Localización 2D de yemas de vid utilizando técnicas de deep learning

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Abstract

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1. Introduction

In this work we propose a solution for the autonomous detection of grapevine buds within 2D images of vineyards captured in natural field conditions. Our proposed approach is based on *Fully Convolutional Networks* (**FCN**) (Long et al., 2015; Shelhamer et al., 2017), a kind of deep learning model specific for computer vision applications. Our solution adds in the historical quest for more and better quality information about different vineyard processes that impact on the productivity of grapevines and quality of their grapes.

For centuries agronomists have been producing models of the most relevant plant processes (i.e. fruit quality and yield, soil profiling, vine health), and vineyard managers have been recollecting a diverse corpus of information for feeding these models. Better and more efficient measuring procedures resulted in more information with its corresponding impact on the quality of models' outcomes, while inspiring researchers to push the boundaries for producing more

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sophisticated models. Such information consists of a large set of variables for assessing different aspects of the parts of the plant involved in these processes: trunks, leaves, berries, buds, shoots, flowers, bunches, canes. Nowadays technology is pushing once again the possibilities in the quality and throughput of these measurements, with digital and autonomous measurement procedures that improve over manual measurement procedures. The discipline is experiencing a transition, with many of its variables, e.g. conteo de yemas no brotadas, número de flores, cantidad de bayas, cantidad de racimos, número de plantas por claro, riqueza de poda, brotes totales, brotes de yemas francas, diámetro del tronco, longitud de entrenudos, longitud de 1er alambre descubierto y longitud del brote, entre tantos otros (Pellegrino et al., 2005; Intrigliolo and Castel, 2007; Reynolds and Heuvel, 2009; Matese and Di Gennaro, 2015; Ozdemir et al., 2017; Poni et al., 2018) are still being measured manually through visual inspection, resulting in large labor costs that limits the measurement campaigns to only small samples of data, that even with the use of statistical inference or spatial interpolation techniques impose a bound in the quality of the outcomes (Whelan et al., 1996; Borgogno-Mondino et al., 2018; Taylor et al., 2019). In some cases this is exacerbated by the need of experts for a proper measurement, such as the case of variables associated to the phenological stages of the plant such as bud swelling, bud burst, inflorescence, flowering, veraison, ripening of berries, among others (Lorenz et al., 1995); or by measurement procedure that requires the destruction of the part of the plant being measured, preventing any tracking of the variables overtime. Such is the case for the measurement of leaves área, bunch weight, berry weight and pruning weight (Kliewer and Dokoozlian, 2005).

Precision viticulture in general (Bramley, 2009), and computer vision algorithms in particular, has been growing in the last couple of decades, mainly for their potential for mitigating these limitations (Seng et al., 2018; Matese and Di Gennaro, 2015). These algorithms come along with a promise of an unprecedented boost in the production of vineyard information, with much expectations not only on possible improvements in the quality of the models' outcomes, but in its potential to produce better models by feeding all this information to big data algorithms.

In this work we contributed to this general endeavour with an algorithm

for measuring variables related to one specific part of the plant: the bud; an organ of major importance for being the grow point of the fruits, containing within all the productive potential of the plant (May, 2000). Our contribution of autonomous bud detection not only enables the autonomous measurement of all bud related variables currently measured by agronomists (see Table 1 for a non-exhaustive list of bud related variables); but has the potential to enable the measurement of novel, yet important variable that are currently impossible to be measured manually. One example is the total sunlight captured by the buds, that depends on the manually unfeasible task of determining the exact location of buds in 3D space. Although the present work focuses on 2D detection, it could be easily upgraded to 3D by, for instance, integrating the 2D detection in the workflow proposed by Díaz et al. (2018) (c.f. Section 1.1 for some more details on this workflow).

Table 1 shows a non-exhaustive list of the most important bud related variables currently measured by vineyard managers (Sánchez and Dokoozlian, 2005; Noyce et al., 2016; Collins et al., 2020), accompanied by an assessment of the extent to which detection contributes in their measurement. The right-most column indicates what information beyond detection is necessary to complete the measurement, while the middle columns labeled (i), (ii), and (iii) indicates the details of what specific aspects of the detection is required for that variable, whether it requires a good *segmentation*, i.e., the discrimination of which pixels in the scene correspond to buds and which ones correspond to the background (no-bud); *individualization*, i.e., discrimination of bud pixels as belonging to different buds; or *localization*, i.e., the localization of the bud within the scene; respectively. For instance, tomemos por caso la variable *buds number*. De ser posible individualizar correctamente las detecciones, the buds number se corresponde directamente con el conteo de detecciones. Por el contrario, para *bud type classification*, además de la individualización, la segmentación de la parte de la imagen correspondiente a la yema es necesaria para poder así alimentar a un clasificador con la información visual relevante, minimizando el ruido producto de pixeles del background. Por último, para medir la *incidence of sunlight on the bud*, no es necesaria la segmentación, sino tan solo una buena localización de la yema, además de la leaves 3D superficial geometry.

