

2016.04 What's New



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## Overview

Red Cedar Technology provides powerful tools for quickly and easily exploring product design options to find the best possible design to meet your needs. HEEDS 2016.04 is packed with great enhancements that continue to streamline design exploration through improved results processing and automated analysis tools.



In this document, you will find information on new capabilities and workflows along with enhancements to existing features. These are separated into the following key areas:

- Process Automation
- Results Processing
- Portals

Any known issues are documented at the end of these notes.

For more detail on utilizing specific capabilities, please refer to the online help.

## **Process Automation**

### Analysis loops

### **DESCRIPTION:**

Loops provide the ability to perform a series of iterations for one or more analysis blocks in a process. A loop can iterate using a continuous, discrete or parameter based values. Loops can generate an array of results for each iteration or select a specific step to be sued for output

#### **BENEFIT:**

Allows easy incorporation of multiple load conditions. Create response curves for results over a range of values (e.g. lift curves, RPM curves, etc).

Ability to iterate mesh detail until a certain goal is reached for each iteration.

Test multiple concepts or configurations per iteration.

### Reuse surrogates

### **DESCRIPTION:**

The Study tab now provides the option to "Create surrogate-based study..." under the Create Study pulldown. This feature creates a new process, responses, and study that mimic the original process, responses, and study except that selected analyses and responses are represented by surrogates.

### **BENEFIT:**

Streamlines the use of surrogates in a study. Using surrogates can make study execution much faster and allow for sensitivity/robustness assessment evaluation in less time.

+ Create Surroga	ate-Based Study	? <mark>x</mark>			
Select analyses to replace with surrogates Select the study and choose how to handle each analyses.					
Study name: Copy data from:	Study_1_Surrogate  Study_1 Ses to replace with surrogat				
Select the analyses to replace with surrogates. Analysis In New Study					
	🖶 Analysis_1	Replace with surrogate 🔻			
	🖶 Analysis_2	Replace with surrogate 🔻			
	🖶 Analysis_3	Replace with surrogate 💌			
	< < Previous Next >>	Finish Cancel			

SW

## Variable hierarchy control

### **DESCRIPTION:**

Variables and responses can now be defined for use internally for a specific analysis or at the global level. The user can filter variables and responses to show specific analysis sets as well as for specific studies.

### **BENEFIT:**

Projects with large numbers of parameters can be difficult to work with. This capability allows the user to provide a scope and organization to the project parameters. With the added organization, the user can more easily focus on the subset of parameters they are working with at any given time.



## Analysis templates

<b>DESCRIPTION:</b>	Add input file
Any analysis can now be saved to a template using the "Save as template" contextual menu.	Cross_
<b>BENEFIT:</b> This avoids the need to repeat re-entering analysis settings across processes or projects.	Copy Analysis Save as template Save as template View tags Delete Del Rename F2 Fabled

8 23

✓ Weight▼

### **Response source definition**

### **DESCRIPTION:**

An extension of the analysis-specific variable support, is the ability to specify the analysis source for a response in the Properties Area.

### **BENEFIT:**

This allows greater response control especially for formula calculations in multiple analysis studies.



C:/Users/ianh/Documents/Red Cedar Technologies/Releases/2016.04/curve\_sample.csv

Pitch 15

191.3804371 1383.685691 **1465.858012** -10902.59.

436.8114454 1940.103404 3251.640754 -14954.72...

522.536613 1877.910248 **3904.797407** -14223.8865

606.5526347 1865.573517 4489.175567 -13740.49...

145.1845475 1151.460032 **1131.546717** -9146.644... -2637.019...

244.9648147 1573.660473 1869.898411 -12413.43...-3485.852...1 304.5813324 1740.445371 2310.057744 -13661.61

369.5101475 1871.143677 2778.192524 -14588.40... -4068.156... 2

696.5265563 1812.72793 5123.444555 -13223.60... -4135.999...1

5803.342158

914.4847304 1715.404096 6548.34091 -12087.20... -4220.091

E 🔻 F

Yaw 15

-3008 062

-3814.51842 1

-4198.840

-4127.458... 2

-4133.553. 1

OK Cancel

Roll 15

Import Preview

Angle of

1 0

2 2.5

6 12.5 7 15

8 17.5

9 20

10 22.5

11 25

Map the imported data columns to the table.

Drag 15

Х 🕶 В 🕶 С 🕶 Ү 🕶

802.5674184 1738.369078

Lift 15

## Curve import mapping

## **DESCRIPTION:**

When importing a file into a Curve, Discrete Set, or User Design Set, or when using the new "Paste special..." context menu item, the user is prompted to map the columns of the imported data to the columns of the target table.

