

Kshitish K Acharya

- **My involvement with NGS & genomics**
- **Can we make a better use of existing data to create a molecular portrait of tissue-specific functions?**

Challenges in Genomics and Computing

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ICTS-TIFR, IISc campus,

Bengaluru -560012

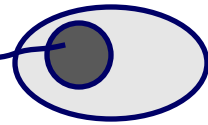


- RNA-sequencing to understand infertility in men
- De novo genomic assembly, gene identification and SNP analysis for novel fish and plant species
- Human gut metagenomics
- ChIP-sequencing data analysis
- miRNA sequence analysis (stress and brain response)
- www.startbioinfo.com



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- My involvement with NGS
- **Can we make a better use of existing data to create a molecular portrait of tissue-specific functions?**
 - **Background**



– Background

– **Cataloging the gene expression**

- Making better use of microarray data

- **Compilation:** 5 years, 20 persons to compile data.

- Current databases miss 50% of published data:
two new databases developed.*

- **A new method of meta analysis.**

- Integrating NGS & mass spec data

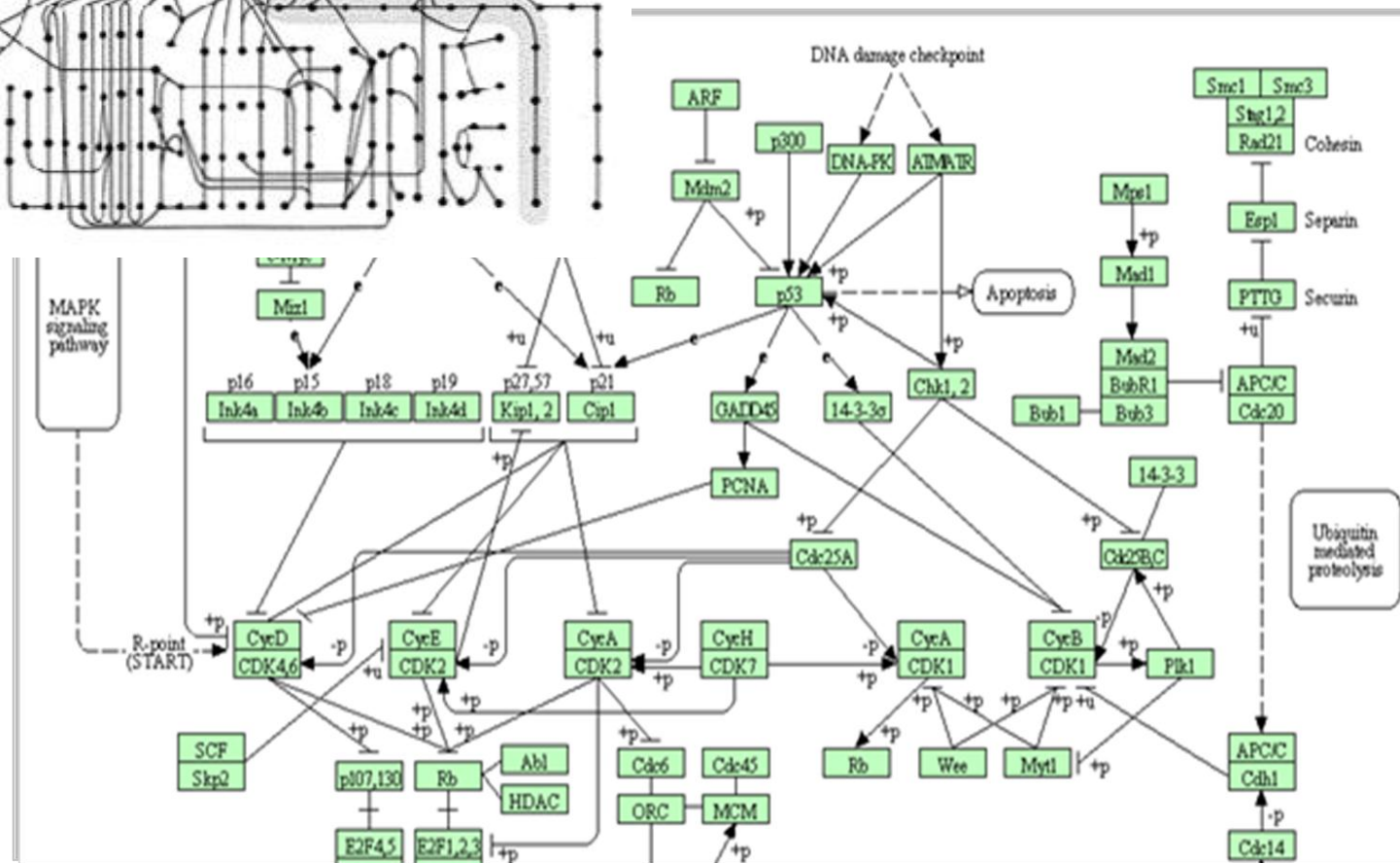
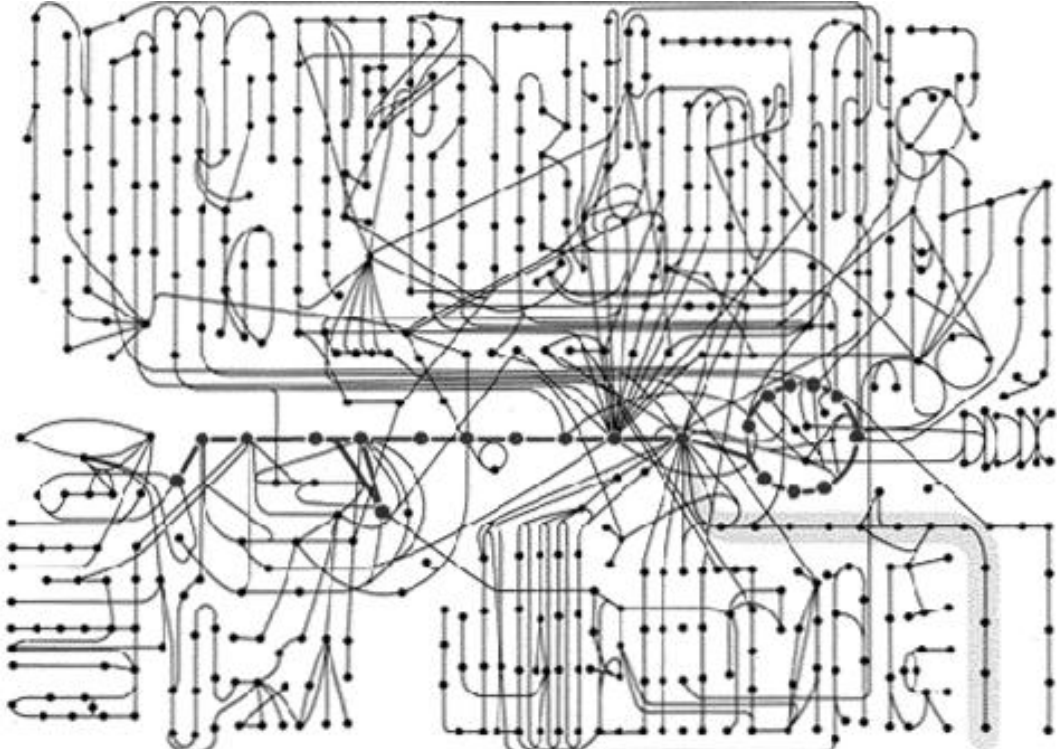
– In depth analysis of molecular interactions

