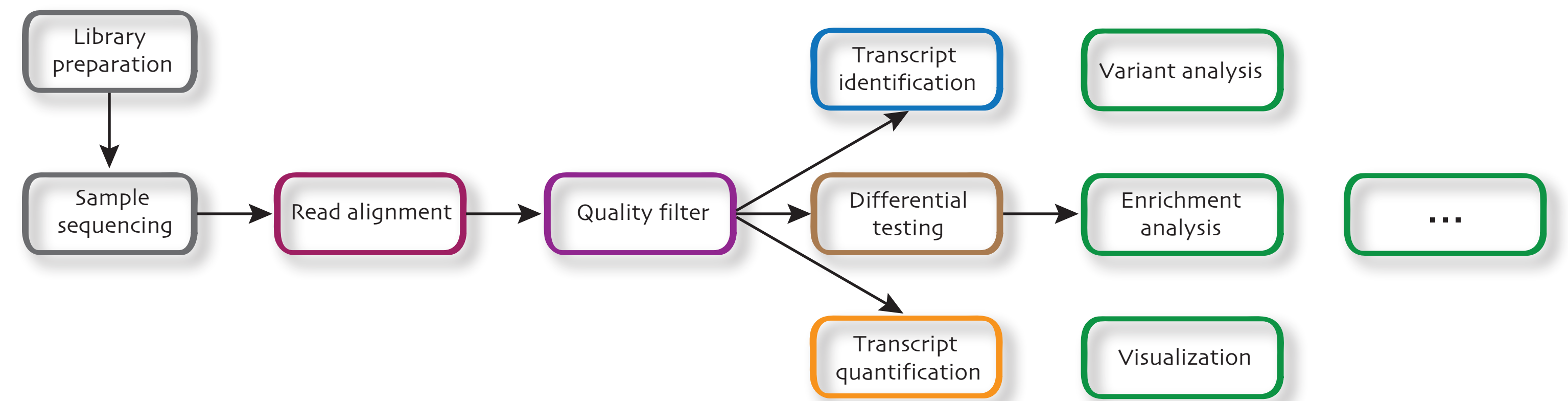
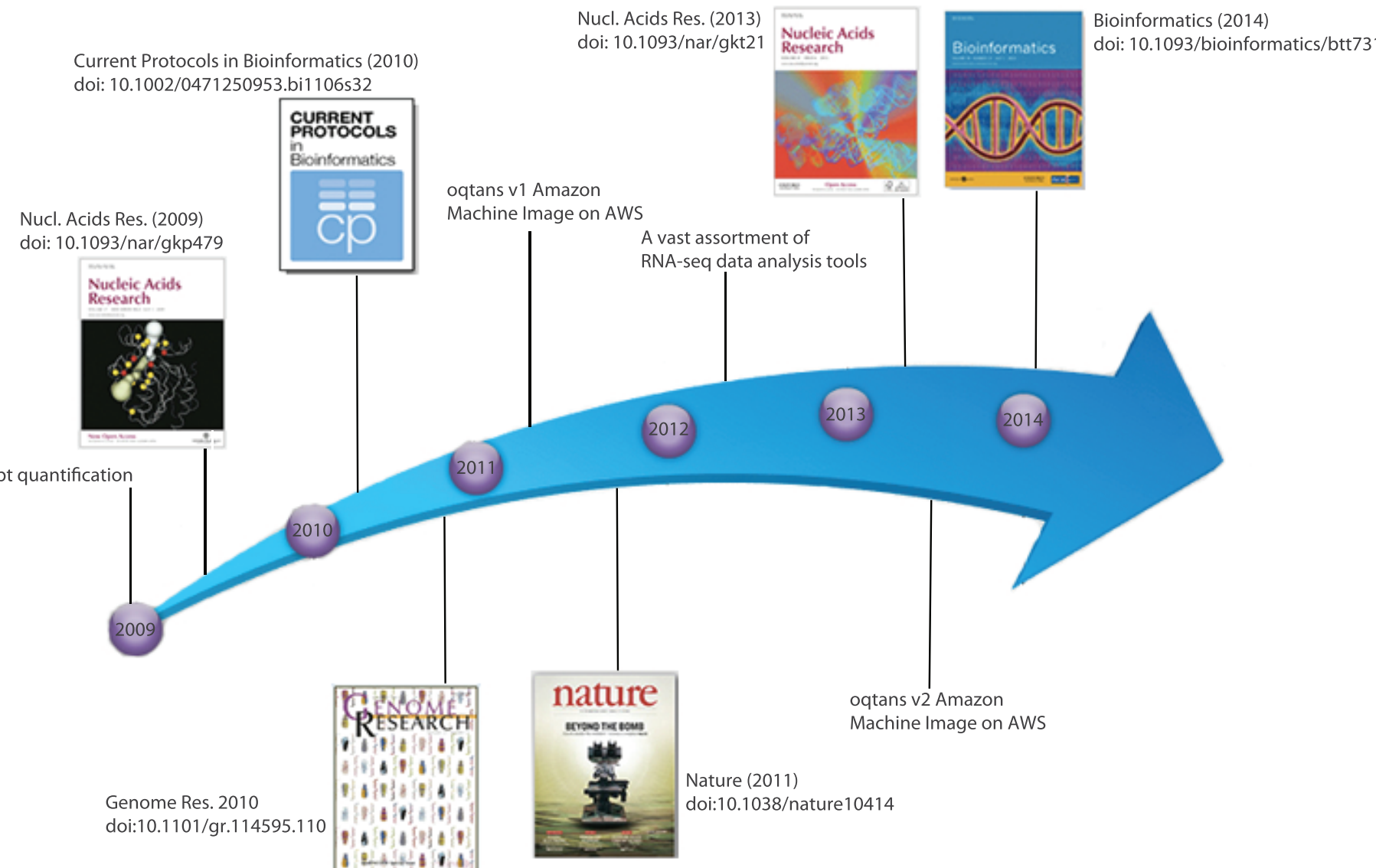


