
ÓMICAS

Graph Subspace Fusion from Super-Pixels for Biomass Estimation in Rice Crops

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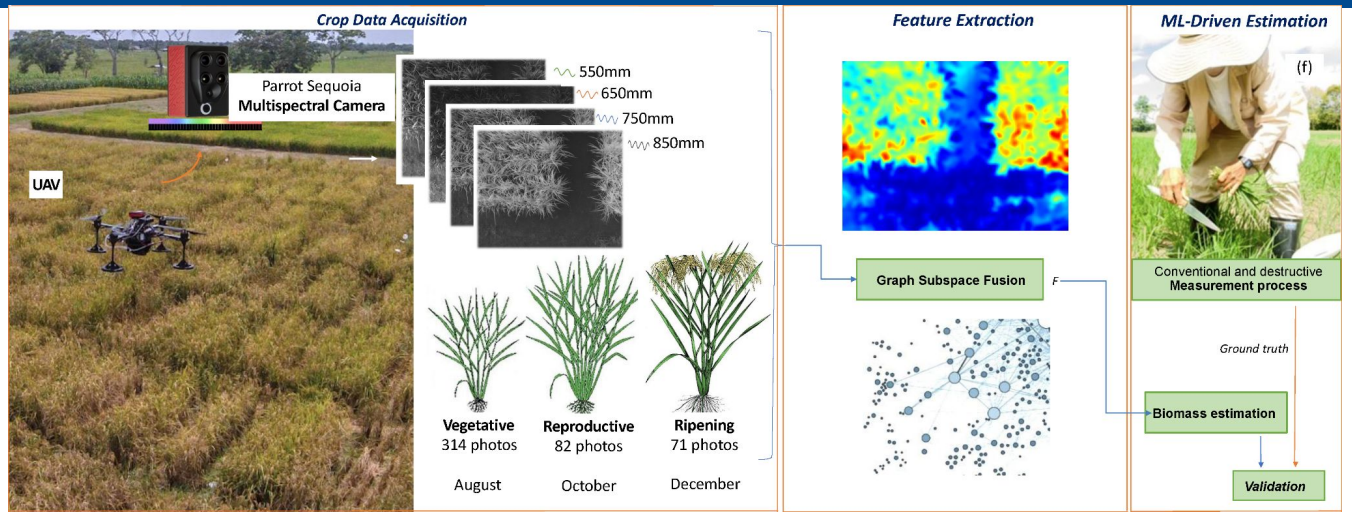
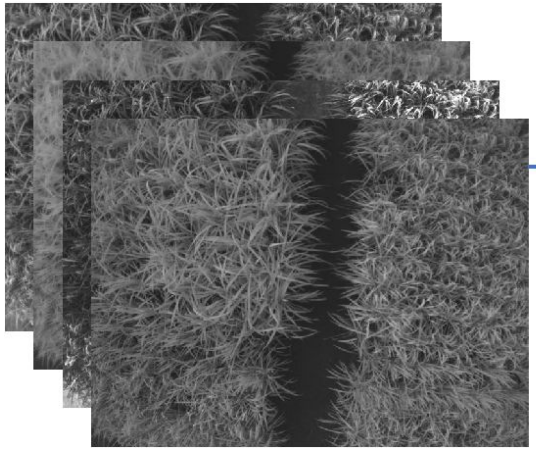


Framework



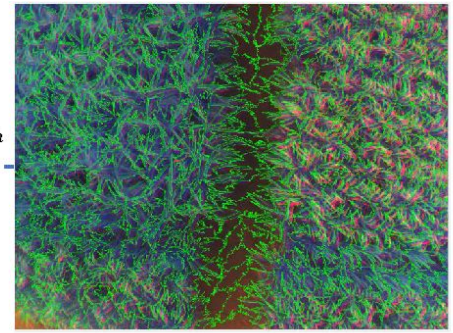
Input image

$X_n^c \in \mathbb{R}^{m \times n}$

Super-Pixels from RGNir channels (GMMSP)

(a)