Variable/Aplicación	(i)	(ii)	(iii)	
Buds number		x		none
Bud area	x	x		none
Bud type classification	x	x		plant structure (trunk and canes)
Bud development stage	x	x		classifier over bud mask
Length between knots (by buds detection)		x	x	plant structure (trunk and canes)
Bud volume				3D reconstruction
Bud development monitoring	x	x	x	
Incidence of sunlight on the bud		x	x	3D reconstruction, leaves 3D superficial geometry

Table 1: Lista (no exhaustiva) de variables asociadas a las yemas, acompañadas de las sub-operaciones detección requeridas para su medición: (i) segmentación; (ii) individualización; y (iii) localización.

A good detector, therefore, should be evaluated on all three aspects of segmentation, individualization and localization. This is easy for our detector as its implementation first produces a segmentation mask, which is then post-processed to produce the individualization and localization. Los detalles de este enfoque se detallan en la Seccion **??**. El análisis de los resultados de detección presentado en la Seccion 3 muestra que este enfoque resulta superador a los algoritmos del estado del arte para la detección de yemas de vid, además de que demuestran ser suficientes para poder medir con buena calidad todas las variables de la Tabla (en algunos casos acompañadas de otros procesos complejos como ser la construcción de un clasificador, por ejemplo). En la Seccion 3.2.3 se discuten el alcance y las limitaciones de los resultados obtenidos para la detección de yemas como también los futuros trabajos y posibles mejoras. Finalmente en la Seccion 4 se presentan las conclusiones más importantes.

1.1. Related work

En la literatura se pueden encontrar una gran variedad de trabajos que emplean algoritmos de computer vision y machine learning para adquirir información sobre los viñedos (Seng et al., 2018), como ser berry and bunch detection (Nuske et al., 2011), fruit size and weight estimation (Tardaguila et al., 2012), leaf area indices and yield estimation (Diago et al., 2012), plant phenotyping (Herzog et al., 2014a,b), autonomous selective spraying (Berenstein et al., 2010), y más (Tardáguila et al., 2012; Whalley and Shanmuganathan, 2013). Entre los algoritmos de computer que se destacan en los últimos años, the *arti-*

ficial neural networks han despertado gran interés en la industria para llevar a cabo diversas tareas de reconocimiento visual (Hirano et al., 2006; Kahng et al., 2017; Tilgner et al., 2019). Particularmente las *Convolutional Neural Networks* (**CNNs**) se han convertido en el enfoque dominante de machine learning para el reconocimiento visual de objetos (Ning et al., 2017). Dos estudios recientes han aplicado exitosamente técnicas de reconocimiento visual basado en *deep learning networks* para identificar variables vitícolas que permitan estimar la producción en viñedos. Uno de ellos Grimm et al. (2019) utiliza una FCN para realizar segmentación de órganos de la planta de vid como los young shoots, pedicels, flower, buds or grapes. El segundo Rudolph et al. (2018) utiliza imágenes de vid en condiciones de campo que son segmentadas utilizando una CNN para detectar inflorescences y sobre esas regiones segmentadas se aplica el algoritmo circle Hough Transform para detectar las flowers buds.

Varios trabajos apuntan tanto a detectar como a localizar buds en diferentes tipos de cultivos mediante sistemas de reconocimiento visual autónomo. For instance Tarry et al. (2014) presents an integrated system for chrysanthemum bud detection that can be used to automate labour intensive tasks in floriculture greenhouses. More recently Zhao et al. (2018) presents a system of computer vision that is used to identify the internodes and buds of stalk crops. Según nuestro conocimiento y el mejor de nuestros esfuerzos de busqueda, existen al menos cuatro trabajos que abordan el problema de la detección de yemas específicamente de la vid mediante sistemas de reconocimiento visual autónomo. Los trabajos presentados por Xu et al. (2014), Herzog et al. (2014b) y Pérez et al. (2017) aplican diferentes técnicas para realizar detección 2D en imágenes que involucra diferentes algoritmos de computer y machine learning. Además, Díaz et al. (2018) introduce un workflow para localizar yemas en el espacio 3D. A continuación se presentan los detalles más relevante de cada uno.

El trabajo de Xu et al. (2014), presenta un algoritmo de detección de yemas utilizando imágenes RGB capturadas indoor y condiciones controladas de iluminación y fondo. Específicamente para establecer un groundwork para un sistema de podado autónomo en invierno. Los autores aplican un filtro por umbral para discriminar el fondo del esqueleto de la planta, resultando en una imagen binaria. Asumen que la forma de las yemas son similares a esquinas y aplican

el algoritmo *Harris corner detector* sobre la imagen binaria para detectarlas. Este proceso obtiene un recall de 0.702, es decir el 70.2% de la yemas fueron detectadas.

El trabajo de Herzog et al. (2014b) presenta tres métodos para la detección de yemas. Todos los métodos utilizados se caracterizan por ser semi-automáticos y requieren intervención humana para validar la calidad de los resultados. El mejor resultado se obtiene utilizando una imagen RGB con un fondo artificial de color negro y corresponde a un recall de 94%. Los autores argumentan que este recall es suficiente para satisfacer el problema de fenotipado de plantas de vid. También discuten que estos buenos resultados pueden explicarse debido al color verde particular y la morfología de las yemas ya brotadas de aproximadamente $2cm$.