The current revolution in sequencing technologies enables a far more detailed picture of the transcriptome. We have developed the integrative online platform, **Oqtans**, for quantitatively analyzing RNA-Seq experiments. It is based on the Galaxy-framework and provides tools for read mapping, transcript reconstruction and quantitation, as well as differential expression analysis.

A fully automated infrastructure installs software, test datasets, and packages from simple configuration scripts.



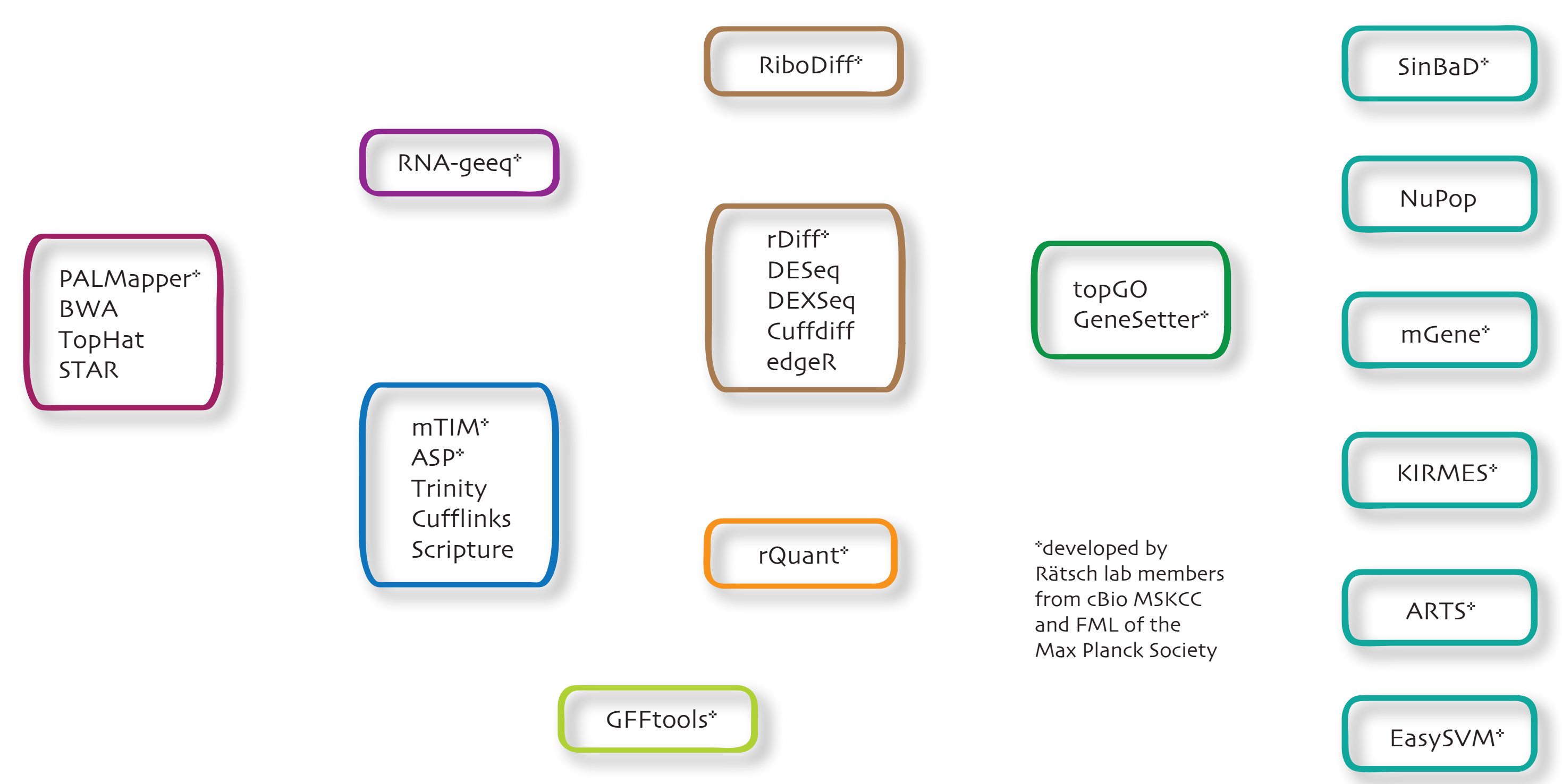
News, Updates



galaxy.cbio.mskcc.org

AWS Cloud: ami-65376a0c

github.com/ratschlab/oqtans



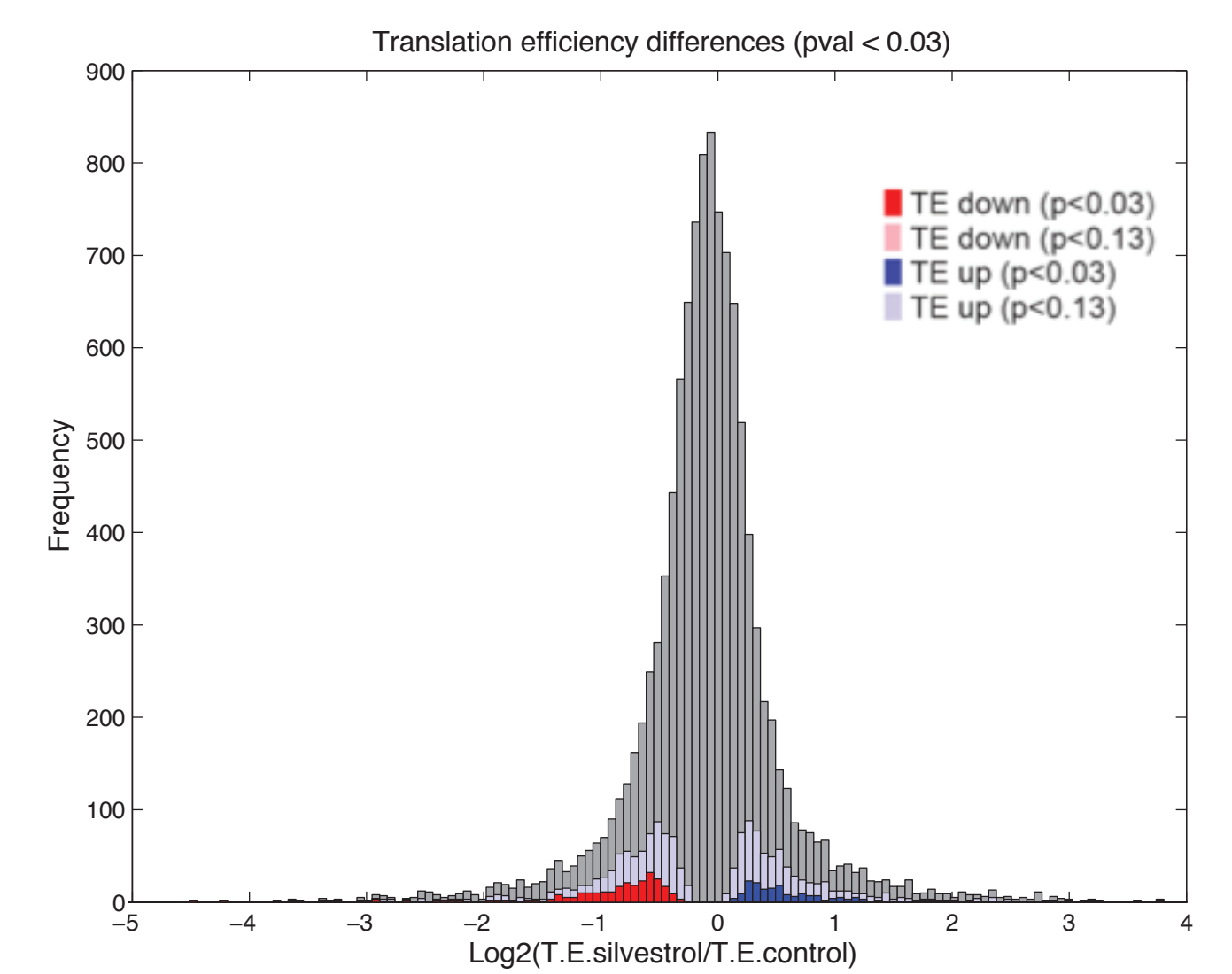
Detection of Protein Translation Efficiency Change based on Ribosome Footprinting

