



Comparing Analysis Method Implementations in Software (CAMIS)

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Motivation

- SAP states:
 - *Using a log-rank test determine to association between survival time and atrial fibrillation. Additionally, calculate Kaplan-Meier estimate of survival time and use Cox proportional hazard model to get the hazard ration and 95% confidence interval*

Summary of Survival Data			
Analysis set: [Analysis set]	[Study Treatment 1]	[Study Treatment 2]	
	###	###	
Event – n (%)	### (<u>xx.x</u> %)	### (<u>xx.x</u> %)	
Censored – n (%)	### (<u>xx.x</u> %)	### (<u>xx.x</u> %)	
Time to event ([months])			
25th percentile (95% CI)	<u>x.xx</u> (<u>xx.x</u> , <u>xx.x</u>)	<u>x.xx</u> (<u>xx.x</u> , <u>xx.x</u>)	
Median (95% CI)	<u>xx.xx</u> (<u>xx.xx</u> , <u>xx.xx</u>)	<u>xx.xx</u> (<u>xx.xx</u> , <u>xx.xx</u>)	
75th percentile (95% CI)	<u>xx.xx</u> (<u>xx.xx</u> , NE)	<u>xx.xx</u> (<u>xx.xx</u> , NE)	
Min, Max	<u>(xx.xx, xx.xx+)</u>	<u>(xx.xx, xx.xx)</u>	
	KM estimators		
Landmark estimates			
[12]-[month] event-free rate (95% CI)	<u>x.xxx</u> (<u>x.xxx</u> , <u>x.xxx</u>)	<u>x.xxx</u> (<u>x.xxx</u> , <u>x.xxx</u>)	
[24]-[month] event-free rate (95% CI)	<u>x.xxx</u> (<u>x.xxx</u> , <u>x.xxx</u>)	<u>x.xxx</u> (<u>x.xxx</u> , <u>x.xxx</u>)	
[36]-[month] event-free rate (95% CI)	<u>x.xxx</u> (<u>x.xxx</u> , <u>x.xxx</u>)	<u>x.xxx</u> (<u>x.xxx</u> , <u>x.xxx</u>)	
p-value ^a	Log-rank test	< 0.xxxx	
Hazard ratio (95% CI) ^b	Cox PH model	<u>x.xxx</u> (<u>x.xxx</u> , <u>x.xxx</u>)	
Key: + = censored observation, NE = not estimable, CI = confidence interval			
^a p-value is from a [stratified/non-stratified] log-rank test.			
^b Hazard ratio and 95% CI from a [stratified/non-stratified] Cox proportional hazards model.			

Motivation - results

```
fit.km <- survfit(Surv(LENFOLY, FSTAT) ~ AFB, data = dat)

## quantile estimates
quantile(fit.km, probs = c(0.25, 0.5, 0.75))
```



\$quantile

	25	50	75
AFB=1	0.26	2.37	6.43
AFB=0	0.94	5.91	6.44



\$lower

	25	50	75
AFB=1	0.05	1.27	4.24
AFB=0	0.55	4.32	6.44



\$upper

	25	50	75
AFB=1	1.11	4.24	NA
AFB=0	1.47	NA	NA

Motivation - results

```
survminer::surv_pvalue(fit.km, data = dat)
```



	variable	pval	method	pval.txt
1	AFB	0.0009646027	Log-rank	p = 0.00096

Motivation - results

```
fit.cox <- coxph(Surv(LENFOLY, FSTAT) ~ AFB, data = dat)
fit.cox %>%
  tidy(exponentiate = TRUE, conf.int = TRUE, conf.level = 0.95) %>%
  select(term, estimate, conf.low, conf.high)
```

```
# A tibble: 1 × 4
  term estimate conf.low conf.high
<chr>    <dbl>    <dbl>    <dbl>
1 AFB0     0.583     0.421     0.806
```



Motivation - Search

SAS/STAT User's Guide

The LIFETEST Procedure

Overview Getting Started Syntax ▾ Details ▾ Examples ▾ References Videos

Overview: LIFETEST Procedure

A common feature of lifetime or survival data is the presence of right-censored observations due either to withdrawal of experimental units or to the end of the experiment. For such observations, you know only that the lifetime exceeded a given value; the exact lifetime remains unknown. Such data cannot be analyzed by ignoring the censored observations because, among other considerations, the longer-lived units are generally more likely to be censored. The analysis methodology must correctly use the censored observations in addition to the uncensored observations.

