

Co-optimization of Fuels and Engines:

Co-Optima Low Greenhouse Gas Fuels Team

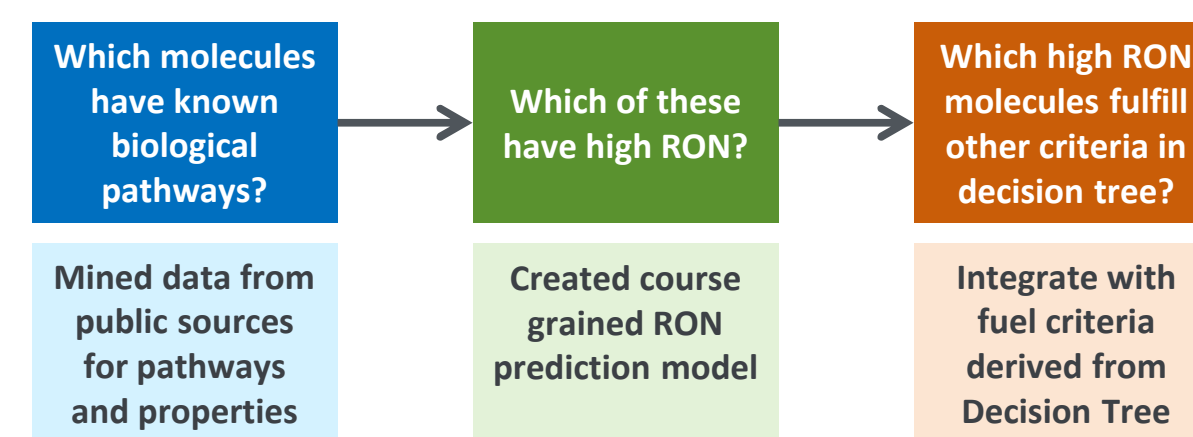
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Overview

- 30 by 30: The primary objective of Co-Optima is a 30% reduction in per-vehicle petroleum consumption by 2030, beyond the “business as usual” case.
- This will be achieved through the co-optimization of both fuels and engines.
- Six teams and 10 national labs are partnering in this multi-year effort.
- Working with the engine development and other Co-Optima teams, the Sandia fuels team is using computational and biochemical methods to produce fuel molecules with optimal performance for engines optimized in this effort.