$M \in \mathbb{R}^{m \times n}$



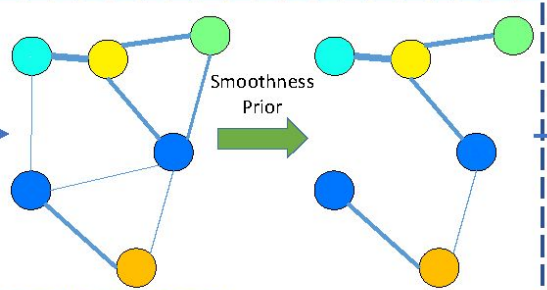
Labels

$M \in \mathbb{R}^{m \times n}$

$X_n^c \in \mathbb{R}^{m \times n}$

Use as node the mean value and the variance of the regions M from X_n^c to learn the graph

(b)



Loop for c = 1, …, C_h to learn the graph per channel

$W^c \in \mathbb{R}^{nr \times nr}$

Graph Subspace Fusion by solving equation (4)

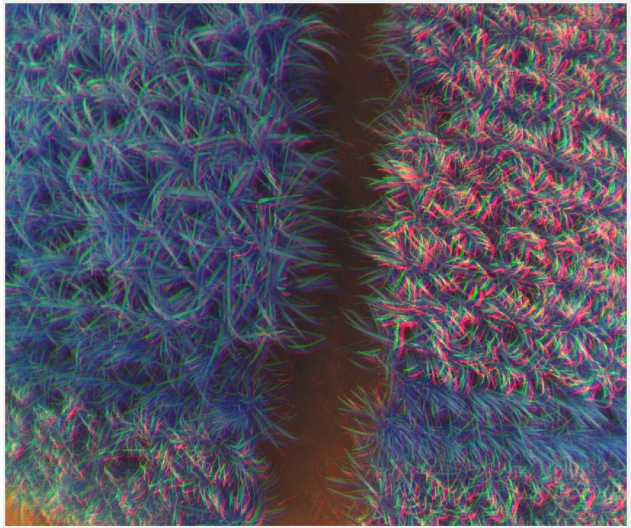
$F \in \mathbb{R}^{1 \times nr}$

(c)

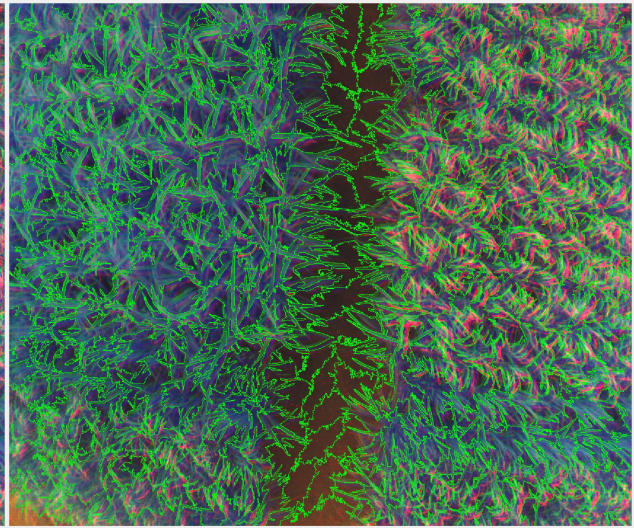
Apply dimensionality reduction (***t*-SNE**) over the feature space F

Gaussian Mixture Model for Super-Pixels (GMMSP)

- *The GMMSP approach associates each superpixel with width v_x and height v_y to a Gaussian distribution and the parameters are tuned by **expectation-maximization** (EM) problem.*
- *We use as input to the GMMSP algorithm the **R-G-NIR** images.*
- *Finally, the graph **nodes** are the descriptors related to the regions (super-pixels) such it is the **mean value** and the **variance**.*