En Pérez et al. (2017), presenta un enfoque para la clasificación de imágenes de yemas en invierno, mediante un enfoque que emplea SVM como clasificador y *Bag of Features* para computar descriptores visuales. Reportan un recall superior a 90% y una precision de 86% cuando se clasifican imágenes que contienen al menos el 60% de una yema y una proporción del 20-80% de pixeles yema vs pixeles no-yema. Argumentan que este clasificador puede ser utilizados en algoritmos para localización 2D del tipo *sliding windows* debido a la robustez ante la variación en tamaño y posición de la ventana. Es esta idea justamente la que se ha reproducido en el presente trabajo para implementar el enfoque de línea base basado en sliding windows y clasificador de patches.

Finalmente, en Díaz et al. (2018) se introduce un workflow para localización de yemas en el espacio 3D. El workflow consta de 5 etapas. La primera realiza una reconstrucción a partir de varias imágenes RGB de una nube 3D de puntos correspondientes a la estructura de la planta de vid. La segunda etapa aplica un metodo de deteccion 2D utilizando una técnica de sliding window y clasificación de patches. La etapa siguiente utiliza un esquema de votos para clasificar cada punto de la nube como yema o no yema. La cuarta etapa aplica el algoritmo de clustering $DBSCAN$ para agrupar puntos de la nube que corresponden a una yema. Finalmente en la quinta etapa se realiza la localización, obteniendo las coordenadas del centro de masa de cada cluster de puntos 3D. Reportan un recall de 45% con una precision de 100% y un error de localización

de aproximadamente 1.5cm, ó 3 diámetros de yema.

Si bien estos trabajos representan un gran avance en relación a la problemática de detección y localización de yemas, todavía sufren al menos una de las siguientes limitaciones: (i) uso de fondo artificial en exteriores; (ii) iluminación controlada en interiores; (iii) necesidad de interacción con el usuario; (iv) detección de yemas en etapas de desarrollo muy avanzado; y (v) bajo recall de detección/clasificación de yemas. Estas limitaciones representan una importante barrera para el desarrollo efectivo de herramientas de medición de variables asociadas a las yemas.

2. Materials and Methods

In this section we describe the main contribution of this work, the deep learning setup for the detection of grapevine buds in 2D images of vine plants captured in natural conditions. We start in the following subsection 2.1.1 with details on the *encoder-decoder* transfer learning architecture and the pre-training chosen for its encoder; followed by subsection 2.1.2 describing our design of the *scanning windows* detection procedure based on the state-of-the-art third-party bud image classifier of Pérez et al. (2017), used as the strongest found competitor to our proposed detection. We then proceed in subsection 2.2 with a description of collection of the images used for training both the deep learning and scanning windows models with details on the procedure used for its capture; and conclude with subsection 2.3 with details on the procedure and parameters for training of both models.

Como se describió en la introducción, el enfoque propone el uso de algoritmos de visión computacional para: (i) *segmentar* las yemas *clasificando* cuales píxeles de la escena corresponden a yema y cuales píxeles corresponden al background (no-yema), (ii) *individualizar* las yemas distinguiendo entre aquellos pixeles que pertenecen a diferentes yemas en la escena observada, y (iii) *localizar* cada yema en la escena. Para la operación de segmentación, i.e., clasificación de pixeles, se toma como base la FCN introducida en (Long et al., 2015), y se entrena para el problema específico de segmentación de yemas de vid (ver sección 2.1.1). La FCN resultante devuelve un mapa de probabilidad de igual escala que la imagen original, donde el valor de un píxel representa la probabilidad de que

el píxel correspondiente en la imágen de entrada pertenezca a una yema. Para obtener una máscara binaria se aplica a cada píxel un umbral de clasificación τ, clasificando al pixel como yema (no-yema) si su probabilidad es mayor (menor) a τ. Para individualizar las yemas se toma esta máscara binaria y se realiza un post-procesamiento para determinar que dos píxeles yema corresponden a una misma yema siempre y cuando pertenezcan a un mismo componente conectado, i.e., si los une alguna secuencia de píxeles yema contiguos. Finalmente, para la localización de objetos existen diversas alternativas entre las que encuentran *bounding box*, *pixel-wise segmentation*, *contorno* y *centro de masa del objeto* (Lampert et al., 2008). En este trabajo se tomó la última, eligiendo localizar a las yemas por el *centro de masa* de su componente conectado.

Los resultados de detección alcanzados por este enfoque son contrastados con el método de detección de yemas introducido en Pérez et al. (2017). En este trabajo los autores proponen el uso de *sliding windows* para subdividir la imagen en un conjunto de *patches* o regiones más pequeñas (Pérez et al., 2017), y luego determina si cierto patch contiene o no una yema usando un clasificador de imágenes construido con el algoritmo *Support Vector Machine* (Vapnik, 2013). Para poder contrastar ambos enfoques cada uno recibe el mismo tipo de entrada, i.e. una imagen de una escena vitícola, y producen las mismas salidas, i.e. una máscara binaria del mismo tamaño que la imagen original cuyos píxeles positivos representan los pixeles del tipo yema, junto a las coordenadas (X,Y) de la localización de estas yemas. A continuación se dan los detalles de cada implementación.

