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

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