Identify the significant change in ribosomal activity taking mRNA abundance into account.

Method 1: Translational Efficiency

$$\text{Translation Efficiency (TE)} = \frac{RPKM_{Ribo}}{RPKM_{mRNA}}$$

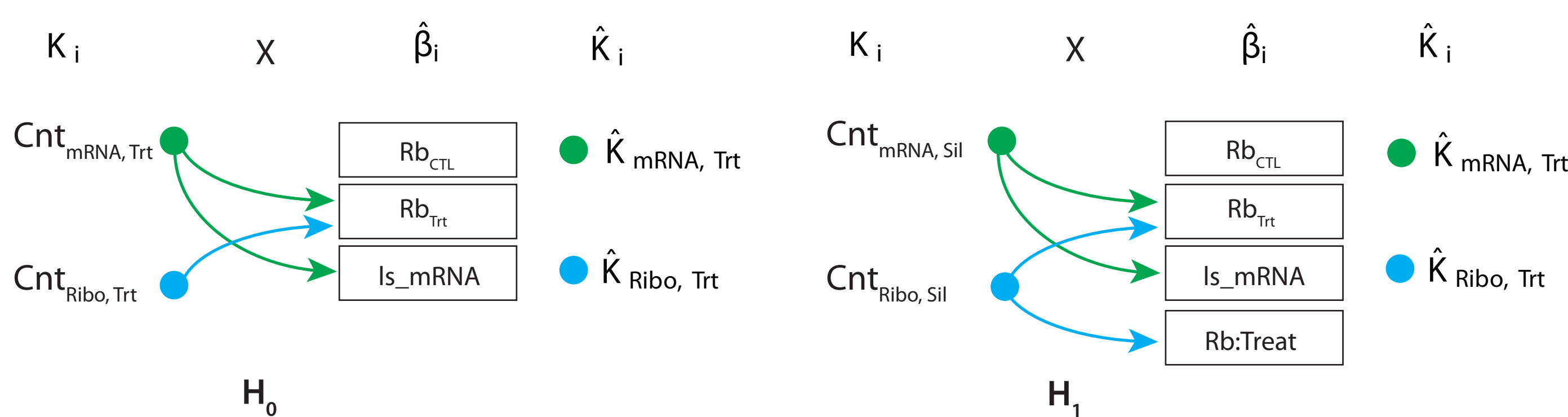
$$\Delta TE = \log \left(\frac{TE_{sil}}{TE_{con}} \right) = \log \left(\frac{RPKM_{Ribo|sil} / RPKM_{mRNA|sil}}{RPKM_{Ribo|con} / RPKM_{mRNA|con}} \right)$$



