

# *Bioconductor* serialization best practices

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# Scenarios

## Personal

- Check-pointing (e.g., for fast computation) or reproducibility

## Package

- Demonstration data, e.g., for vignettes & examples
- Package-specific resource, e.g., reference data
- Project-wide benefit, e.g., EnsDb

# Where

< 1 Mb

- Package-specific resource? in the package

1 - 100 Mb

- AnnotationHub or ExperimentHub

> 100 Mb

- Hmm, time to reconsider

# How?

## R formats

- 'Rda' files containing `data.frame`, `GRanges`, `SummarizedExperiment`, ...

## Pros

- Fast and easy to load

## Cons

- Only useful in *R*
- Complex (e.g., S4) objects: updated class definitions require methods to update the objects

## Community-standard formats

- `csv`, `bed`, `hdf5`, ...

## Pros

- Constant format, so consistent import
- Useful outside *R*

## Cons

- Cost of importing or constructing complex objects 'on the fly'

# Unserializing *R* objects

`readRDS()` (better than `data()` / `load()`)

- Reads the object into R
- (S4) attaches the necessary package(s)
- No automatic validation or updating

`updateObject()`

- Convention
- `BiocGenerics::updateObject` generic
- Object-specific methods defined by the developer, e.g.,  
`selectMethod("updateObject", "GRanges")`

# Best practices

Where?

- <1 Mb, useful in a single package or package hierarchy: package
- >1 Mb, or useful across packages: AnnotationHub or ExperimentHub

How?

- Community standard formats, unless ingestion into *R* is (time or space) expensive

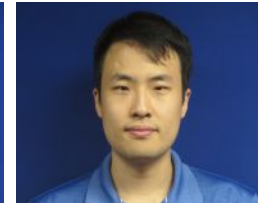
# Conclusions and acknowledgements

*Bioconductor* core team & close collaborators

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World-wide community of users & developers

[Technical](#) and [scientific](#) advisory boards



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