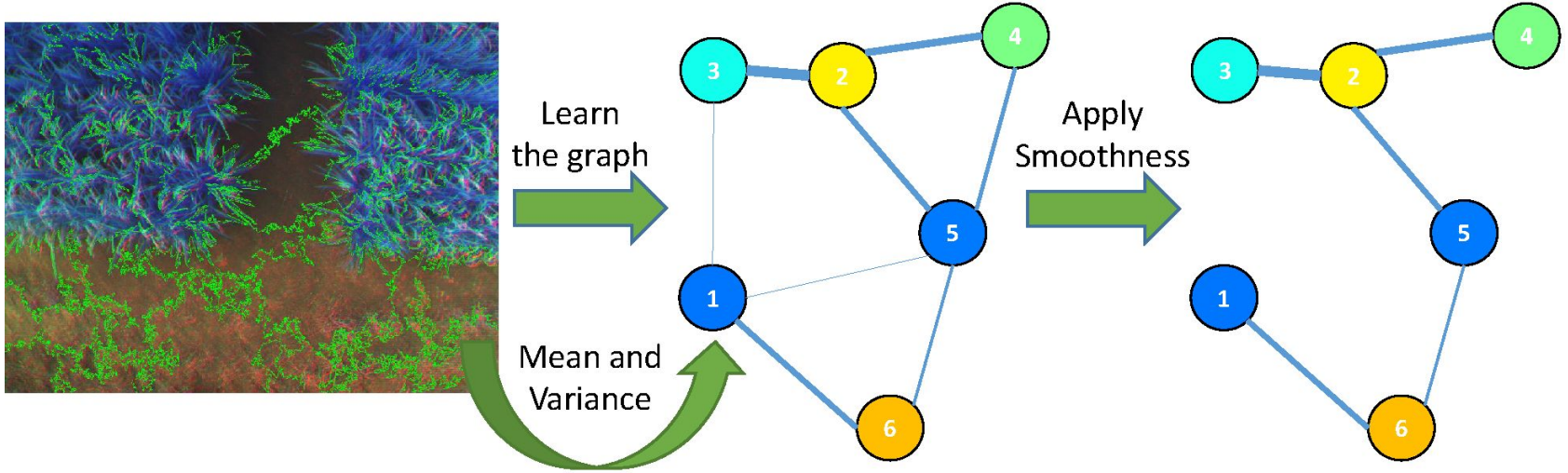


R-G-NIR image



Super-Pixels

Graph Learning with Smoothness Prior



- *In (2)* ***W_1, … , W_4 are the graphs*** *related to the Red, Green, NIR, and Red Edge channels respectively.*
- *V_1 to V_4 are the* ***eigenvectors*** *of Wi respectively.*
- *F are the fused* ***features*** *of all graphs that are* ***co-living*** *in the same subspace.*

$$
\begin{aligned}
F \quad = \arg\min_{F,S} & \frac{\lambda_1}{2} \left\| W_1 - F V_1^\top \right\|_{\mathcal{F}}^2 + \frac{\lambda_2}{2} \left\| W_2 - F V_2^\top \right\|_{\mathcal{F}}^2 \\
& + \frac{\lambda_3}{2} \left\| W_3 - F V_3^\top \right\|_{\mathcal{F}}^2 + \frac{\lambda_4}{2} \left\| W_4 - F V_4^\top \right\|_{\mathcal{F}}^2 \\
& + \lambda_5 \left\| S \right\|_{\mathrm{TV}} + \frac{\mu}{2} \left\| S - F - L_m \right\|_{\mathcal{F}}^2 ,
\end{aligned}
$$

*Then, we **fixed** one variable an compute the **derivative** with respect to the other (cyclic descent algorithm).*

$$F = \frac{\lambda_1 W_1 V_1 + \cdots + \lambda_4 W_4 V_4 + \mu(S - L_m)}{\lambda_1 + \lambda_2 + \lambda_3 + \lambda_4 + \mu}.$$

Finally, we update the Lagrangian multiplier.