Method 2: Generalized Linear Model (GLM)

For each gene, read count $K_i \sim \text{Negative Binomial}(\mu, \alpha)$, $\mu = E(K) = \log(\eta)$

Linear predictor: $\eta = \beta \cdot X$, where X denotes state of system, α is chosen as a dispersion prior.



Likelihood ratio test or F-test to capture the significance.

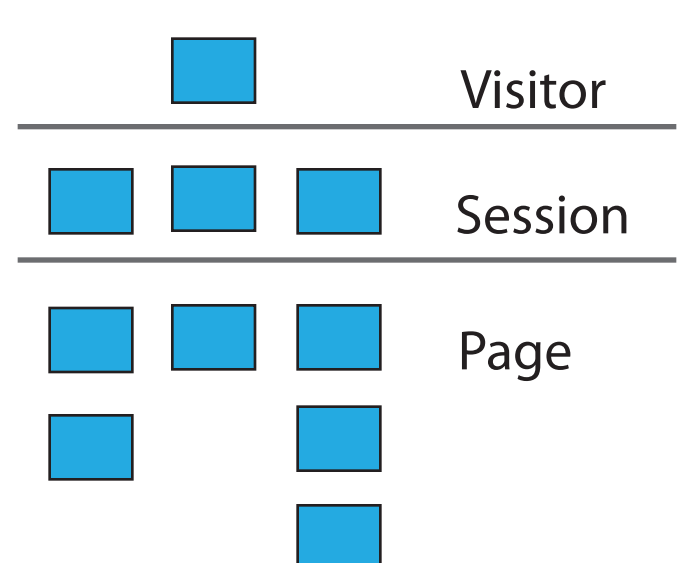
Utilize negative binomial distribution to approximate the read count statistics.

GLM takes both mRNA and Ribo footprint read counts into account.

GLM captures the significant interaction between treatment and footprint condition.