2.1. Models

2.1.1. Fully Convolutional Network with MobileNet (FCN-MN)

Como clasificador de píxeles se utilizaron las tres versiones 32s, 16s y 8s de las FCN introducidas originalmente por Long et al. (2015), por haber sido utilizadas con excelentes resultados en muchas aplicaciones de segmentación de imágenes Litjens et al. (2017); Garcia-Garcia et al. (2018); Kaymak and Uçar (2019). Estas redes presentan arquitecturas características con dos partes bien distinguibles: *encoder* y *decoder* (ver 1). El encoder consiste en una CNN que realiza un *downsampling* de una imagen de entrada en un conjunto de features mediante operaciones de convolución, para producir un conjunto de *feature*

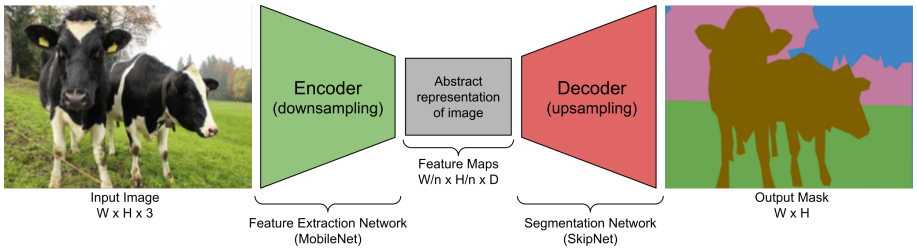


Figure 1: Esquema de la arquitectura de red FCN-MN utilizada en este trabajo, basada en la FCN propuesta por Shelhamer et al. (2017), reemplazando su encoder de extracción de features por las redes MobileNet Howard et al. (2017), lo que produce features maps con un factor de downsampling n. Como decoder para la producción del mapa de segmentación se utiliza la red SkipNet Siam et al. (2018), implementando las variantes 32s, 16s y 8s.

maps, i.e. una representación abstracta de la imagen que captura información semántica y contextual, pero que descarta información espacial de grano fino. Estas operaciones reducen las dimensiones espaciales de la imagen a medida que se avanza más profundo en la red, resultando en feature maps de tamaño 1/n del tamaño de la imagen de entrada, donde n es el factor de downsampling. El decoder es una subred de *upsampling*, que toma el conjunto de feature maps de baja resolución y los proyecta al espacio de píxeles, aumentando la resolución para producir una máscara de segmentación (o clasificación densa de píxeles) con las mismas dimensiones de la imagen de entrada. Esta operación se implementa como una red de transposed convolutions con parámetros entrenables, también conocidas como upsample convolutions Shelhamer et al. (2017).

Por otra parte, para refinar la calidad de la segmentación, se suelen utilizar conexiones que sobrepasan al menos una capa de la red, llamadas *skip connections*. Éstas se utilizan para transferir información espacial local desde las capas internas del encoder directamente al decoder. En general, estas conexiones mejoran los resultados de segmentación, ya que mitigan la pérdida de información espacial permitiendo al decoder incorporar información de feature maps internos, aunque su impacto puede variar según la skip architecture que se proponga. En Long et al. (2015) se proponen tres skip architectures: la 32s sin información de capas internas del encoder; la 16s que suma información espacial de capas profundas del encoder; y la 8s, que suma información espacial de capas profundas y menos profundas del encoder. Los detalles de estas arquitecturas quedan fuera del alcance de este trabajo, pero pueden consultarse en Long et al. (2015)

y Shelhamer et al. (2017). Dado que los resultados reportados en la literatura no son concluyentes respecto a que arquitectura es mejor Long et al. (2015); Shelhamer et al. (2017), en este trabajo se consideran las tres alternativas.

A pesar de haber alcanzado excelentes resultados en la práctica, estas arquitecturas conllevan una importante carga de recursos computacionales. Con esto en mente, en este trabajo se reemplazó el encoder VGG Simonyan and Zisserman (2015) propuesto originalmente por Long para las FCN, por la red MobileNet Howard et al. (2017), una red que se destaca por tener tan solo 4.2 millones de parámetros frente a los 138 millones de parámetros de VGG, permitiendo que el proceso de entrenamiento y testeo sea considerablemente más rápido, con requerimientos de memoria muy inferiores, pero manteniendo la performance. El uso de MobileNet como encoder en las FCN de Long et al. (2015) no es novedoso, sino que ha sido ya propuesto para la arquitectura 8s por Siam et al. (2018) en su arquitectura SkipNet. Técnicamente, la propuesta de Siam et al. (2018) es sumamente sencilla, por lo que nos atrevemos aquí a extenderla a las arquitecturas 16s y 32s propuestas originalmente por (Long et al., 2015). Debido a estos cambios es que nos referimos a estas redes como FCN-MN de aquí a lo que resta del paper.

2.1.2. Sliding Windows y Clasificador de patches (SW-C)

En esta sección se describe el enfoque propuesto por Pérez et al. (2017) para clasificación de imágenes de yema y una implementación del mismo para detección basada en sliding windows descrita en el trabajo original.

Este enfoque opera en tres pasos: (i) aplica el algoritmo de sliding windows sobre una imagen para extraer patches (sub-imágenes o regiones rectangulares); (ii) clasifica (todos los píxeles de) cada patch en yema o no-yema mediante el algoritmo presentado en Pérez et al. (2017); y (iii) produce la máscara de segmentación final mediante un esquema de votación. A continuación se dan los detalles de cada paso.