Methodologies

- Computational methods



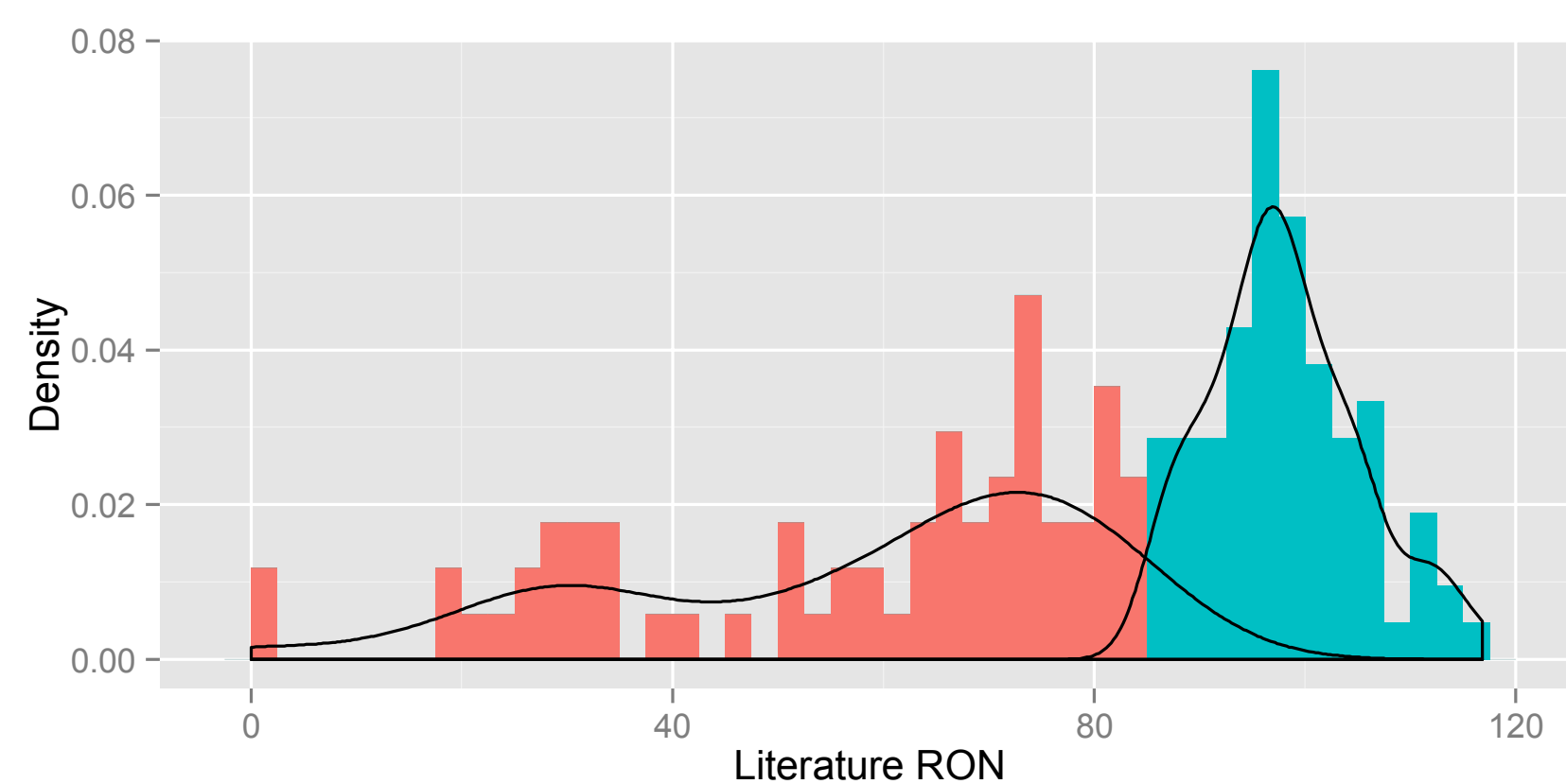
- Biochemical production

Red Yeasts:	Produce fuel molecules derived from isoprene metabolism in suitable organisms and develop these as chassis organisms	
Bioprospecting:	isolate organisms growing on actual hydrolysate and naturally producing fuel molecules, develop selected organism as chassis if needed & feasible	
Corynebacterium:	Utilize industrial model organisms and engineer for production of fuel molecules (i.e. fusel alcohols)	

Discussion

- Thus far engine performance has been limited by the type of fuel available (i.e. petroleum). Biology allows for the production of molecules not heretofore considered as fuels. We asked the question: what fuel properties does an engine need for higher performance and efficiency?
- In Co-Optima criteria were developed for what makes a good fuel. We developed methods to screen for all known biochemical pathways to produce these fuels in chemical databases, including research octane number (RON), where available. These were used to develop a RON prediction model.
- Molecules which were predicted to have high RON were targeted for biological production, and routes to terpenes and mixed alcohols demonstrated.