Rectification Measurements for Possible Web Security Threats

Session Management

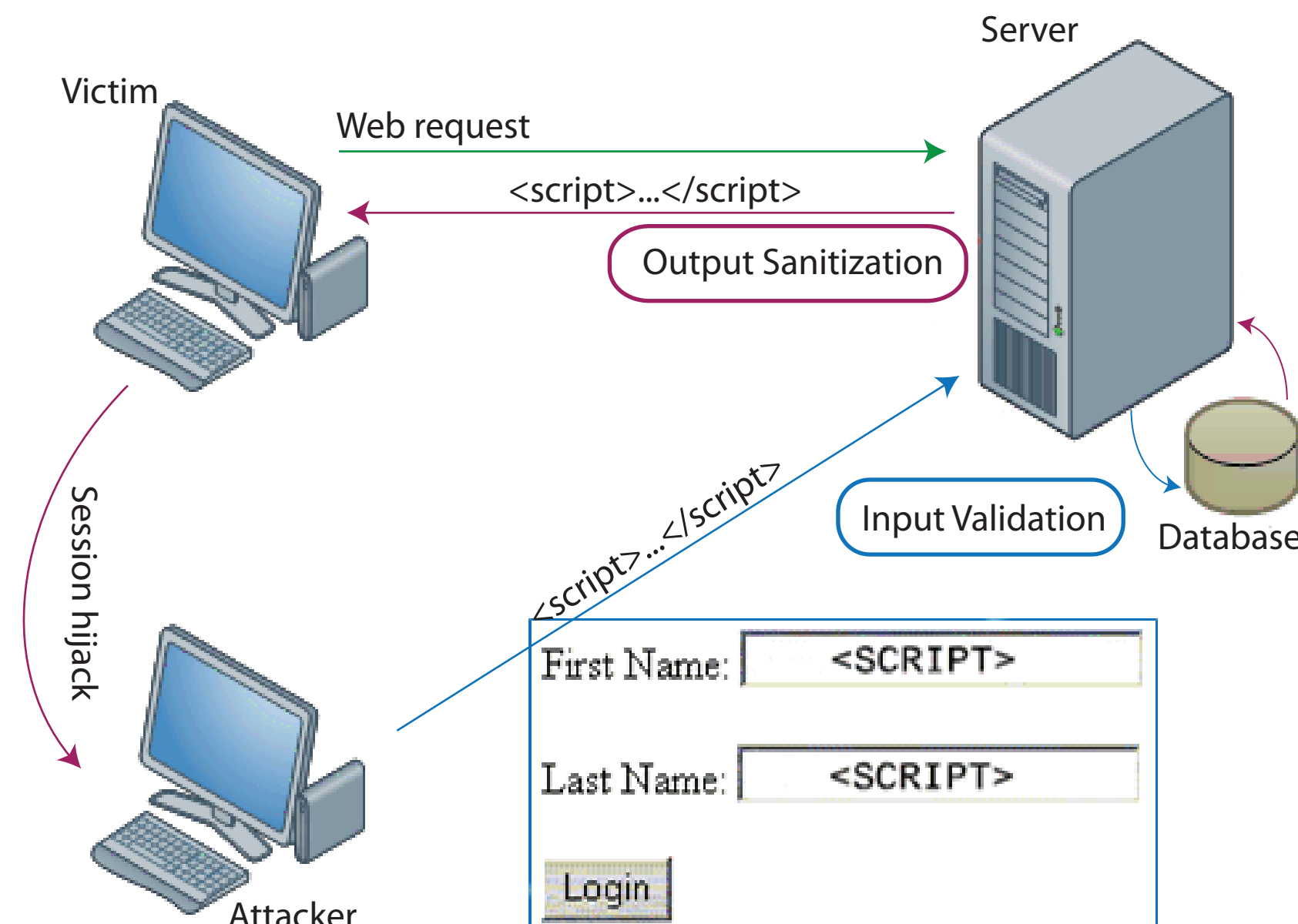


User authentication and subsequent session transmissions were not encrypted.