Las técnicas sliding windows comprenden una familia de algoritmos ampliamente utilizados en el pasado como parte de diversos enfoques para localización de objetos con bounding boxes (Divvala et al., 2009; Wang et al., 2009; Chum and Zisserman, 2007; Ferrari et al., 2007; Dalal and Triggs, 2005; Rowley et al., 1996). En estos algoritmos, cada imagen es escaneada densamente desde un ex-

tremo de la imagen (e.g. esquina superior izquierda) hasta el otro extremo (e.g. esquina inferior derecha) mediante una ventana deslizante rectangular en diferentes escalas y diferentes desplazamientos, extrayendo sub-imágenes o patches de la imagen original. En este trabajo, se definen 10 tamaños de ventana de igual alto y ancho, a saber 100, 200, 300, 400, 500, 600, 700, 800, 900 y 1000 píxeles, con un desplazamiento horizontal del 50% el ancho de la ventana y un desplazamiento vertical del 50% el alto de la ventana, lo que produce una superposición del 50% entre parches contiguos. Estos valores se eligen sobre la base del análisis de robustez del clasificador que presenta Pérez et al. (2017) para la geometría de la ventana. Este análisis muestra que el clasificador (explicado en la sección 2.3.2) es robusto para los patches que contienen al menos 60% de los píxeles de una yema, y estos deben cubrir al menos el 20% del patch. Si consideramos los casos extremos, i.e. el diámetro de yema más pequeño 100px y el más grande 1600px, tamaños de ventana de 100px y 1000px podrían contener al menos el 60

El segundo paso de este enfoque consiste en determinar si un patch es de clase yema o no-yema. El clasificador de Pérez et al. (2017) toma los patches producidos por el sliding windows y para cada uno realiza las siguiente operaciones: (i) computa features visuales de bajo nivel mediante el algoritmo *Scale Invariant Feature Transform* (SIFT) Lowe (2004); (ii) construye un descriptor de alto nivel para cada patch empleando el algoritmo *Bag of Features* (BoF) Csurka et al. (2004) sobre los features SIFT del paso anterior; y (iii) determina la clase de cada patch usando el descriptor BoF sobre un clasificador construido mediante el algoritmo *Support Vectors Machine* Vapnik (2013). Los detalles del entrenamiento de este clasificador se posponen hasta la sección 2.3.2 (Entrenamiento SW-C).

Finalmente, el tercer paso del enfoque consiste en construir la máscara binaria donde se encuentran etiquetados los píxeles que pertenecen a la clase yema y no-yema. Esta máscara es construida a través de un esquema de votación donde cada píxel suma un voto por cada patch que lo contiene clasificado como yema, el cual podría ser de un máximo de 4 para algunos píxeles debido a que el deslizamiento propuesto entre patches presenta solapamiento tanto horizontal como vertical. Luego, se establece un umbral de votos mínimos ν que puede

tomar los valores del 1 al 4, de tal manera que los píxeles con una cantidad de votos igual o mayor a ν son clasificados como yema, caso contrario se clasifican como no-yema.

2.2. Colección de imágenes

La colección de imágenes utilizada en este estudio es la misma colección utilizada originalmente en Pérez et al. (2017), el cual se ha descargado de la URL indicada por los autores http://dharma.frm.utn.edu.ar/vise/bc. La colección completo está compuesta por 760 imágenes capturadas en condiciones natural de campo, en invierno. Sin embargo en este trabajo solo se tomaron las 698 imágenes que contienen exactamente una yema. Cada imagen está acompañada del ground truth, es decir una máscara con la segmentación manual de la yema. Estas imágenes y sus máscaras fueron empleadas durante el entrenamiento y evaluación de los modelos de detección. Para esto, el corpus de imágenes se separó en dos subconjuntos disjuntos: el *trainset* con el 80% de las imágenes y el *testset* con el restante 20%. Esto resultó en un trainset de 558 imágenes y un testset de 140 imágenes, ambos con sus respectivas máscaras ground truth. De esta manera, los dos enfoques propuestos utilizan exactamente las mismas 558 imágenes durante el entrenamiento, y las mismas 140 imágenes durante la evaluación.

2.3. Entrenamiento de los modelos

En esta sección se dan los detalles del proceso de entrenamiento para cada enfoque empleando las 558 imágenes del trainset.

2.3.1. Entrenamiento enfoque FCN-MN.

Para el entrenamiento de este enfoque se utilizaron las 558 imágenes reservadas para este propósito, las mismas que se usaron para el entrenamiento del enfoque anterior. Estas imágenes presentan diferentes resoluciones, sin embargo las FCN-MN requieren una entrada de tamaño fijo. Por esto, todas las imágenes (incluida sus máscaras) fueron escaladas a una resolución de 1024×1024 píxeles usando un método de interpolación bilinear (Han, 2013). Además, para las imágenes del trainset se realizó un scaling en los valores de intensidad RGB de los píxeles de [0,255] a [-1, 1].