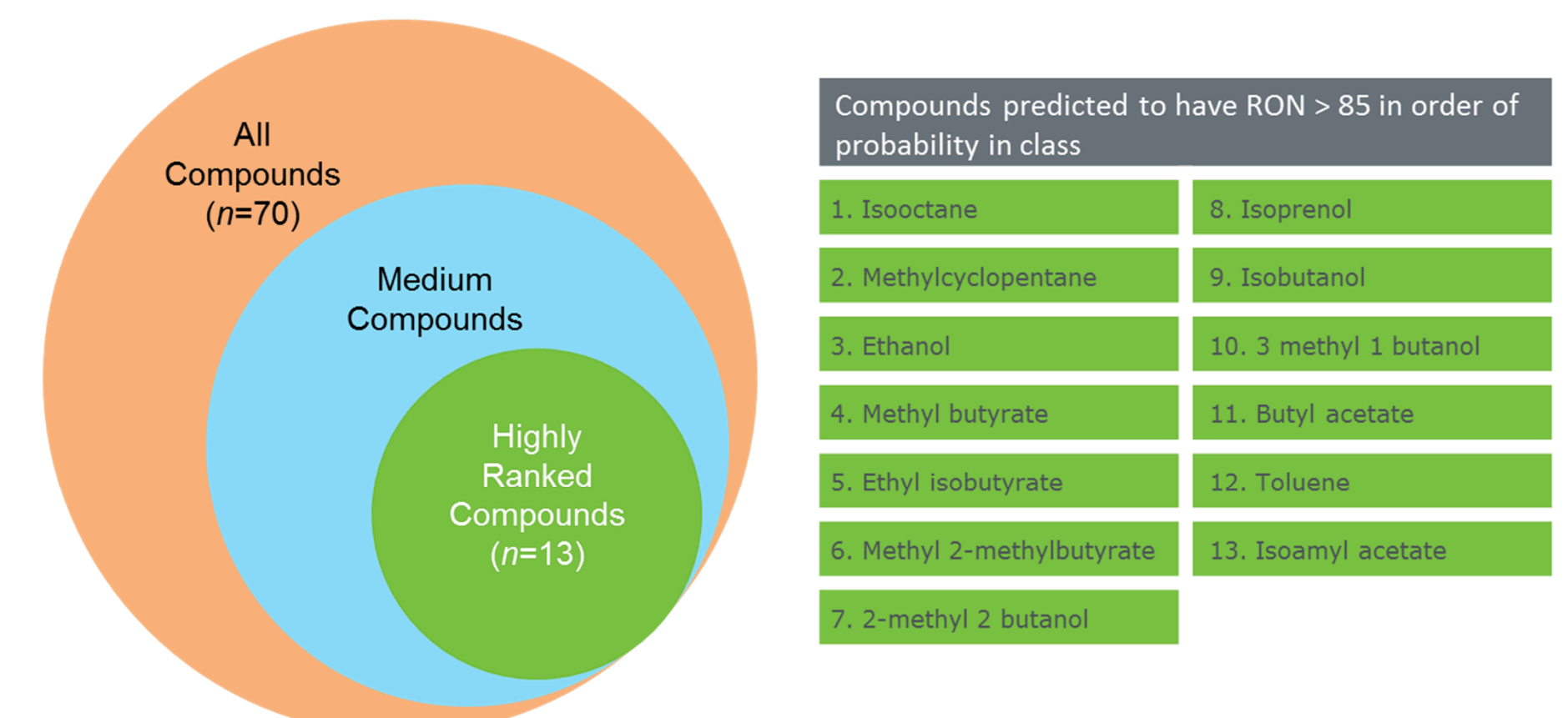
Computation Results



- Literature RON values were used with a machine learning technique to build a RON prediction model, enabling high throughput RON evaluation.
- This technique will be used to predict other largely unavailable fuel properties, such as flame speed.

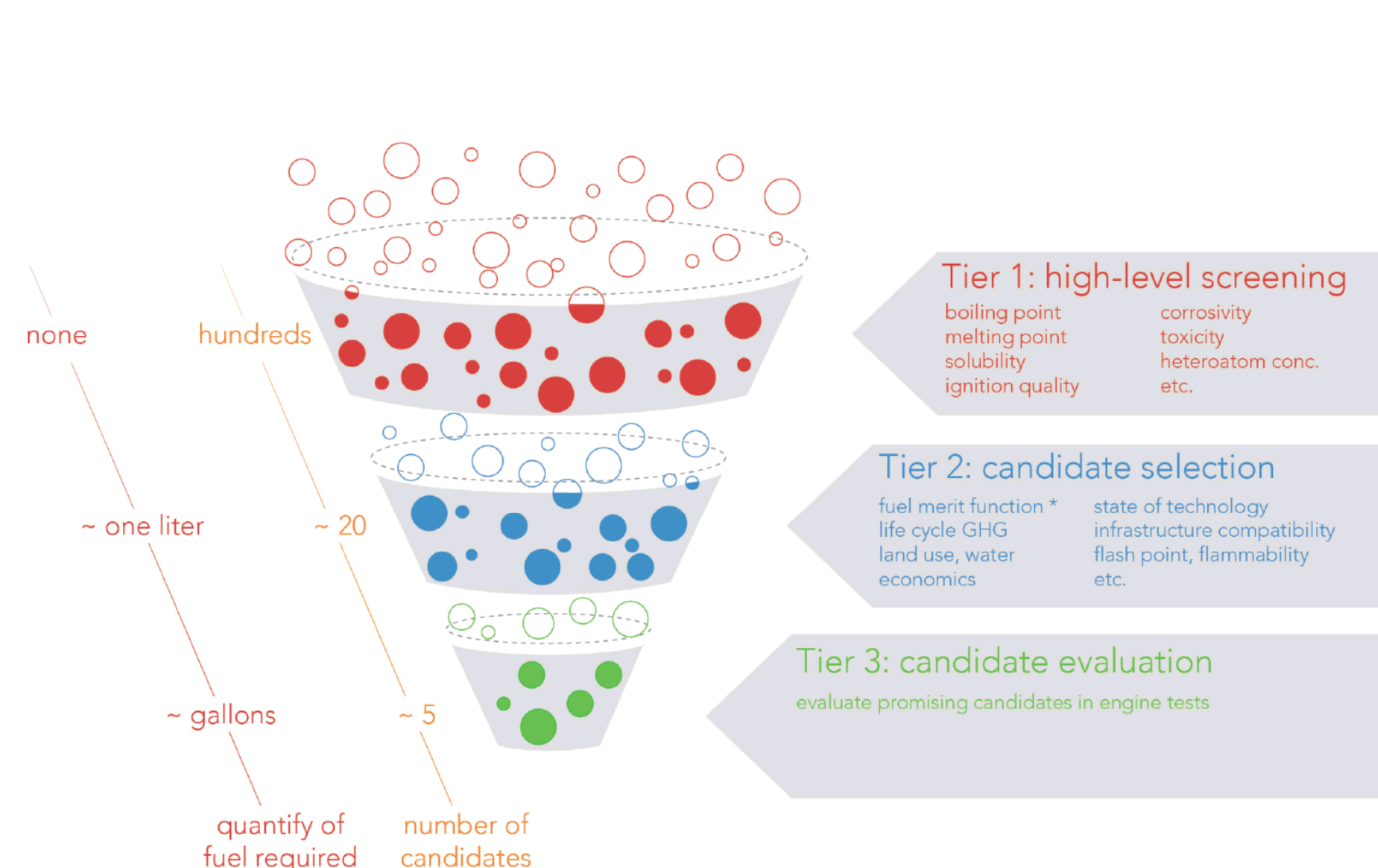
Features	Weight	Type
OH Rate Constant	0.0382	Physical
Surface Tension	0.0368	Physical
SMARTS Pattern: C-C-C-C-C-C	0.0349	Structural
KOC (pH 5.5)	0.0323	Physical
Vapor Pressure (mmHg at 25°C)	0.0313	Physical
SMARTS Pattern: C-C-C-C-C	0.0313	Structural
Octanol-Water Partition Coefficient (pH 7.4)	0.0302	Physical

