

# Package: exonr (via r-universe)

July 24, 2024

**Title** Scientific Data Processing

**Version** 0.9.0

**Description** This package provides a set of tools for processing scientific data. It's based on the exon Rust package.

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**Suggests** testthat (>= 3.0.0), duckdb (>= 0.8.0)

**Config/testthat/edition** 3

**Repository** <https://where>true.r-universe.dev>

**RemoteUrl** <https://github.com/where>true/exon>

**RemoteRef** HEAD

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## Contents

ExonDataFrame . . . . .	2
exonr . . . . .	3
ExonRSessionContext . . . . .	3
read_bed_file . . . . .	4
read_fasta_file . . . . .	4
read_fastq_file . . . . .	5
read_genbank_file . . . . .	5
read_gff_file . . . . .	6
read_inferred_exon_table . . . . .	6
read_inferred_exon_table_r . . . . .	6
read_mzml_file . . . . .	7
read_sam_file . . . . .	7
read_vcf_file . . . . .	8

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ExonDataFrame	<i>An ExonDataFrame is a data frame that is backed by an Exon engine.</i>
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## Description

An ExonDataFrame is a data frame that is backed by an Exon engine.

## Methods

### Public methods:

- [ExonDataFrame\\$new\(\)](#)
- [ExonDataFrame\\$to\\_arrow\(\)](#)
- [ExonDataFrame\\$to\\_record\\_batch\\_reader\(\)](#)
- [ExonDataFrame\\$clone\(\)](#)

**Method** `new()`: Initialize the ExonDataFrame object.

*Usage:*

```
ExonDataFrame$new(result)
```

*Arguments:*

`result` Dataframe that serves as the base for ExonDataFrame.

**Method** `to_arrow()`: Convert the ExonDataFrame to an Arrow table.

*Usage:*

```
ExonDataFrame$to_arrow()
```

*Returns:* An Arrow table.

**Method** `to_record_batch_reader()`: Convert the ExonDataFrame a stream of record batches.

*Usage:*

```
ExonDataFrame$to_record_batch_reader()
```

*Returns:* A stream of record batches.

**Method** `clone()`: The objects of this class are cloneable with this method.

*Usage:*

```
ExonDataFrame$clone(deep = FALSE)
```

*Arguments:*

`deep` Whether to make a deep clone.

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exonr	<i>ExonR</i>
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## Description

ExonR

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ExonRSessionContext	<i>An ExonRSessionContext is a context for an Exon session.</i>
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## Description

An ExonRSessionContext is a context for an Exon session.

## Methods

### Public methods:

- [ExonRSessionContext\\$new\(\)](#)
- [ExonRSessionContext\\$sql\(\)](#)
- [ExonRSessionContext\\$execute\(\)](#)
- [ExonRSessionContext\\$clone\(\)](#)

**Method** `new()`: Initialize the ExonRSessionContext object.

*Usage:*

```
ExonRSessionContext$new()
```

**Method** `sql()`: Execute an SQL query.

*Usage:*

```
ExonRSessionContext$sql(query)
```

*Arguments:*

`query` The SQL query to execute. Returns an ExonDataFrame.

**Method** `execute()`: Execute an SQL query.

*Usage:*

```
ExonRSessionContext$execute(query)
```

*Arguments:*

`query` The SQL query to execute. Runs eagerly.

**Method** `clone()`: The objects of this class are cloneable with this method.

*Usage:*

```
ExonRSessionContext$clone(deep = FALSE)
```

*Arguments:*

`deep` Whether to make a deep clone.

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read_bed_file	<i>Read BED File</i>
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**Description**

This function reads a BED file from a file and returns a RecordBatch stream.

**Usage**

```
read_bed_file(file_path)
```

**Arguments**

file\_path      The path to the BED file.

**Value**

A RecordBatch stream representing the contents of the BED table.

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read_fasta_file	<i>Read FASTA File</i>
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**Description**

This function reads a FASTA file from a file and returns a RecordBatch stream.

**Usage**

```
read_fasta_file(file_path)
```

**Arguments**

file\_path      The path to the FASTA file.

**Value**

A RecordBatch stream representing the contents of the FASTA table.

---

read_fastq_file	<i>Read FASTQ File</i>
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**Description**

This function reads a FASTQ file from a file and returns a RecordBatch stream.

**Usage**

```
read_fastq_file(file_path)
```

**Arguments**

file_path	The path to the FASTQ file.
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**Value**

A RecordBatch stream representing the contents of the FASTQ table.

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read_genbank_file	<i>Read GenBank File</i>
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**Description**

This function reads a GenBank file from a file and returns a RecordBatch stream.

**Usage**

```
read_genbank_file(file_path)
```

**Arguments**

file_path	The path to the GenBank file.
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**Value**

A RecordBatch stream representing the contents of the GenBank table.

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read_gff_file	<i>Read GFF File</i>
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**Description**

This function reads a GFF file from a file and returns a RecordBatch stream.

**Usage**

```
read_gff_file(file_path)
```

**Arguments**

file_path	The path to the GFF file.
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**Value**

A RecordBatch stream representing the contents of the GFF table.

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read_inferred_exon_table	<i>Copy the inferred exon table from the given path into the given stream.</i>
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**Description**

Copy the inferred exon table from the given path into the given stream.

**Usage**

```
read_inferred_exon_table(file_path, stream_ptr)
```

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read_inferred_exon_table_r	<i>Copy the inferred exon table from the given path into the given stream.</i>
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**Description**

Copy the inferred exon table from the given path into the given stream.

**Usage**

```
read_inferred_exon_table_r(file_path, pointer_addr)
```

**Arguments**

file_path	The path to the inferred exon table.
stream_ptr	The pointer to the stream to copy the inferred exon table

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read_mzml_file	<i>Read MzML File</i>
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**Description**

This function reads a MzML file from a file and returns a RecordBatch stream.

**Usage**

```
read_mzml_file(file_path)
```

**Arguments**

file\_path      The path to the MzML file.

**Value**

A RecordBatch stream representing the contents of the MzML file.

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read_sam_file	<i>Read SAM/BAM File</i>
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**Description**

This function reads a SAM file from a file and returns a RecordBatch stream. It will also read BAM files.

**Usage**

```
read_sam_file(file_path)
```

**Arguments**

file\_path      The path to the SAM/BAM file.

**Value**

A RecordBatch stream representing the contents of the SAM/BAM file.

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read_vcf_file	<i>Read VCF/BCF File</i>
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**Description**

This function reads a VCF/BCF file from a file and returns a RecordBatch stream.

**Usage**

```
read_vcf_file(file_path)
```

**Arguments**

file\_path      The path to the VCF/BCF file.

**Value**

A RecordBatch stream representing the contents of the VCF/BCF file.



# Index

ExonDataFrame, [2](#)  
exonr, [3](#)  
ExonRSessionContext, [3](#)

read\_bed\_file, [4](#)  
read\_fasta\_file, [4](#)  
read\_fastq\_file, [5](#)  
read\_genbank\_file, [5](#)  
read\_gff\_file, [6](#)  
read\_inferred\_exon\_table, [6](#)  
read\_inferred\_exon\_table\_r, [6](#)  
read\_mzml\_file, [7](#)  
read\_sam\_file, [7](#)  
read\_vcf\_file, [8](#)