Dado que la cantidad de imágenes en el trainset se considera escasa, para lograr un entrenamiento robusto se emplearon dos técnicas ampliamente utilizadas en la práctica: *transfer learning* Pan and Yang (2009) y *data augmentation* Shorten and Khoshgoftaar (2019). El proceso de transfer learning se realizó de la siguiente manera: (i) se implementa la red MobileNet original propuesta en Howard et al. (2017); (ii) se inicializa la red con los parámetros pre-entrenados sobre el dataset de benchmark ImageNet Kornblith et al. (2019); (iii) se reemplaza la capa de clasificación multiclase de MobileNet por una capa de clasificación binaria; (iv) se entrena la red como un clasificador de patches yema y no-yema de forma análoga al entrenamiento de SVM, empleando el trainset de patches balanceado luego de escalar todas sus imágenes a 224×224 píxeles; y (v) se toman los parámetros obtenidos en este pipeline para inicializar el encoder de nuestra FCN-MN, introducido en la sección 2.1.1. El proceso de data augmentation se aplicó on the fly durante el entrenamiento, i.e. en la medida que el proceso requería nuevas imágenes. Por cada imagen del traiset se generaron 200 nuevas imágenes (111600 en total) aplicando simultáneamente las siguientes siete operaciones, donde sus valores se tomaron de forma aleatoria con probabilidad uniforme: *rotación* de hasta 45°; *traslación horizontal* de hasta 40%; *traslación vertical* de hasta 40%; *shear* de hasta 10%; *Zoom* de hasta 30%; *flip horizontal*; y *flip vertical*. En general, para el entrenamiento de una FCN-MN se requiere especificar el *método de optimización* y el valor de *dropout*, dos parámetros típicamente definidos por el usuario. En este trabajo, los métodos de optimización que se tuvieron en cuenta fueron: *Adam* con parámetros $LearningRate = 0.001$, $beta1 = 0.9$ y $beta2 = 0.999$; *RMSProp* con parámetros $LearningRate = 0.001$ y $rho = 0.9$; y *Stochastic Gradient Descent* con parámetros $LearningRate = 0.0001$ y $Momentum = 0.9$. Para el caso de dropout se definieron los valores 0.5 y 0.001. Estos valores fueron preseleccionados por experimentaciones preliminares que no se discuten aquí.

La mejor combinación entre método de optimización y valor de dropout se estableció en tiempo de entrenamiento sobre un conjunto de validación, utilizando el enfoque *4-fold cross validation* por 60 epochs, variando sobre los tres métodos de optimización y los dos valores de dropout. Los valores seleccionados fueron aquellos que maximizan el promedio de la Jaccard's *Intersection-over-*

	Mean IoU	
Optimizer	**Dropout = 0.001**	**Dropout = 0.5**
RMSprop	0.44253	0.3117
Adam	0.240277	0.315714
SGD	0.000886	0.00151

Table 2: Promedio de IoU sobre las 3 variantes para cada combinación de parámetros.

Union (IoU) (Jaccard, 1912), en los 4-folds sobre las 3 variantes, siendo IoU una medida de evaluación típica de problemas de segmentación (ver sección 3.1.2). Observamos en la Tabla 2 que la combinación de parámetros con la que se alcanza mayor IoU promedio es RMSProp con dropout de 0.001.

Finalmente se procedió a entrenar las 3 variantes con RMSProp como método de optimización y un valor de dropout de 0.001 sobre el conjunto de entrenamiento completo por 200 epochs.

2.3.2. Entrenamiento enfoque SW-C

La etapa de entrenamiento para este enfoque se realiza de la misma manera que para el workflow original propuesto en Pérez et al. (2017). Esto implica entrenar un clasificador binario para que aprenda el concepto de yema versus no-yema a partir de un corpus de patches rectangulares que contienen o no una yema. Durante el entrenamiento, los patches yema deben ser regiones que circunscriben perfectamente la yema (ver 2). Los patches no-yema deben ser regiones que no contienen ni un solo píxel de yema (ver 2). Por lo tanto, para construir el corpus de patches, se procesaron las 558 imágenes y sus máscaras siguiendo el mismo protocolo que en Pérez et al. (2017), obteniendo un total de 558 patches que circunscriben a cada yema (existe una por imagen) y más de 25000 patches no-yema (el área no-yema es mucho mayor al área que ocupa una yema en la imagen). El tamaño de estos patches es variable, con resoluciones entre 0.1 y 2.6 megapíxeles aproximadamente (patches de 100×100 a 1600×1600 píxeles).

A partir de este corpus de patches, se creó un trainset de patches balanceado, i.e. con 558 patches de cada clase, donde los patches no-yema fueron tomados al

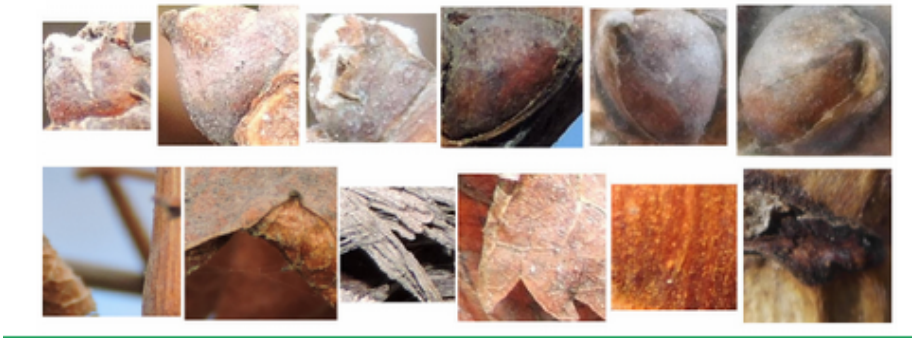


Figure 2: Collection of patches used in this work. The first row corresponds to bud patches. The second and third rows correspond to the non-bud patches.