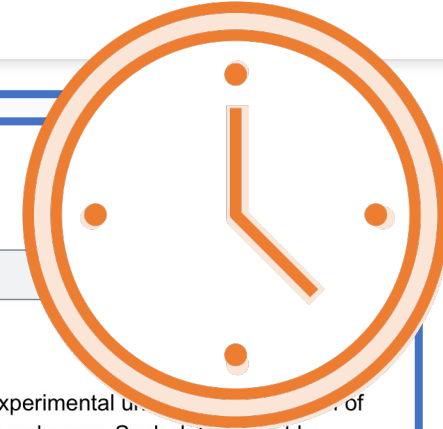
Texts that discuss the survival analysis methodology include Collett (1994), Cox and Oakes (1984); Kalbfleisch and Prentice (1980); Klein and Moeschberger (1997); Lawless (1982); Lee (1992). Users interested in the theory should consult Fleming and Harrington (1991); Andersen et al. (1992).

Usually, a first step in the analysis of survival data is the estimation of the distribution of the survival times. Survival times are often called *failure* times, and *event* times are uncensored survival times. The survival distribution function (SDF), also known as the survivor function, is used to describe the lifetimes of the population of interest. The SDF evaluated at t is the probability that an experimental unit from the population will have a lifetime that exceeds t —that is,

$$S(t) = \Pr(T > t)$$

where $S(t)$ denotes the survivor function and T is the lifetime of a randomly selected experimental unit. The LIFETEST procedure can be used to compute nonparametric estimates of the survivor function either by the product-limit method (also called the Kaplan-Meier method) or by the life-table method (also called the actuarial method). The life-table estimator is a grouped-data analog of the Kaplan-Meier estimator. The procedure can also compute the Breslow estimator or the Fleming-Harrington estimator, which are asymptotic equivalent alternatives to the Kaplan-Meier estimator.

Some functions closely related to the SDF are the cumulative distribution function (CDF), the probability density function (PDF), and the hazard function. The CDF, denoted $F(t)$, is defined as $1 - S(t)$ and is the probability that a lifetime does not exceed t . The PDF, denoted $f(t)$, is defined as the derivative of $F(t)$,



assumed to be open on the left and closed on the right. (start = end = 1. For counting

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Methods

R SAS Comparison

Survival Models

Kaplan-Meier Log-rank test and Cox-PH

[R](#) [SAS](#) [R vs SAS](#)

Accelerated Failure Time

Non-proportional hazards methods

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Reasons

The reasons for the differences are because the default methods for handling ties in Cox model and confidence interval calculation in KM estimators in the two languages are different.

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- R: change to “breslow”

```
fit.cox <- coxph(Surv(LENFOLY, FSTAT) ~ AFB, ties = "breslow", data = dat)
```

- R: change to “log-log”

```
fit.km <- survfit(Surv(LENFOLY, FSTAT) ~ AFB, conf.type = "log-log", data = dat)
```

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- R: change to “breslow”

```
fit.cox <- coxph(Surv(LENFOLY, FSTAT) ~ AFB, ties = "breslow", data = dat)
```



- R: change to “log-log”

```
fit.km <- survfit(Surv(LENFOLY, FSTAT) ~ AFB, conf.type = "log-log", data = dat)
```



Welcome to the CAMIS repository !