### **BENEFIT:**

Provides more flexibility when importing data into MDO.

## Curve fitting

### **DESCRIPTION:**

A new column has been added to curve properties to optionally define a weight value for each curve point (shown as the green line on the plot). The weight factor affects the influence of each portion of the curve when used in a curve fit response and can be used to normalize the curve data.

The curve fit response has a new "Normalize difference" option that enables users to designate the curve data used for RMS error calculation. The sample curve shows the RMS formula.

### **BENEFIT:**

A higher importance can be given to fit key portions of a data curve.

Greater normalization flexibility.



### Copy analysis

### **DESCRIPTION:**

When copying an analysis, the user can now specify any process for the target.

### **BENEFIT:**

Streamlines the work for reusing existing analysis settings in a new process.

<ul> <li>✓ Process Automation</li> <li>✓ Flap1</li> <li>✓ SolidWorks_2</li> <li>✓ Wind Tunnel</li> </ul>	the Copy Analysis
► Controls ▲ ➡ Flap2 ▲ Analysis_3	New analysis name: SolidWorks_4
<ul> <li>▲ □ Parameters</li> <li>▷ □ Variables</li> <li>▷ □ Responses</li> </ul>	► Flap1 ► Flap2 OK Cancer
Exploration	

## **Objective options**

### **DESCRIPTION:**

Two new objective control options are available to set the goal relative to a specific target value:

- Minimize Difference: Make the objective as closes to the target value as possible.
- Maximize Difference: Make objective as far away from the value as possible.

The ability to define an equality constraint has also been added. This is equivalent to defining both the upper and lower bounds to the same value.

### **BENEFIT:**

Improved flexibility in objective goals and constraint definitions.

Comme	nts				
Objectiv	/e	Option			Target
🛛 🎯 volume		Minimize Differen	Minimize Difference 🔹 🔻		
		Minimize Value Maximize Value			
		Minimize Differen	ce		
		March Diff.			
			ice		
Lower	≤	Constraint			Upper
Lower	≤	Constraint		· 5000	Upper
Lower	≤	Constraint		· 5000 · 0.1	Upper

### More easily extract responses

### **DESCRIPTION:**

There is also a new option to extract responses from existing output files. When evaluating responses, the dialog now remains visible for all scenarios.

### **BENEFIT:**

This enables more efficient testing of individual analyses, evaluating baseline values, and to extract response values from updated output files without the need to re-run the analysis.

Select Analyses to Evaluate
Evaluate responses from all analyses
Evaluate tagged responses from a single analysis:
Analysis: 🛑 cbeam 👻
Options:
<ul> <li>Extract responses from current output files</li> </ul>
$\odot$ Run the analysis to generate new output files

Keyword access for analysis execution	
<b>DESCRIPTION:</b> A button has been added to the analysis execution options to insert keywords. Similar functionality already existed in the Advanced section for pre and post execution commands.	Design_Num Design_Path Analysis_Name Job_Name Job_D Study_Path Project_Path Project_Path Project_Path Project_Path Project_Path Project_Path Project_Path Project_Path
<b>BENEFIT:</b> Consistent access to keywords Increase visibility and awareness of using keywords	Compute resource: Local 2 Execution command: %HEEDS_STARCCM_CMD% Command options: %CMD_OPTIONS% %INPUTFILE% -batch updateSTARCCMModel.java Finished con Num. designs to execute simultaneously: 1 Success con

## Analysis connector enhancements

#### **DESCRIPTION:**

Hovering over a connector now displays a tooltip indicating the analysis blocks being connected. Multiple connectors can also now be defined to an input file. However, if the setup is invalid, the study will give error messages that must be resolved before the study will run.

### **BENEFIT:**

Define more efficient workflows where there are multiple conditional sources. Improved visual feedback on what is being transferred.



### View vector responses

### **DESCRIPTION:**

HEEDS now supports display of vector results. These can be viewed when evaluating responses or in post processing by hovering over a value and the tooltip will list the vector values.

Vector responses have square brackets appended to the name.

The context menu in any plot or parameter table has a new "Response explorer..." menu item

The Response Explorer interface enables the user to view the vector responses for any specified design id (filtered with a design set), for a selected set of responses.

This data can be imported to a spreadsheet or a user plot.

### **BENEFIT:**

Increased visibility and insight to responses with multiple values.