azar entre miles de patches. El entrenamiento se realizó tal como se detalla en el pipeline propuesto en Pérez et al. (2017): (i) se extrajeron descriptores SIFT todos los patches del trainset; (ii) se aplicó BoF con tamaño de vocabulario igual a 25, dado que fue el modelo con mejores resultados según los autores; y (iii) se entrenó el clasificador SVM sobre los descriptores BoF de cada patch, empleando un kernel *Radial Basis Function*, donde el valor de los parámetros γ y C se estableció mediante un 5-fold cross-validation sobre los mismos rangos de valores, i.e. $\gamma = \{2^{-14}, 2^{-13}, \ldots, 2^{-7}\}$ y $C = \{2^5, 2^6, \ldots, 2^{14}\}$.

3. Experimental results

In this section we present a systematic evaluation of the quality our proposed procedure FCN-MN for bud detections quality, which, according to the discussion in the introduction, can be decomposed on the three aspects that impact on the relevant bud related variables listed in Table **??**: *segmentation*, *individualization*, and *localization*.

For that, we start in the following subsection by presenting metrics that quantify the quality for these aspects, followed by the results subsection 3 that presents details on the metric values obtained for different experiments over the test set of images.

3.1. Performance metrics

3.1.1. Individualization metrics

Individualization of buds, in both FCN-MN and SW, is the result of two steps: (i) the thresholding of the algorithm's output mask into a *binary mask*, keeping all pixels of ν the probabilistic mask output by FCN-MN with values higher than τ and keeping all pixels belong to at least ν patches rendered positive by SW, and (ii) the association of each *connected component* of the binary mask to exactly one (detected) bud.

An incorrect individualization is thus the result of incorrect matching of detected components with actual buds in the image. This matching can get very complicated when there is an unknown number of true buds in the scene as can be seen by the large amount of possible detection metrics defined in Oguz et al. (2017). To simplify the analysis our image corpus contains a single bud per image, avoiding the need of all metrics that report the confusing situation of a component overlapping more than one true bud. This results in the following simplified list of possible metrics:

- **Correct Detection** (CD) is the best case, and counts all images in the test corpus for which the detected binary mask presents a single connected component, and this connected component overlaps with the true bud of the image. This would correspond with a *true positive* situation.

- **Split** (S) occurs when there is more than one detection per bud, which happens when the mask contains multiple connected components, all of which overlaps the true bud. This metric counts the total number of such components over all images in the test corpus.

- **False Alarm** (S), is equivalent to a *false positive* situation, and corresponds to connected components not overlapping with the true bud. As for splits, it counts, for each image, the number of such components.

- **Detection Failure** (DF), is equivalent to a *false negative* situation,when the detection mask presents no connected components. It counts one each image satisfying this condition.

All four of these cases are mutually exclusive, that is, no image can satisfy any two (or more) of these definitions simultaneously. To quantify the individualization quality one could simply report these quantities counted over the test set, with the best case consisting in a CD value equal to the cardinality of this set. However, determining the overall individualization quality from the analysis of 4 quantities can get rather complicated. One alternative is reporting the well-known precision and recall, denoted P_D and R_D and referred to as *detection-precision* and *detection-recall* to distinguish them from the segmentation precision and recall defined later below. For that, we have to address first the fact that we have two differing true positive counts: CD and S. We solve this by first counting as true positives not only the CD type of images, but the S ones, i.e., we count as one true positive any image with either a correct detection or a split case, resulting in:

$$P_D = \frac{true\ positives}{true\ positives + false\ positives} = \frac{CD + S}{CD + S + FA} \tag{1}$$

$$R_D = \frac{true\ positives}{true\ positives + false\ negatives} = \frac{CD + S}{CD + S + DF}, \tag{2}$$

and then account for the split type of errors by explitictely reporting S.

Given these quantities we also report the *F1-measure* computed as their harmonic average:

$$F1 = 2 \times \frac{precision \times recall}{precision + recall}.$$

3.1.2. Segmentation metrics

Individualization metrics, although informative, relies on the overlap between the detected and true buds, regardless of how minimal the overlap. This could miss several possible pixelwise detection errors, resulting in rather coarse comparisons between competing detection algorithms. For instance, a correct detection could present a very small overlap with the true bud, with many or even a majority of the true bud's pixels missing (i.e., several *false negatives* pixels), or could be erroneously reporting several pixels as bud pixels (i.e., several *false positives* pixels). Clearly, the best case scenario would be a case of correct detection with no false negative or positive pixels, that visually would correspond to a perfect overlap of the detected connected component and the true

bud. Similarly, a pixel wise comparison of the masks could help assess the quality of the splits. The best split, for instance, would be one completely enclosed within the true mask, i.e., with none of its connected components presenting false positive pixels; while covering as much of the true bud mask as possible, i.e., presenting just enough false negatives to disconnect its components. Finally, a false alarm case, clearly presenting only false positive pixels, could be further assessed by the number of (false positive) pixels in its components.

