



OVERVIEW OF PROTEIN – PROTEIN INTERACTION PROJECT

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25/07/2020

MAIN OBJECTIVE

- Obtain complete information about how two specific proteins are interacting.
- For a specific pair of interacting proteins we want to know if they have a Domain Domain Interaction (DDI) or Domain Linear-Motif Interaction (DLI).

WHY?

- There are several databases with specific information, but we want to obtain a complete and integrated output.
- Find the more likely way for two specific proteins to interact.
- Allows to find a relationship between interaction strength and modular architecture of PPI network.
- It will help to have a better understanding of protein interactions and regulation mechanisms.

PROTEIN INTERACTION GROUPS

Physical characteristics of PPI are determined by interface structure. There are two main groups:

- **DDI:** Domain Domain Interaction. Typical case of big/strong interfaces between two globular domains. Tend to connect proteins within the same biological modules. Stronger fold affinities than DLI.
- **DLI:** Domain Linear-Motif Interaction. Common in small and weak interfaces between short peptides. Enriched in interactions connecting different functional groups.

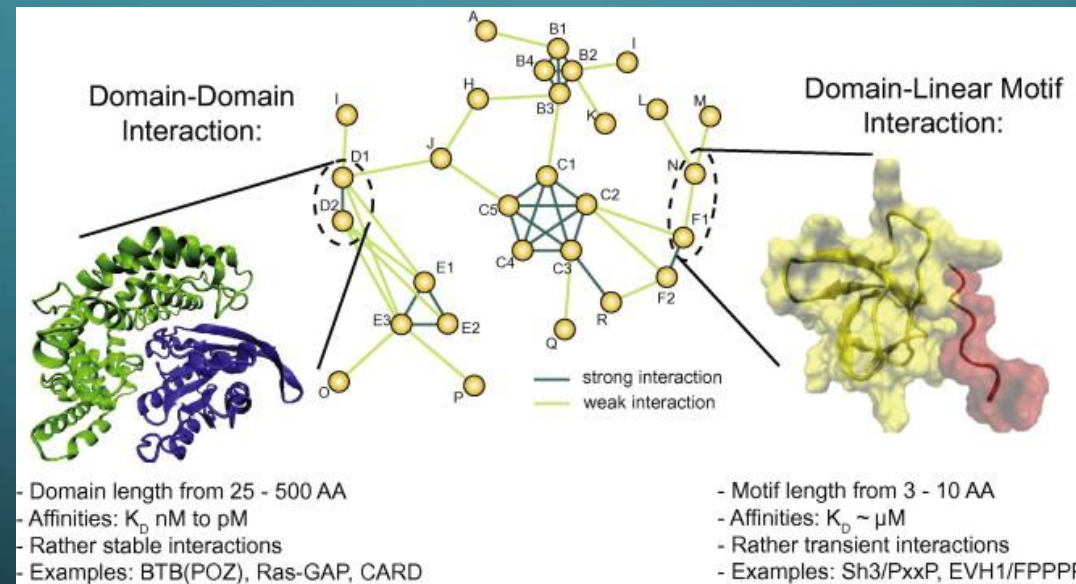
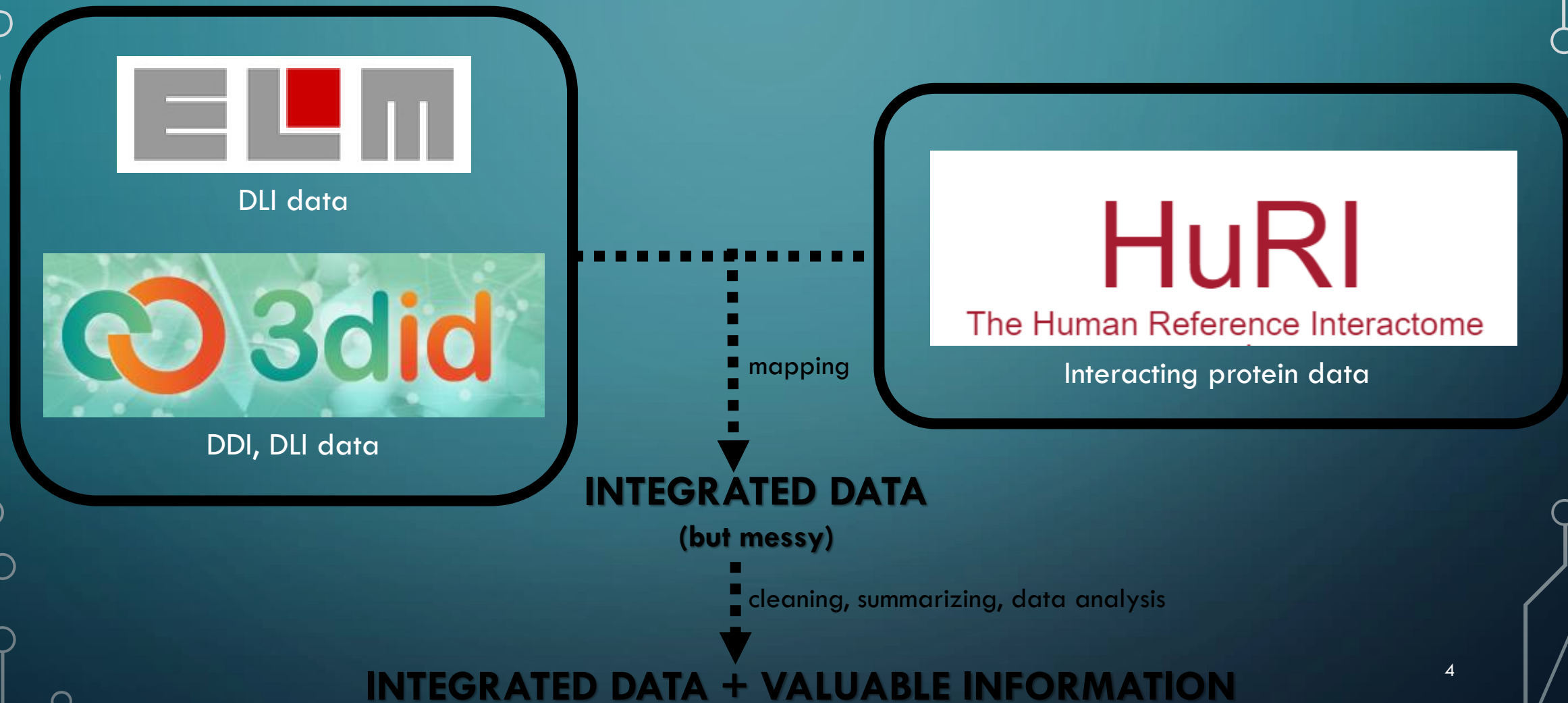


Figure 1. Two different PPI groups illustrated. On the left we have an example of a DDI. On the right a DLI is shown. Extracted from: (<http://www.sciencedirect.com/science/article/pii/S0014579308001208>)

GENERAL VIEW



ABOUT DATABASES



- Eukaryotic Linear Motif
- Contains experimentally validated **SLiMs** (compact protein interaction sites composed of short parts of adjacent aa).
- Located in intrinsically altered proteome regions, important for cell signalling/protein regulation.
- SLiM-based interactions are **DLI** type and are not easily detected.
- Many diseases alter their function.
- Pathogens mimic them to hijack host system.



- 3D Interaction Domains
- Collection of DDI which high-resolution 3D structure is known.
- Also contains Domain Motif Interactions.
- Gives information about critical molecular details.

ABOUT DATABASES

HuRI

- Human Reference Protein Interactome
- ORF Sequences and PPIs are mapped with Ensembl.
- For each interacting protein pair it displays experimental information, protein Ids and isoform-specific ORF.
- The integration with genome, transcriptome and proteome enables the study of cellular function in physiological/pathological contexts.