Enables user to inspect all response values for each design.

Ø	Methods	X Var	iables		🖌 Respons	ses	Rented	ents		
T.	. Available	Response	s T		Туре	A	nalysis	Va	lue	
$\checkmark$	🛯 🖉 Year		Tag	9		Analys	is_1	[9 value	il	
V	Predic	ted Popu	la Ta	a		Analys	is 1	[9 value	:1	
	RMS		Cu	Sho Set	ate anaysis w model default ima	Analys anics	is_1	0.90017	Values: 78.6955 68.441 59.466 51.625 44.7853 38.8272 33.6431 29.1373 25.2244	
			<b>.</b>	ines	ponse expi					
				Cop	ру	C	trl+C			
				Exp	ort selectio	n				
esp	onse Explorer: St	tudy_1			_					X
Res	ponses: 🔛 colu	umn_1, 🏰 🔻	] 🕼 📎		Design set:		•	Design id: 6		2
	🕼 column_1	🖞 column_2	🕼 colur	mn_3						<u>^</u>
1	7.85 0	)	61.6225							
2	8.85 1	15.13	78.3225							
3	9.85 3	30.26	97.0225							Ξ
4	10.85 4	15.39	117.722							
	11.85 6	50.52	140.423							
5	12.95 7	75.65	165.123							
5 6	12.00 /									
5 6 7	13.85 9	90.78	191.822							
5 6 7 8	13.85 9 14.85 1	90.78	191.822 220.523							
5 6 7 8 9	13.85 9 14.85 1 15.85 1	90.78 105.91 121.04	191.822 220.523 251.222							
5 6 7 8 9	13.85 9 13.85 9 14.85 1 15.85 1 16.85 1	90.78 105.91 121.04 136.17	191.822 220.523 251.222 283.923							

## Input file source & target control

#### **DESCRIPTION:**

The Input File Details dialog has been simplified to place the Source and Target settings on separate tabs. A new option to rename the file has been added.

### **BENEFIT:**

Clearer differentiation between source and target preferences.

Prevents modification to original source files

Joan	Le larget
File	Source - Where does HEEDS find the input file?
0	Project folder - file is stored in the project folder
	C:/Users/jasond/DataSamples/MDO/cbeam
$\bigcirc$	Study folder - file is copied to the study folder (stored in project folder)
	C:/Users/jasond/DataSamples/MDO/cbeam/[Study]
۲	Other analysis - file is generated by another analysis:
	<b>v</b>
0	Relative path - a child folder of the analysis folder:
۲	Fixed path - the file is referenced from a fixed location:
	C:/Users/jasond/DataSamples/MDO/cbeam

## Consistent feedback on changed parameters in Analysis Portals

### **DESCRIPTION:**

In the HEEDS options for Analysis Portals, the Solver install, Execution command, Command options, and Icon entries will be displayed in italics if the user has a value different from the default settings. The default is displayed in a tooltip and can be restored using the reset button.

#### **BENEFIT:**

This provides feedback to identify what is different from the defaults and what will be changed when the reset button is pressed.

Solver install:	; Program Files CD-adapco STAR-CCM+11.02.010-R8 star bin starccm+.exe" 🛅	(j)
Execution command:	Original value: "C:\Program Files\CD-adapco\STAR-CCM+8.02.008\starccm+"	(j)
Command options:	%CMD_OPTIONS% %INPUTFILE% -batch updateSTARCCMModel.java	(i)
Icon:	portals:starccm.png	

Study restart options dialog	
DESCRIPTION: The Study Restart Options dialog has been rearranged to display the backup option nested under the write and restart option. This reinforces that backups only happen when writing the input files. BENEFIT: Minimizes confusion over what each option will do.	<ul> <li>Study Restart Options</li> <li>Resume - continue the study from where it left off The search will be initialized with the designs from the initial run identified below.</li> <li>Use all designs</li> <li>Specify design ids: 1-10,25-30 (1)</li> <li>Use POST design set: </li> <li>Extend - add more evaluations to the study</li> <li>Additional evaluations: 150</li> <li>Options:</li> <li>Use write the input files</li> <li>Write the input files and restart the study</li> <li>Backup existing results data</li> </ul>

• Y. ①

## Use any file for input condition

### **DESCRIPTION:**

The user is permitted to specify file names that are not part of the project in Manage Conditions section. These can only be used in the Finished or Success conditions. A Run condition requires a file selected from the project.

### **BENEFIT:**

Increased flexibility in checking completion. Alleviates the need to add the file to the project.