- CAMIS: Comparing Analysis Method Implementations in Software
- A PHUSE DVOST working group project
- A cross-industry collaboration formed of members statistical and programming associations such as PHUSE, PSI, IASCT and ASA.
- Aims:
 - To create a white paper
 - To create a github repository to store how to apply statistical methods in various software and document any differences observed in the results obtained



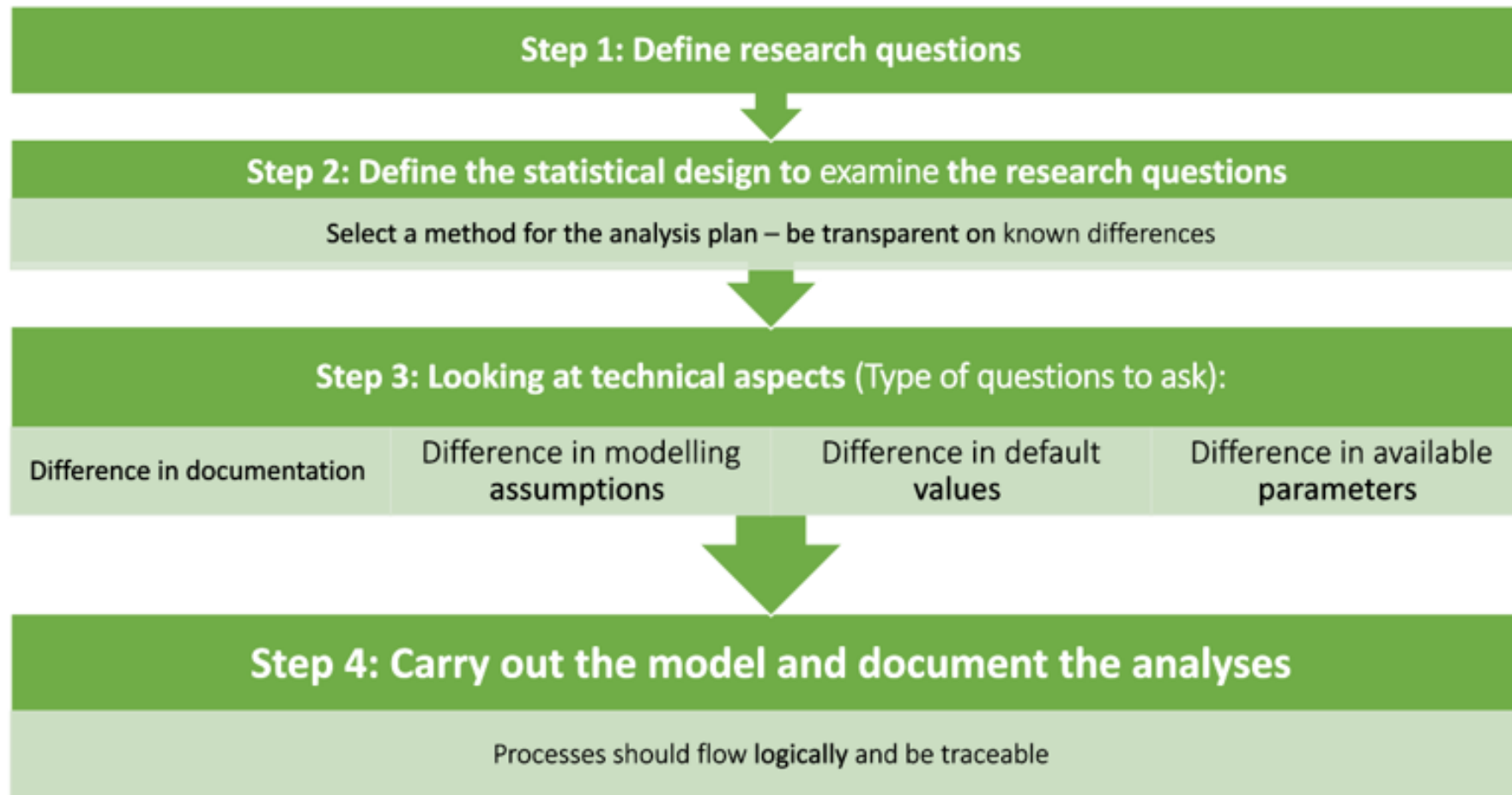
White Paper



Key Considerations When Understanding Differences in Statistical Methodology Implementations Across Programming Languages – An Introduction to the CAMIS Project

