$Supported_data_table$

Supported Datasets

Dataset Name	Genotypes	Environment	Phenotype (label)	Label Type	Description	Supported
Baryshnikovna_2010	6,022	1	smf	global	growth rate	✓
Costanzo_2016_smf	21,718	2	smf	global	growth rate	\checkmark
$Costanzo_2016_dmf$	20,705,612	2	smf	global	growth rate	\checkmark
Costanzo_2016_dmi	20,705,612	2	dmi	edge	gene interaction	\checkmark
$Kuzmin_2018_smf$	1,539	1	smf	global	growth rate	\checkmark
$Kuzmin_2018_dmf$	410,399	1	dmf	global	growth rate	\checkmark
$Kuzmin_2018_tmf$	91,111	1	tmf	global	growth rate	\checkmark
Kuzmin_2018_dmi	410,399	1	dmi	edge	growth rate	\checkmark
$Kuzmin_2018_tmi$	91,111	1	${ m tmi}$	hyper edge	growth rate	\checkmark
$Kuzmin_2020_smf$	480	1	smf	global	growth rate	\checkmark
$Kuzmin_2020_dmf$	256,862	1	dmf	global	growth rate	\checkmark
$Kuzmin_2020_tmf$	537,911	1	tmf	global	growth rate	\checkmark
Kuzmin_2020_dmi	256,862	1	dmi	global	gene interaction	\checkmark
$Kuzmin_2020_tmi$	537,911	1	${ m tmi}$	hyper edge	gene interaction	\checkmark
SGD_essential	1,101	1	viable	global	viability	\checkmark
SynthLethalYeast	1,400	?	viable	global	viability	\checkmark
SynthRescueYeast	6,948	?	viable	global	viability	\checkmark
$scmd2_2005$	4,718	1	morphology	global	cell morphology	\checkmark
$scmd2_2018$	1,112	1	morphology	global	cell morphology	\checkmark
$scmd2_2022$	1,982	1	morphology	global	cell morphology	\checkmark
ODuibhir_2014	1,312	1	smf	global, node	growth rate	\checkmark
Kemmeren_2014	1,484	1	expr	global, node	sm microarray expression	\checkmark
Sameith_2015	72	1	expr	global, node	dm microarray expression	\checkmark
Zelezniak_2018	97	1	prot abund., met conc.	global, node	sm kinase deletion mutants	\checkmark
Wildenhain_2015	195	4,915	smf	global	smf drug tolerance	in progress
Lian_2017	18,000	1	AID	global	AID furfural tolderance	\checkmark
FitDb	6,000	1,144	smf	global	growth rate	in progress

- Just approximate on ${\tt Kuzmin_2020}$ for now
 - 537,911 dmf, dmi
 - -256,862 tmf, tmi
 - -480 smf

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Costanzo_2016_dmi	20,705,612	2	dmi	$_{ m edge}$	gene interaction	\checkmark
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$Kuzmin_2018_dmf$	410,399	1	dmf	global	growth rate	\checkmark
Kuzmin_2018_tmf	91, 111	1	tmf	global	growth rate	\checkmark
Kuzmin_2018_dmi	410,399	1	dmi	$_{ m edge}$	gene interaction	\checkmark
Kuzmin_2018_tmi	91, 111	1	${ m tmi}$	hyper-edge	gene interaction	\checkmark
Kuzmin_2020_smf	480	1	smf	global	growth rate	\checkmark
Kuzmin_2020_dmf	256,862	1	dmf	global	growth rate	\checkmark
Kuzmin_2020_tmf	537, 911	1	tmf	global	growth rate	\checkmark
Kuzmin_2020_dmi	256,862	1	dmi	global	gene interaction	\checkmark
Kuzmin_2020_tmi	537, 911	1	${ m tmi}$	hyper-edge	gene interaction	\checkmark
SGD_essential	1, 101	1	viable	global	viability	\checkmark
SynthLethalYeast	1,400	?	viable	global	viability	\checkmark
SynthRescueYeast	6,948	?	viable	global	viability	\checkmark
$scmd2_2005$	4,718	1	ellipse (e_1, e_2)	global	cell morphology	\checkmark
scmd2_2018	1,112	1	ellipse (e_1, e_2)	global	cell morphology	\checkmark
$\operatorname{scmd2}_{-2022}^{-}$	1,982	1	ellipse (e_1, e_2)	global	cell morphology	\checkmark
ODuibhir_2014	1,312	1	smf	global, node	growth rate	\checkmark
Kemmeren_2014	1,484	1	expr	global, node	sm microarray expression	\checkmark
Sameith_2015	72	1	expr	global, node	dm microarray expression	√

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