Documentation update	
<ul> <li>DESCRIPTION:</li> <li>The Create Project Archive capability has been enhanced such that: <ul> <li>If the path to the zip utility executable includes a space then it should be wrapped in double quotes.</li> <li>i.e. "C:\Program Files\7-Zip\7z.exe"</li> </ul> </li> <li>If 7-zip is used to create .zip archives then the -tzip argument is used. <ul> <li>"C:\Program Files\7-Zip\7z.exe" a -tzip %ARCHIVE% %FILES%</li> </ul> </li> </ul>	Create Project Archive          P S3          Project:       C:/Users//Models/Vector_test/PopulationModeling/Population2.heeds          Archive:       Jsers/anh/Documents/Models/Vector_test/PopulationModeling/Population2.zp          Contents:          P population2.heeds          Image: Contents:          P opulation2.heeds          Image: Contents:
<b>BENEFIT:</b> Less customization needed for specific machine configuration.	

Manage Conditions

 Name

K Condition\_1

Properties of Condition\_1

🕂 Add Item

if... File exists 

cbeam.txt

and 🔹 File contains 🔹 💐 cbeam.out (cbe 👻 🏹 Enter text to find

## **Results Processing**

## Self-Organizing Map (SOM) Plot

### **DESCRIPTION:**

The Self-Organizing Map (SOM) is a way of displaying patterns and relationships in data aimed at design explorations with multiple objectives and responses. A SOM plot can show data relationships that are otherwise difficult to visualize. It is particularly helpful for higher-dimensional data, where 2D and 3D plots are insufficient. For example, a SOM plot allows you to identify tradeoffs among multiple objectives.

Results are displayed as either:

- A) Pie wedges to indicate the normalized parameter values for the designs in that cell.
   Each segment of the pie represents one parameter. The range of parameter values in a cell are represented by the darker outer portion of the pie piece
- B) Colored cells to overlay the variation of one parameter with respect to the vertex parameters (i.e. a heatmap).

### **BENEFIT:**

Visual way to explore relationships and dependency for complex systems.



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## Display of video files

### **DESCRIPTION:**

Many simulation tools provide animation outputs. HEEDS POST now supports playback of video files generated from an analysis.

### **BENEFIT:**

Increased visualization capabilities of results.



View vector responses	
<b>DESCRIPTION:</b> Vector responses can also be displayed in a 2D user plot.	Response: Column_1
<b>BENEFIT:</b> Enable user to inspect all response values for each design.	x-y table     Indi       Data File from Design
	Response: Column_1 Design: 15 Synchronized Independent Series Data

### Gaussian surrogate fitting

### **DESCRIPTION:**

The 'Gaussian Process' tuning option for Kriging surrogates has been added. The Gaussian Process option allows a relaxed fit of the data, meaning the surrogate is not required to exactly interpolate data points.

Gaussian process tuning computations take 2-6 times more processing time than the normal Kriging tuning. Gaussian process tuning gives a smoothing effect when used on noisy or irregular data.

Gaussian process tuning will closely match smooth data, but may not interpolate it as precisely as Kriging tuning.

#### **BENEFIT:**

Provides a smoother surrogate response surface for noisy or irregular data.

Select	
opecity mot	
Model:	Kriging 🗸
Function:	Gaussian
Shape Facto	or: 1
Tuning:	Kriging
Order:	None Kriging Gaussian Process

## Analysis loops

#### **DESCRIPTION:**

The user is allowed to select a specific loop case to override the preferred study case across the entire study

When the selected case for a loop is changed the study immediately updates. Designs sets, custom performance, surrogates, and used data are recalculated. Plot display is updated to reflect the new data.

#### **BENEFIT:**

A fast and efficient way to review all results for different loop iterations.



### Surrogate export

### **DESCRIPTION:**

You can now export function-based surrogate models in a form that can be directly evaluated by other applications. Surrogate export now supports additional common formats such as Python, Java and Modelica.

### **BENEFIT:**

Allows you to export and re-use HEEDS surrogates in analyses or applications such as Excel.



### Design names

### **DESCRIPTION:**

Design names (defined by user in an eval study or when sharing/injecting designs) will appear in the design tooltips in plots.

Design names can also be used to include/exclude designs in a design set. Individual names, wildcards, or name ranges can be specified. For example:

- "sweep\*" will select all designs that start with "sweep".
- "sweep\_10-sweep\_25" will select all of the designs between, and including, the designs named "sweep\_10" and "sweep\_20".