**Min-Hua Jen, Brian Varney, Kyle Lee, Benjamin Arancibia, Mia Qi, Lyn Taylor,
Christina Fillmore, Joseph Rickert, Mike Stackhouse, Michael Rimler**

White Paper



PSIAIMS / CAMIS

Q

Type ↵ to search

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⌂

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📧

<> Code

⌚ Issues 49

🔗 Pull requests 5

💬 Discussions

🎬 Actions

📁 Projects

📖 Wiki

🛡 Security

📈 Insights

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🍴 Fork 7 ▾

★ Starred 11 ▾

🔗 main ▾

🔗 14 branches

🏷 0 tags

Go to file

Add file ▾

<> Code ▾

 DrLynTaylor Merge pull request #114 from PSIAIMS/molmac-patch-1 ...

✓ 1b8e587 2 weeks ago ⌚ 306 commits

📁 .github/workflows	back to previous action	last month
📁 Comp	Merge pull request #101 from PSIAIMS/mcnemar_mol	2 months ago
📁 R	modify data call for renv status	last month
📁 SAS	Merge pull request #101 from PSIAIMS/mcnemar_mol	2 months ago
📁 data-info	Update lock file 🔒	9 months ago
📁 data	Update stat_method_tbl.csv	2 months ago
📁 images	Merge pull request #101 from PSIAIMS/mcnemar_mol	2 months ago
📁 minutes	Update CAMIS team members.csv	2 weeks ago
📁 non_website_content	added PHUSE SDE 2023 Mississauga conference presentation	2 months ago
📁 renv	Update on renv	last month
📁 templates	Add contribution information	9 months ago
📄 .DS_Store	abc	5 months ago
📄 .Rprofile	Update with renv	9 months ago
📄 .gitignore	Adding site to ignore	9 months ago

About ⚙

🔗 psiaims.github.io/CAMIS/

📖 Readme

📈 Activity

★ 11 stars

👁 3 watching

🍴 7 forks

Report repository

Releases

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Contributors 12





















Website - How to Use it



How

× Cancel

3 matching documents

Deriving Quantiles or Percentiles in R
Percentiles can be calculated in R using the quantile function. The function has the argument type which allows for nine different percentile definitions to be used. The default is type = 7, which uses a piecewise-linear estimate of the cumulative...

Deriving Quantiles or Percentiles in SAS
Percentiles can be calculated in SAS using the UNIVARIATE procedure. The procedure has the option PCTLDEF which allows for five different percentile definitions to be used. The default is PCTLDEF=5, which uses the empirical distribution function to fi...

Deriving Quantiles or Percentiles in R vs SAS
quantiles in SAS, R, and Python Sample quantiles: A comparison of 9 definitions Hyndman, R. J., & Fan, Y. (1996). Sample quantiles in statistical packages. The American Statistician, 50(4), 361-365.



Call for Action – How you can help?

Documenting how to perform statistical methods in R, SAS or comparing them

Adding to the repository differences between R & SAS that know about

Adding content for Python, Julia or other software

Review/ revision of existing CAMIS content.

You can be a contributor or
JOIN US
on the PHUSE working
group



Website - How to Contribute



Search: Type / to search

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Edit Pins Watch 4 Fork 8 Starred 20

Fork your own copy of PSIAIMS/CAMIS

Go to file Add file >> Code About

psiaims.github.io/CAMIS/

Readme Activity 20 stars 4 watching 8 forks Report repository

Releases

1 ...	✓ 2f025a1 20 hours ago	🕒 311 commits
us action		last month
quest #101 from PSIAIMS/mcnemar_mol		2 months ago
all for renv status		last month
quest #101 from PSIAIMS/mcnemar_mol		2 months ago
le 🔒		9 months ago
nethod_tbl.csv		2 months ago

Website - How to Contribute

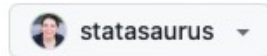


Create a new fork

A *fork* is a copy of a repository. Forking a repository allows you to freely experiment with changes without affecting the original project. [View existing forks.](#)

Required fields are marked with an asterisk ().*

Owner *



Repository name *

/ CAMIS

✓ CAMIS is available.