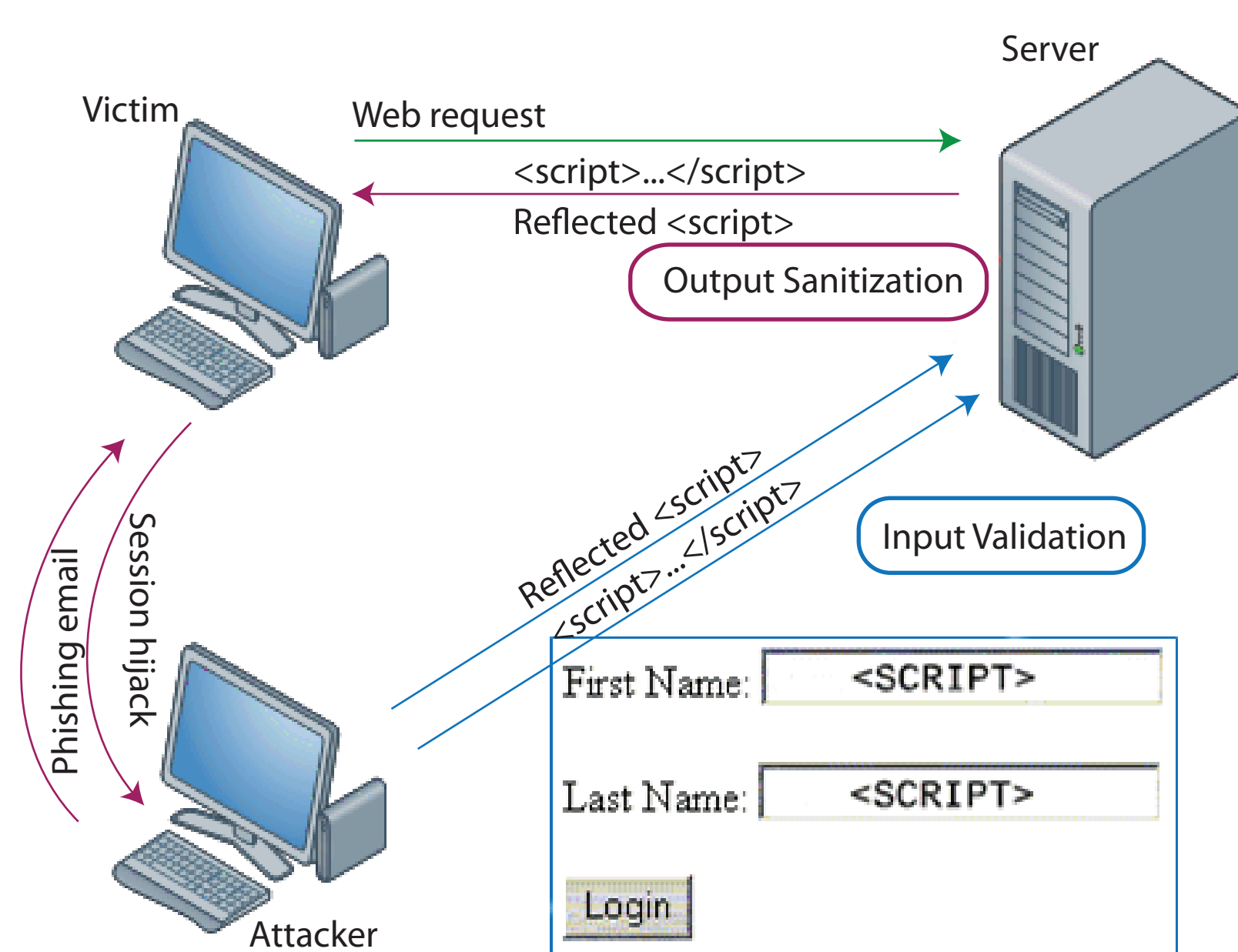
SSL encryption of all transmissions from the point of authentication.

Cross-Site Scripting (XSS)

a) Stored Cross-Site Scripting



b) Reflected Cross-Site Scripting



Minimizing the vulnerability of Stored and Reflected XSS involves validating the input data at the server-side using ModSecurity with customized rules.

Authentication



User passwords stored insecurely.

hash = salt + sha256(salt + password)

[1] Sreedharan V et. al., Oqtans: The RNA-seq Workbench in the Cloud for Complete and Reproducible Quantitative Transcriptome Analysis, Bioinformatics, 2014 doi: 10.1093/bioinformatics/btt731.

[2] Blankenberg, D. et al., Galaxy: a web-based genome analysis tool for experimentalists, Curr Protoc Mol Biol, 2010 doi: 10.1002/0471142727.mb1910s89.

[3] Wolfe, A., Singh, K., Zhong, Y. et al., RNA G-quadruplexes cause eIF4A-dependent oncogene translation in Cancer, Nature in press 2014, doi: 10.3038/nature13485.