### **BENEFIT:**

Increased visualization and design set filtering controls make it easier to focus on particular areas of interest.

50					
	urce	0			Rul
	DesignSet_	_5 - S	ummary		
	Included		Excluded		
	37		48		
	1 (design_1)	)	11 (sweep_	6) 🔺	
	2 (design_2)	)	12 (sweep_	6)	
	3 (design_4)	)	22 (h1.9)		
	4 (design_5)	)	23 (h1.9)		
	5 (sweep_6)		24 (h1.9)		
	6 (sweep_6)		25 (h1.9)		
	/ (sweep_6)		26 (h1.9)		
	8 (sweep_6)		27 (h1.9)		
	9 (sweep_0)	5	28 (h1.9) 20 (h1.0)		
	10 (Sweep C	,	29 (111.9)		
t Desia	n 🗾 Design	n Id	🗾 Desig		Desid
. D'obigi	Design	10	Desig	in bource	-
line	Design	n Flag	Desig	n Rank	
	Plot Data				
e	Plot Data val: Design T	able			
e Di	Plot Data <b>val: Design T</b> esign Id	able Sourc	ce	volume	
e De 1	Plot Data <b>val: Design T</b> esign Id	able Sourc Set_1	ce (design_1)	volume 266.4	
e D 1 2	Plot Data <b>val: Design T</b> esign Id	able Sourc Set_1 Set_1	ce (design_1) (design_2)	volume 266.4 24.48	
e D 1 2 3	Plot Data <b>val: Design T</b> esign Id	Source Source Set_1 Set_1 Set_1	ce (design_1) (design_2) (design_4)	volume 266.4 24.48 665.3	
e D 1 2 3 4	Plot Data <b>val: Design T</b> esign Id	Source Set_1 Set_1 Set_1 Set_1 Set_1	ce (design_1) (design_2) (design_4) (design_5)	volume 266.4 24.48 665.3 1224	
e D 1 2 3 4 5	Plot Data <b>val: Design T</b> esign Id	able Source Set_1 Set_1 Set_1 Set_1 Set_1 Set_1	te (design_1) (design_2) (design_4) (design_5) (sweep_6)	volume 266.4 24.48 665.3 1224 120.2	
e D 1 2 3 4 5 6	Plot Data <b>val: Design T</b> esign Id	able Source Set_1 Set_1 Set_1 Set_1 Set_1 Set_1 Set_1	ce (design_1) (design_2) (design_4) (design_5) (sweep_6) (sweep_6)	volume 266.4 24.48 665.3 1224 120.2 216	

## Portals

Portals for ES-ICE, pro-STAR, STAR-CD (MDO)	
DESCRIPTION:	
Portals were added for the ES-ICE, pro-STAR and STAR-CD applications. These applications are commonly used together.	
<b>BENEFIT:</b> Streamlines tagging of files for these applications.	A_ESICE_Pre B_proSTAR C_STARCD D_ESICE_Post

AVL-EXCITE	
DESCRIPTION:	
AVL-EXCITE now supports input and output tagging.	
BENEFIT:	
Streamlines tagging of files for these applications.	
	AVL_1

Autodesk Moldflow	
<b>DESCRIPTION:</b> A portal was added for the Moldflow application.	
Moldflow supports input and output tagging.	
<b>BENEFIT:</b> Streamlines tagging of files for these applications.	Moldflow_1

## **Known Issues**

**DESCRIPTION:** Clicking on X to close the left pane in the Help does not work

## WORKAROUND:

This is a limitation specific to Chrome due to the Robohelp version used. It works correctly in Internet Explorer 11.

# 2016.04.1 Updates

Issue	Description
4050	Support deletion of several types of analysis items from process at once.
4085	Remove trailing spaces from cluster Job ID's to allow successful use in a job completion check
4091	Stability issue with 3D function plot generated using wizard
4088	Prevent "performance" from getting included in the list of study responses
4078	Occasional crash at the end of study using Excel in visible mode.
4096	Excessive CPU consumption when running in serial mode
4135	Incorrect warnings displayed for curve fitting
4170	Upstream STAR-CCM+ sim files not correctly transferred to remote machine
4110	Stop condition for loop not detected
3894	Improve serial mode for loop execution
4178	Add API option to delete/keep results at end of study
4182	Portal Analysis Runtime error (SolidWorks, Python and MATLAB) causing study to stop
4190	Improved API support for parallel license usage
3684	Add support to Creo portal to keep session open for study.
3685	Add support for Creo design outputs to be used as response parameters