Metric	Mean value	Std. dev
Accuracy	0.80	0.09
Precision	0.82	0.12
Sensitivity	0.80	0.16
Receiver Operator Characteristic (AUC)	0.88	0.07



- >2000 QSAR and structural features were correlated to RON. It was possible to describe which features most heavily contributed to RON. This will enable more detailed investigation into RON chemistry and allow improved fuel selection.
- The model enables down-selection from 1000s of molecules to a number that can feasibly be investigated experimentally.

Screening and production



- Red Yeasts**
- Organisms producing **carotenoids** have good metabolic flow through **isoprene biosynthesis** pathways.
 - A variety of fuel molecule candidates can be derived from isoprene biosynthesis pathways
 - Strain engineering efforts are focused on two yeasts:

	<p><i>Xanthophyllomyces dendrorhous</i> (Agaricomycotina)</p> <ul style="list-style-type: none"> Oleaginous yeast, demonstrated to utilize xylose for growth Used in commercial carotenoid production Major Carotenoids (in this sequence): Astaxanthin, HO-ketotorulene, Cantaxanthin 20 MB genome, published and very well annotated Lots of molecular tools for strain engineering published, including many case studies increasing flux into carotenoid pathway
	<p><i>Rhodospiridium rubrum</i> (Pucciniomycotina)</p> <ul style="list-style-type: none"> Oleaginous yeast, demonstrated to utilize xylose for growth Used in commercial carotenoid production Major Carotenoids (in this sequence): Torularhodin, Torulene, Beta carotene 20 MB genome published Transformation methods established but only few methods available

Carene	PaJF67	Picea abies		Myrcene	ama1e20	Antirrhinum majus	
	TpsB	Salvia stenophylla			amaOC15	Abies grandis	
Cineole	hyp3	Hypoxylon sp. E74060B		Ocimene	ag2.2	Abies grandis	
	SSCG_00536	Streptomyces clavuligerus			ama0a23	Antirrhinum majus	
Limonene	ag10	Abies grandis		Pinene	ag3.18	Abies grandis	
					pt30	Pinus taeda	
Linalol	PaTPS-Lin	Picea Abies		Sabinene	RlemTPS2	Citrus jambhiri	
					SabS1	Salvia pomifera	
				Thujene	LoTPS2	Licea cubeba	

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