connectivity

Firing patterns

Izhikevich models

In vivo recordings

Cognome

Molecular markers

Synaptic physiology









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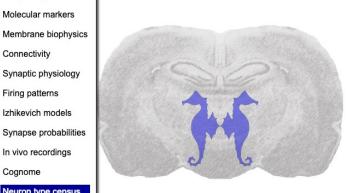
Neuron type census If you have feedback on either functionality or content like to be informed when the first official version is released. out the <u>feedback form</u> or email us at <u>Hippocampome.org@gmail.com</u>.

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# Hippocampome.org









#### Browse neuron type census matrix

	Neuron Type	Rats	Mice
DG(18)	<u>Granule</u>	962200	394502
	Hilar Ectopic Granule	90	37
	Semilunar Granule	163633	67090
	Mossy	25573	10485
	Mossy MOLDEN	5206	2134
	AIPRIM	8559	3509
	DG Axo-axonic	235	96
	DG Basket	1612	661
	DG Basket CCK+	128	52
	HICAP	833	342
	<u>HIPP</u>	6006	2462
	HIPROM	10	4
	MOCAP	9067	3717
	MOLAX	<u>5421</u>	2223
	MOPP	377	155
	DG Neurogliaform	599	246
	Outer Molecular Layer	10	4
	Total Molecular Layer	7989	3275
CA3(25)	CA3 Pyramidal	183844	75376
	CAR Duramidal	44123	18000

Legend: +/green: Excitatory -/red: Inhibitory

#### Attili et al., 2022: method

- we assigned a variable for each neuron type
- in order to account for information regarding neuronal groups in certain layers that did not correspond to any Hippocampome.org neuron type, we added nine ancillary variables
- divisive scaling factor of 0.41 to convert mouse data to rat
- Numerical densities were converted into neuronal numbers
- Relationships are converted in equations

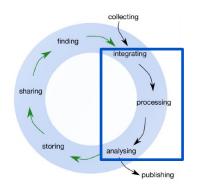


$$\begin{array}{c} \text{Equation} \\ x_{69} + x_{72} + x_{75} + x_{9} + x_{81} \\ + x_{84} + x_{86} + x_{87} \\ + x_{91} + x_{94} + x_{96} \\ + x_{97} + x_{100} + x_{114} \\ + x_{131} = 324,000 \\ \end{array} \\ \begin{array}{c} \text{Normalized form} \\ \text{Normalized form} \\ & \begin{array}{c} (x_{69} + x_{72} + x_{75} + x_{79} + x_{81} \\ + x_{84} + x_{86} + x_{87} \\ + x_{91} + x_{94} + x_{96} \\ + x_{97} + x_{100} + x_{114} \\ + x_{131})/324,000 - 1 = 0 \\ \end{array} \\ \begin{array}{c} \text{Least squares} \\ \text{form} \\ \end{array} \\ \begin{array}{c} ((x_{69} + x_{72} + x_{75} + x_{79} + x_{81} \\ + x_{84} + x_{86} + x_{87} \\ + x_{91} + x_{94} + x_{96} \\ + x_{97} + x_{100} + x_{114} \\ + x_{131})/324,000 - 1)^2 = 0 \\ \end{array} \\ \begin{array}{c} \frac{30x_8}{31x_8} - 1 = 0 \\ \frac{x_7 + x_8}{3,680} - 1 \le 0 \\ \frac{x_7 + x_8}{3,680} - 1 \ge 0 \\ \frac{x_7 + x_8}{3,68$$

$$\mathbf{r} = \sum_{i}^{n} w_i \left( \left( z_i^{type} - z_i^{data} \right) / z_i^{data} \right)^2$$
, overall residual to be minimized by numerical optimization

# Integrating, processing, and analysing

- Data are often heterogeneous
- Convert data into the same format and granularity
- Uniform metadata (Interoperability)
- Recording and reporting how data is processed and analysed
- Full reproducibility requires access to the software, software versions, workflow, dependencies and operating system used as well as the data and software code itself
- Hosting source code in a repository where it receives a unique identifier and is under version control (e.g. GitHub)





## **Publishing**

- Journals increasingly recommend or require deposition of raw data in a public repository
- The vast majority of scientific journals require inclusion of processing and analysis methods in 'sufficient detail for reproduction'



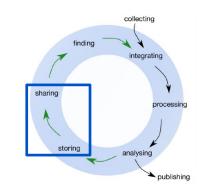
- 'data journals': scientific journals that publish papers describing datasets. This
  gives authors a vehicle to accrue citations for data production alone, which is
  typically not well recognized under the traditional publishing model
- Open Access Publishing
- Publications have unique ID (PubMed ID, DOI) as well as researchers (ORCID)



Legend: challenge, solution

## Storing, sharing

- Public repositories
- Local data storage solutions during the processing and analysis stages
- Some domains require large storage resources
- Human data require privacy regulations