$$L_m = L_m + F - S$$

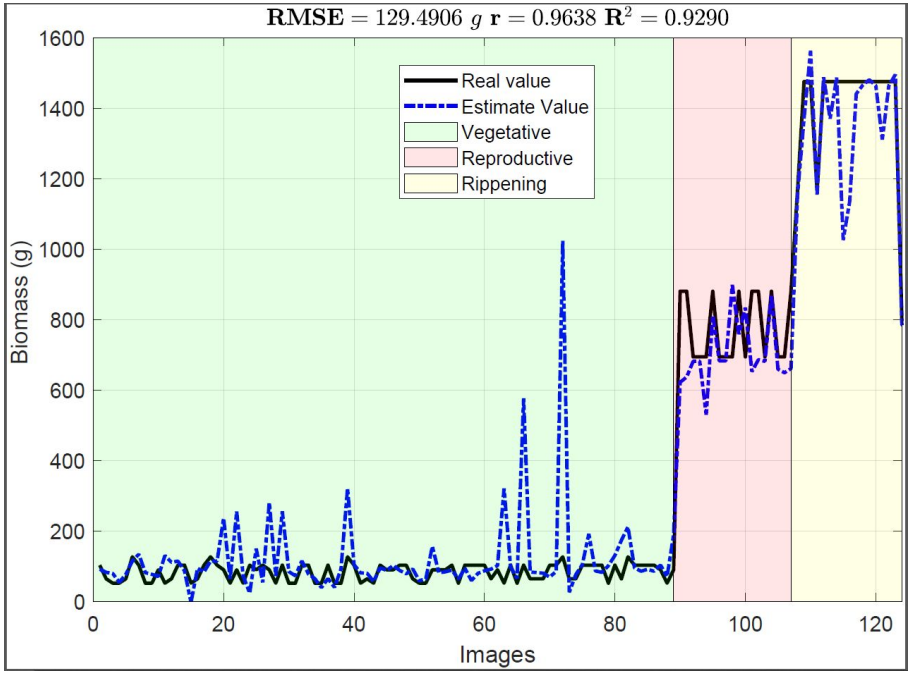
$$S = \text{SplitBregman}(L_m + F, \mu/\lambda_5).$$

Experimental Set-Up

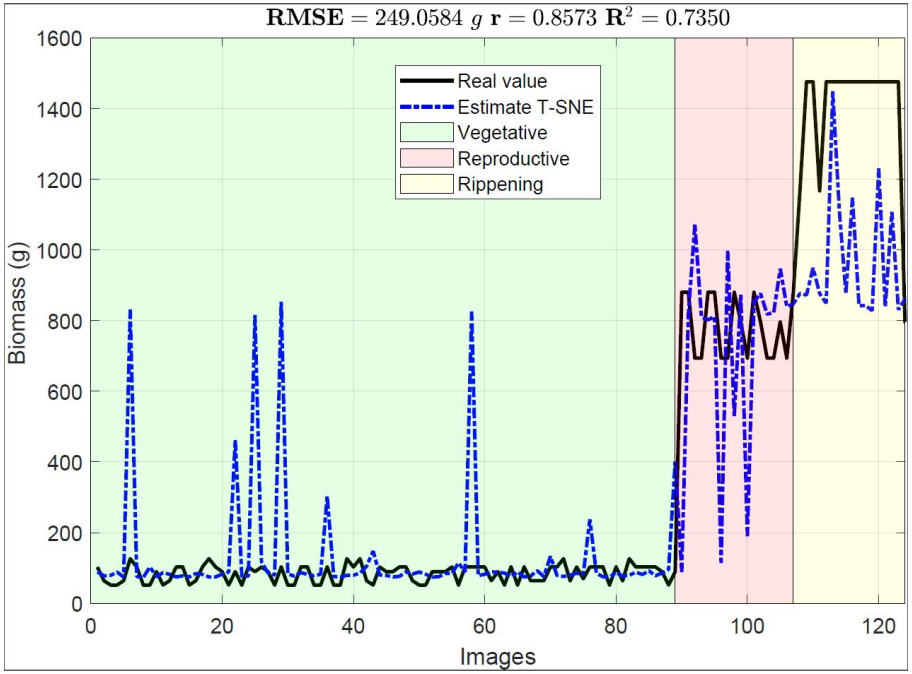
- *Set of images with 314 for the vegetation stage, 82 for the reproductive, and 71 for the ripening.*
- *The captured images have a resolution of 960×1280 pixels, geo-referenced with the corresponding biomass measurements in grams (g) from the Ground-Truth*
- *We trained **regressors**: classical **SVM** and a robust nonlinear autoregressive network with exogenous inputs (**NARX**), both accounting for **70%** of the dataset for the **training**, and the remaining **30%** for **testing** and **validation**.*
- *The performance of the models was measured in terms of the root mean squared error (**RMSE**), the **linear correlation** (r), and the **coefficient of determination** (R^2)*

Parameter	Value
$v_x = v_y$	35
λ_1 to λ_5	1
μ	0.01
CD iterations	30
S and L_m initialization	Ones