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 - Compilation: 5 years, 20 persons to compile data
 - current databases miss 50% of published data:*
 - two new databases developed*
 - **Current computational approaches cannot provide an alternative to biocuration.**
 - There is a **‘silent flood of bioinformatics resources’**.
 - A new method of meta analysis
 - Integrating NGS & mass spec data
- In depth analysis of molecular interactions

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 - Making better use of microarray data
 - Current computational approaches cannot provide an alternative to biocuration.
 - ‘Silent flood of bioinformatics resources’
 - Integrating NGS & mass spec data
- **In depth analysis of molecular interactions**
 - **Transcriptional regulation**
 - **miRNAs and piRNAs**
 - **Protein-protein interactions**
 - **Pathway and process analyses**



- Can we make a better use of existing data to create a molecular portrait of tissue-specific functions?
 - **Cataloging the gene expression**
 - Making better use of microarray data
 - Compilation of data
 - New meta analysis
 - Current computational approaches cannot provide an alternative to biocuration.
 - ‘Silent flood of bioinformatics resources’
 - Integrating NGS & mass spec data
 - **In depth analysis of molecular interactions**
 - Known interactions of DNA, RNA and proteins

Can we make a better use of existing data to create a
molecular portrait of tissue-specific functions? **YES!**



Darshan SC



Akhilesh,
Sruvanthi
&
many others

Neelima Ch



THANK YOU!

GLORIAD

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