By default, forks are named the same as their upstream repository. You can customize the name to distinguish it further.

Description (optional)

☒ Copy the **main** branch only

Contribute back to PSIAIMS/CAMIS by adding your own branch. [Learn more.](#)

You are creating a fork in your personal account.

Create fork

stataaurus / CAMIS

Q Type / to search

>_

<> Code

Pull requests

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forked from [PSIAIMS/CAMIS](#)

Pin

Watch 0

Fork 9

Star

main

1 branch

0 tags

Go to file

Add file

<> Code

This branch is up to date with PSIAIMS/CAMIS:main.

Contribute

Sync fork

stataaurus Merge pull request [PSIAIMS#115](#) from PSIAIMS/LT1

...

2f025a1 20 hours ago

311 commits

.github/workflows	back to previous action	last month
Comp	Merge pull request PSIAIMS#101 from PSIAIMS/mcnemar_mol	2 months ago
R	modify data call for renv status	last month
SAS	Merge pull request PSIAIMS#101 from PSIAIMS/mcnemar_mol	2 months ago
data-info	Update lock file	9 months ago
data	Update stat_method_tbl.csv	2 months ago
images	Merge pull request PSIAIMS#101 from PSIAIMS/mcnemar_mol	2 months ago
minutes	Merge pull request PSIAIMS#115 from PSIAIMS/LT1	20 hours ago
non_website_content	added PHUSE SDE 2023 Mississauga conference presentation	2 months ago

About

[psiaims.github.io/CAMIS/](#)

Readme

Activity

0 stars

0 watching

9 forks

Releases

No releases published

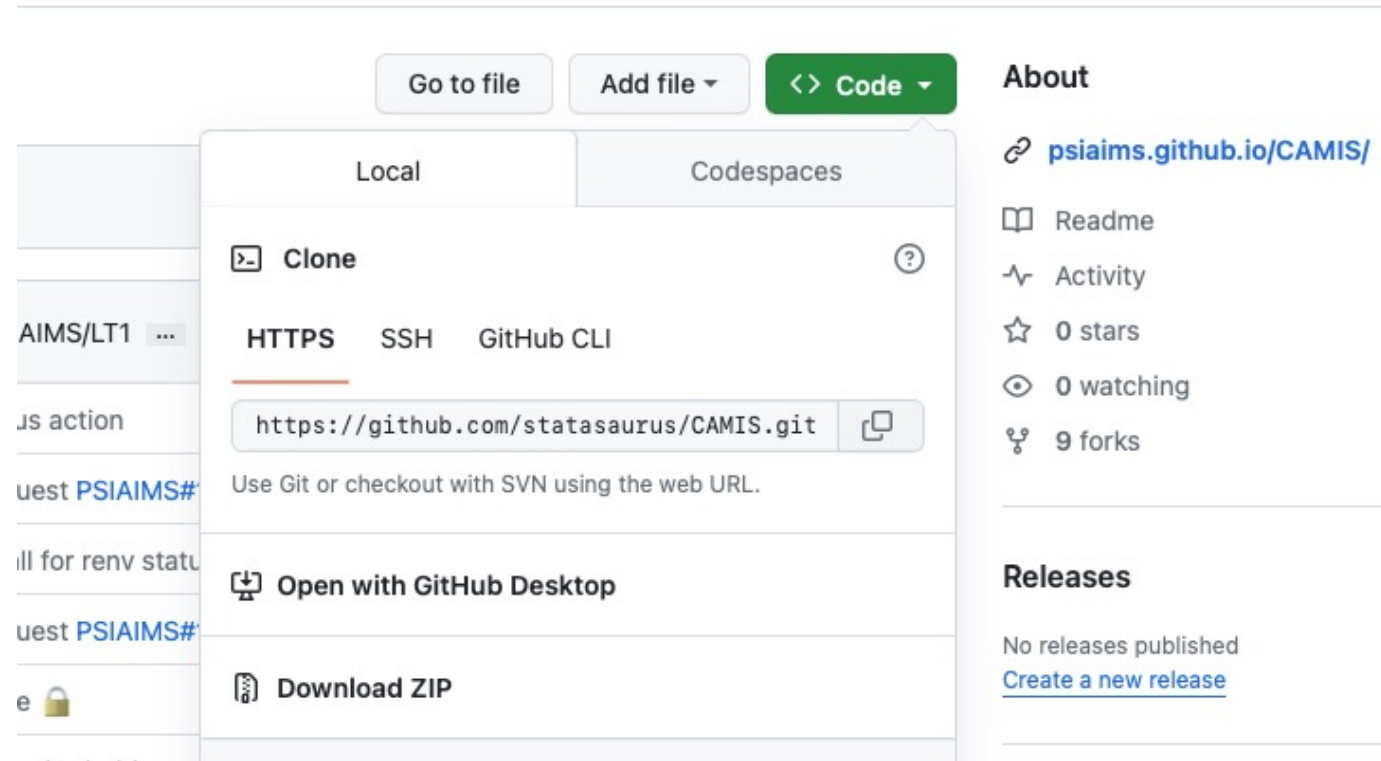
[Create a new release](#)