Qualitative Results for SVM

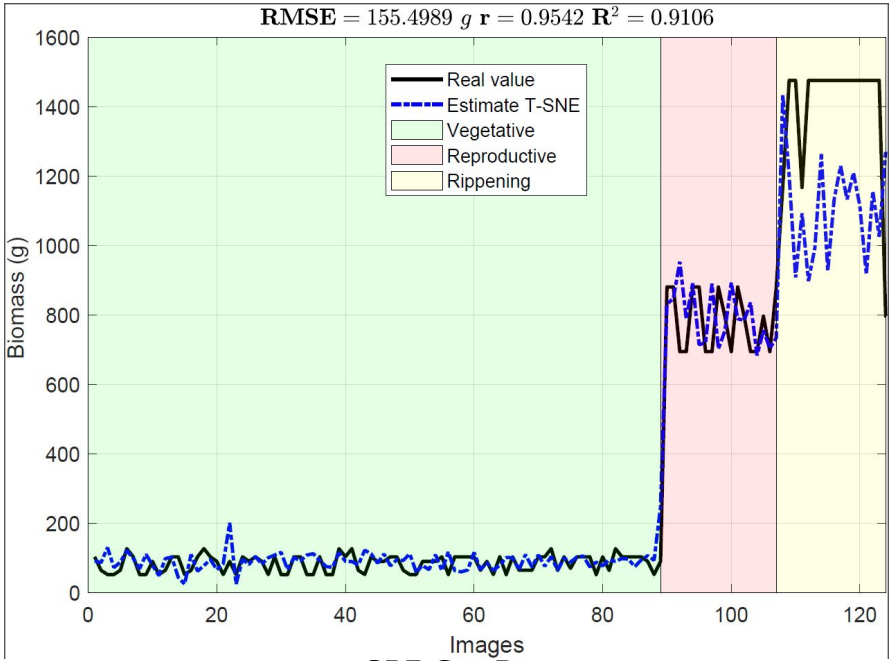


GFKuts

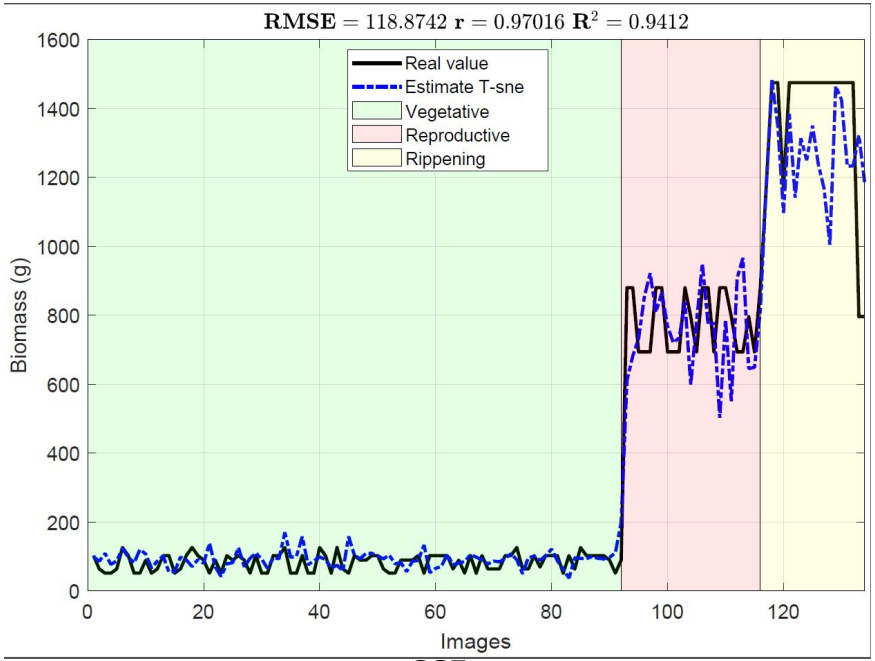


GBF

Qualitative Results for SVM

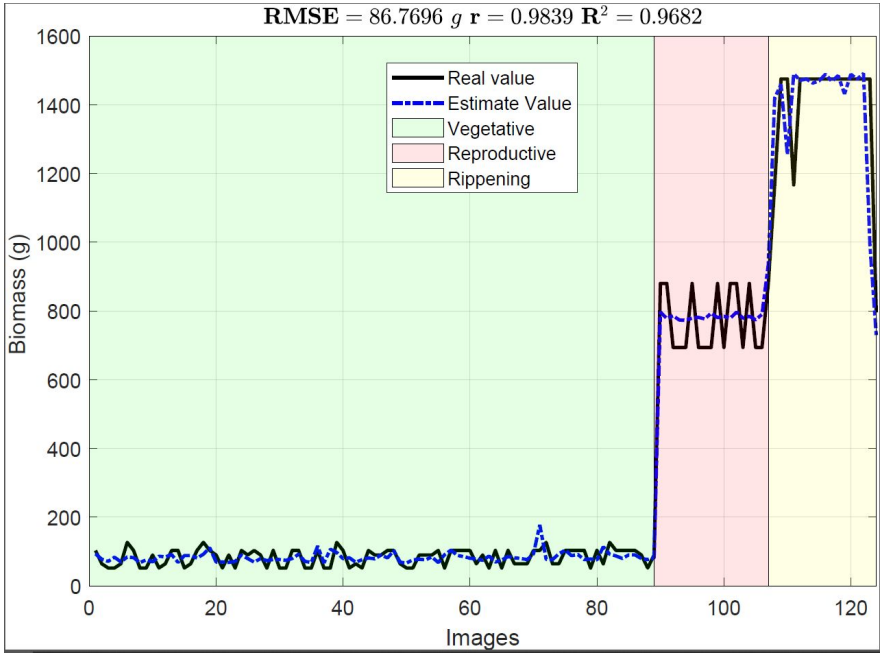


GBF-Sm-Bs

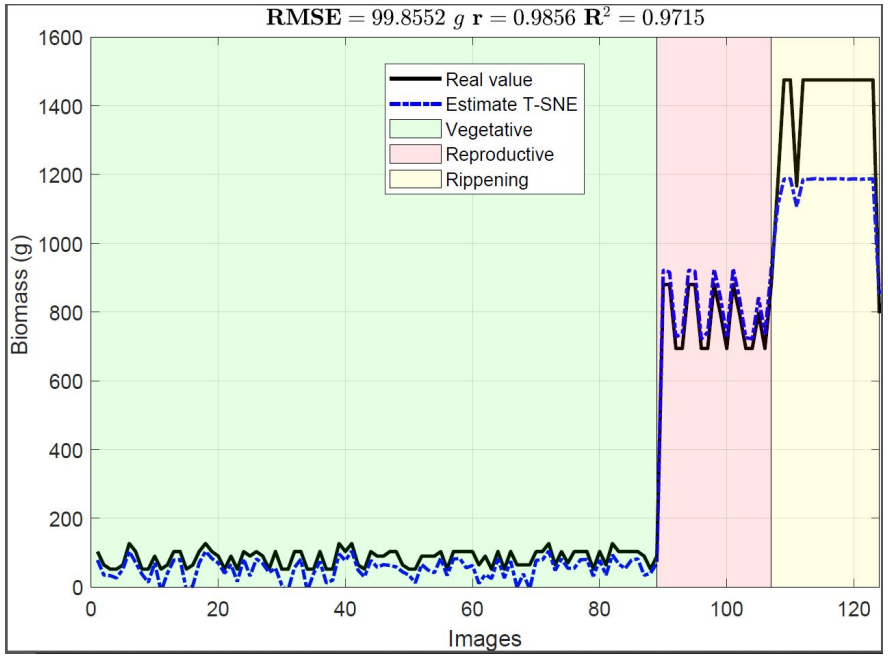


GSF

Qualitative Results for NARX

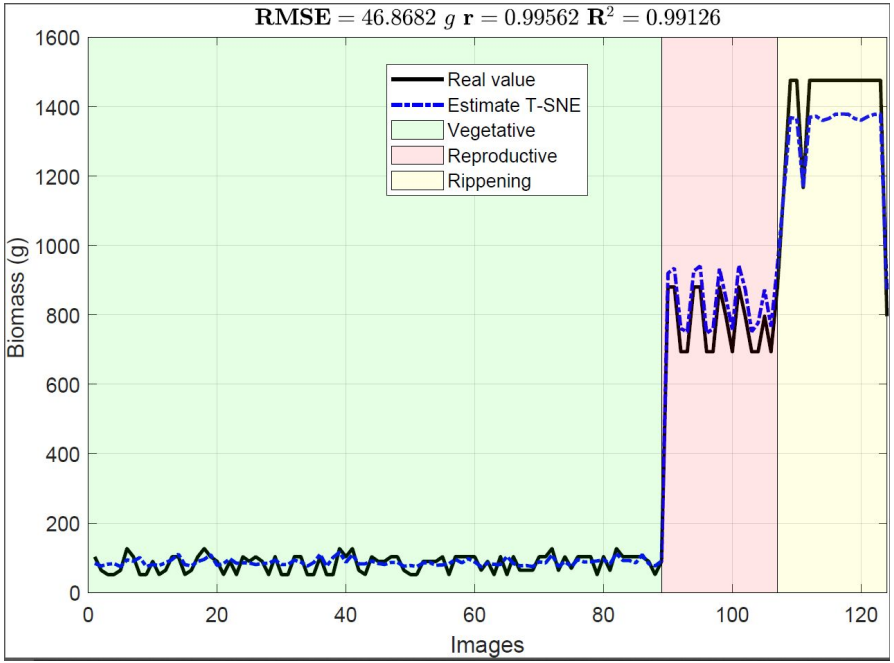


GFKuts

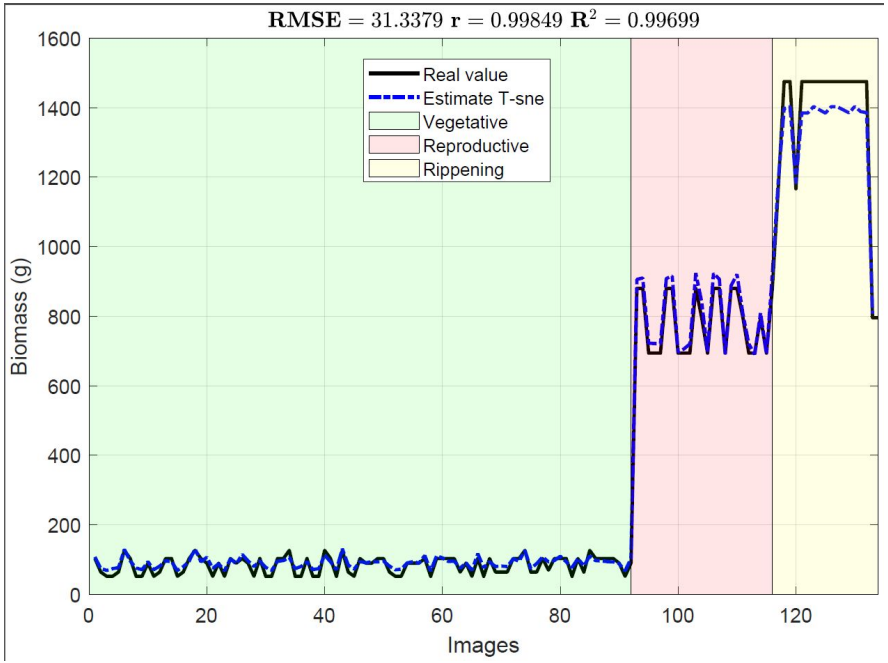


GBF

Qualitative Results for NARX



GBF-Sm-Bs



GSF

Model/Regressor	RMSE (in grams [g])	r	R^2
GFKuts /SVM	129.490	0.963	0.929
GBF /SVM	249.058	0.857	0.735
GBF-Sm-Bs /SVM	155.498	0.954	0.910
GSF/SVM	**118.8742**	**0.970**	**0.9412**
GFKuts /Narx	86.769	0.983	0.968
GBF /Narx	99.855	0.9856	0.971
GBF-Sm-Bs /Narx	45.358	0.995	0.991
GSF/Narx	**31.337**	**0.998**	**0.996**

Conclusions

- *In this work, we proposed a **subspace fusion** generated by graphs that contains structural information of a multi-spectral image given by **super-pixels**.*

- *The experimental results confirmed that by using the proposed **GSF** method we can extract relevant features that are good predictors of the biomass growth than features such as VI, and eigenvectors related to graph fusion presented in previous works. More precisely, the **GSF** achieved the lowest **RMSE = 118.8742g** and **RMSE = 31.3370g** for the SVM and NARX regressors respectively.*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