#### **Box 2** | The FAIR Guiding Principles

#### To be Findable:

- F1. (meta)data are assigned a globally unique and persistent identifier
- F2. data are described with rich metadata (defined by R1 below)
- F3. metadata clearly and explicitly include the identifier of the data it describes
- F4. (meta)data are registered or indexed in a searchable resource

#### To be Accessible:

- A1. (meta)data are retrievable by their identifier using a standardized communications protocol
- A1.1 the protocol is open, free, and universally implementable
- A1.2 the protocol allows for an authentication and authorization procedure, where necessary
- A2. metadata are accessible, even when the data are no longer available

#### To be Interoperable:

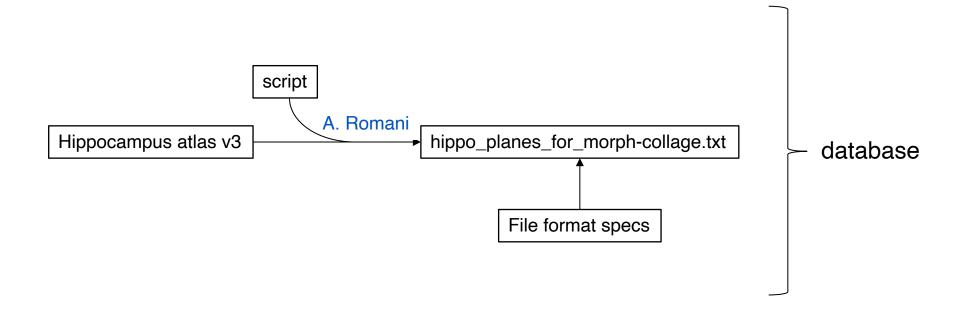
- 11. (meta)data use a formal, accessible, shared, and broadly applicable language for knowledge representation.
- I2. (meta)data use vocabularies that follow FAIR principles
- 13. (meta)data include qualified references to other (meta)data

#### To be Reusable:

- R1. meta(data) are richly described with a plurality of accurate and relevant attributes
- R1.1. (meta)data are released with a clear and accessible data usage license
- R1.2. (meta)data are associated with detailed provenance
- R1.3. (meta)data meet domain-relevant community standards

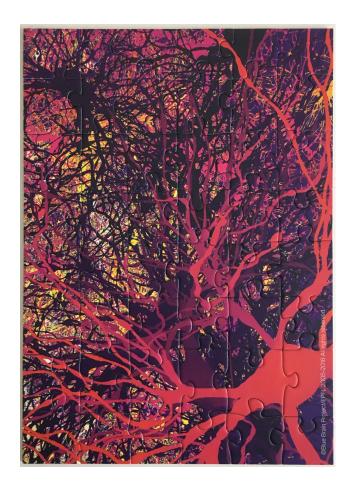


# It's time to fix my problem...



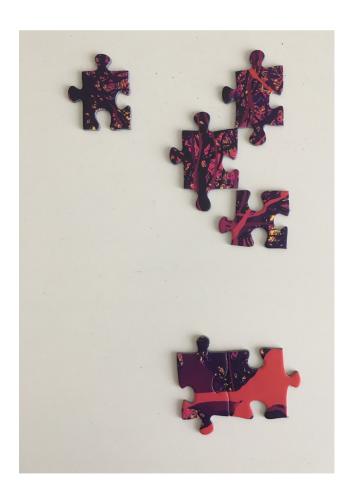


# What you would like





# The reality

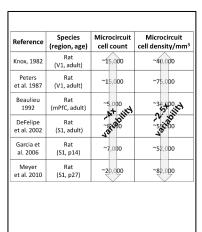




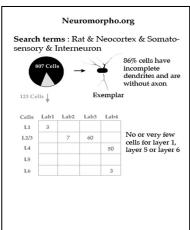
## How to overcome sparsity and reproducibility of data?

Examples of some issues with existing data

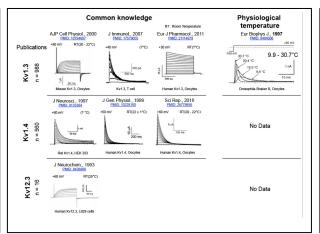
#### **Cell densities**



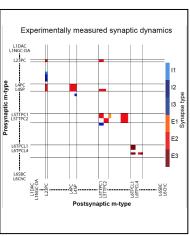
#### **Morphologies**



Ion channel kinetics



Synaptic physiology



Numbers in literature can **vary** up to **4 fold** 

Usually data is incomplete or missing

Data often is **inconsistent** and raw data largely not publicly **available** 

Very few pathways have been characterized. Data can be very **sparse** 



## What you have learnt

- Data is not enough, it is important to have metadata.
- Rich metadata and standardizations enable reproducibility.
- MINDS.
- Ontology, provenance, standard vocabulary...
- FAIR principles.
- Lifecycle of the data.
- Data sparseness.