Packages

No packages published

[Publish your first package](#)

Website - How to Contribute



Website - How to Contribute



New Project Wizard

Back Clone Git Repository



Repository URL:

Project directory name:

Create project as subdirectory of:
 Browse...

☐ Open in new session

Create Project Cancel

Website - How to Contribute



Add in chi-sq comp #120

Edit <> Code

Open statasaurus wants to merge 1 commit into PSIAIMS:main from statasaurus:main

Conversation 0

Commits 1

Checks 0

Files changed 1

+51 -0



statasaurus commented now

Member ...

No description provided.



Add in chi-sq comp

50d5d2f



statasaurus requested a review from DrLynTaylor now

Reviewers



DrLynTaylor

At least 1 approving review is required to merge this pull request.

Still in progress? [Convert to draft](#)

Assignees

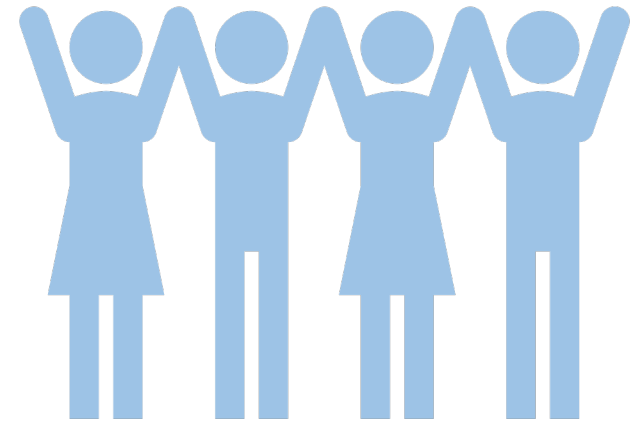
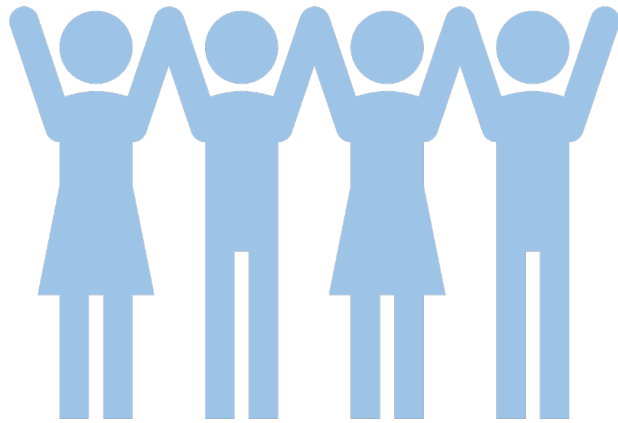


No one—[assign yourself](#)

Summary



- CAMIS is here to help
 - ... but, we need your help too



Thank you

