

de.NBI – German Network for Bioinformatics Infrastructure

# RNA Bioinformatics Center

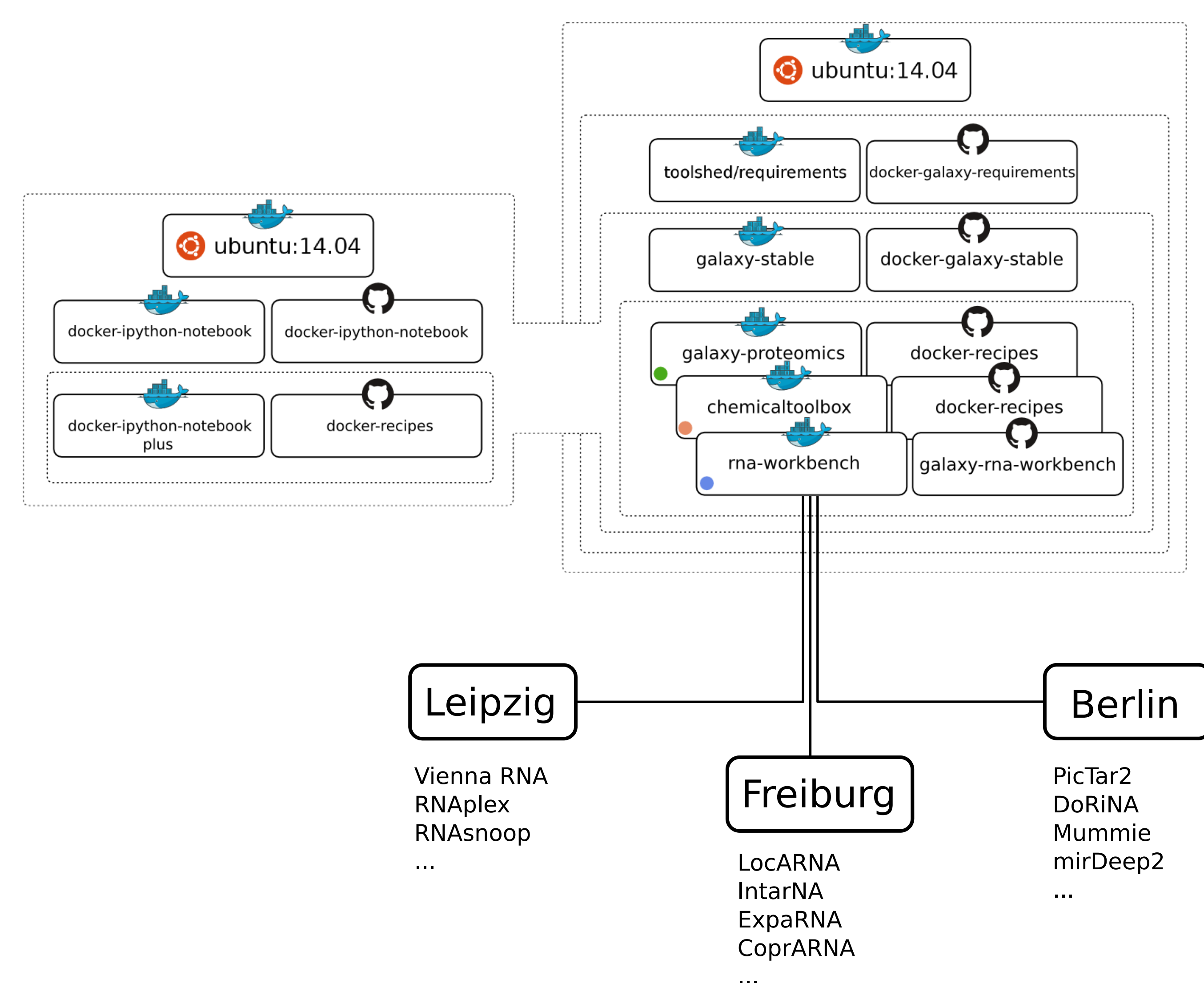
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## Background

Genome-wide sequencing revealed pervasive transcription, where the majority of the DNA encodes non-coding RNAs. Non-coding RNAs and RNA-protein interactions play a fundamental role in cellular regulation; consequently they have received increasing attention over the past decade. A series of recent discoveries (due to high-throughput genome-wide identification of miRNAs and RNA-protein interactions) have shown that the complexity of post-transcriptional gene regulation equals the one of transcriptional gene regulation. For example, the human genome encodes thousands of miRNAs and approximately 800 RNA binding proteins. Based on those insights, many human diseases could be linked to post-transcriptional gene regulation already.

## Docker, Galaxy, and RNA: Tool Integration and Deployment



## Mission

The RNA Bioinformatics Center (RBC) is going to cover all aspects of RNA bioinformatics in the upcoming German Centre of Bioinformatic Infrastructure (de.NBI), which aims at establishing a solid bioinformatics infrastructure in Germany. In more detail, the RBC will cover infrastructure and services for the study of RNA-protein interactions by the analysis of CLIP-seq data, detection of RNA motifs and miRNA binding sites; the study of Ribozymes and RNAs as decoys, involving the analysis of RNA-protein interactions, detection of non-coding RNAs, RNA structure prediction, and RNA conservation; and research on guide RNAs, comprising miRNA and ncRNA target prediction, and their detection. Accumulating knowledge in these diverse areas of RNA bioinformatics, the RBC consists of the major German RNA-bioinformatics groups. Its mission is to establish an integrated workbench for RNA analysis; the application of recent software tools will make the tools easily accessible, support their integration into bioinformatics workflows and facilitate their deployment. By providing an integrated RNA Bioinformatics infrastructure with high usability as well as training of users, the project will generally raise the awareness of the importance of the analysis of RNA-related regulation.