The community has proposed several metrics to quantify segmentation errors. The most obvious ones are those that report the *fraction* of the whole image corresponding to *true positive* pixels, denoted TPF; *false positive* pixels, denoted FPF; and *false negative* pixels, denoted FNF. As for the individualization metrics, one can simplify the analysis by considering the pixelwise precision and recall, denoted P_S and R_S and referred to as *segmentation precision* and *segmentation recall*, defined formally as:

$$\begin{aligned} P_S &= TPF/(TPF + FPF) \\ R_S &= TPF/(TPF + FNF), \end{aligned}$$

$$2 \times precision \times recall/(precision + recall), \tag{3}$$

proposed independently by Dice (1945), thus usually referred to as the *Dice measure*. A common alternative to the Dice measure is the Jaccard's *intersection-over-union* (Jaccard, 1912), equivalent to $TPF/(TPF + FPF + FNF)$.

With these metrics, one could quantify the refinements discussed in the first paragraph above, by simply applying them, no to the whole mask, but to the individual individualization cases. For instance, reporting the mean Dice measured over all correctly detected components; or, to refine the assessment of how bad is a split, one could report the mean Dice measure to all components of some split, or the mean Dice measure over all split components of all split images.

The case of false alarms is rather monotonous and not very informative, with zero precision and recall for all such components. Indeed, a pixelwise assessment

of the gravity of a false alarm requires a quantification of the number of false positive pixels. One could simply consider the FPF, the fraction of all the image pixels that are false positives. Instead, we considered a normalization against the size of the bud to be more informative, resulting in the *normalized area*, denoted NA and defined formally as *the total area of the component corresponding to its total number of pixels, normalized by the area of the true bud.*

3.1.3. Localization metrics

As a localization metric we propose the *normalized distance*, denoted ND, defined formally as *the distance between the center of mass of the component, to the center of mass of the true bud, divided by the diameter of the true bud (defined as the maximum distance between any two border points of the true bud).*

3.2. Resultados Sistemáticos

We proceed now to assess the validity of our main hypothesis, namely, that FCN-MN is a better detector than its SW counterpart over each of the metrics defined in the previous section.

For a thorough comparison we considered several cases for each algorithm, training 27 FCN-MN detectors and 40 SW detectors over the training set of 558 images, one for each combination of their respective hyper-parameters. For FCN-MN these hyper-parameters are the three architectures 8s, 16s, and 32s, and the 9 values $\{0.1, 0.2, \ldots, 0.9\}$ for the binarization threshold τ; whereas for SW these hyper-parameters are the 10 patch sizes $\{100, 200, \ldots, 1000\}$ and the 4 values $\{1, 2, 3, 4\}$ of the voting threshold ν.

Table 3 shows the results for the best detectors of each algorithm, reporting all performance metrics of the three aspects of detection: individualization, segmentation and localization. The first column shows the label of the selected detectors, with the subscript indicating the architecture and patch size for the case of FCN-MN and SW, respectively, while the superscript indicating the thresholds τ and ν, respectively.

The table includes all metrics defined in Section 3.1 required for a thorough comparison of FCN-MN against SW. First, we include four individualization metrics: detection precision P_D, detection recall R_D, the F1-measure $F1$, and

S (the total count of split components). For a thorough analysis of the segmentations we discriminated the segmentation metrics for the correctly detected, splitted and false alarms. For the detections, i.e., correctly detected and splits, we report segmentation precision, segmentation recall, and the Dice measure denoted in the table by P_S^{CD}, R_S^{CD} and $Dice^{CD}$ for the correctly detected, and P_S^S, R_S^S and $Dice^S$ for the splits. Each of the three correctly detected cells report the mean value of the measure computed for each correctly detected test image, i.e., each image with only one component overlapping the true bud, including the corresponding standard deviation in parenthesis. For the split group, the mean and standard deviation are computed over the measures computed only for the split images, i.e., over the images containing at least two components overlapping the true bud. Here, the segmentation metrics are computed over the union of all split components. For the false alarms we reported the mean *normalized area*(NA), in this case computed individually for each false alarm component, reporting at each cell its mean over all false alarm components of all test images.

Finally, for localization the table reports the *normalized distance*(ND) only for false alarms, considering that correctly detected and splits, as they overlap the true bud, should be close enough to render it unnecessary further analysis. Instead, a false alarm can be arbitrarily far from the true bud. We thus report in the column ND the mean normalized distance of each false alarm connected component that appears in any test image.

The table is a summary, as it includes only a subset of all 27 FCN-MN cases, and a subset of all 40 SW cases. A detector was considered for inclusion in the table if, when compared to its counterparts of the same algorithm, it resulted in the higher value for at least one of the metrics. The corresponding cell was marked in bold in the table. For instance, the detectors FCN-MN$_{16s}^{0.8}$ is included because its detection precision P_D of 97.7 is the largest among the detection precision of all 27 FCN-MN detectors. Similarly, the detectors SW$_{1000}^{1}$ has been included because its precision P_D = 67.0is the largest among all 40 SW detectors.

The table shows a clear improvement of FCN-MN over SW. For all metrics it is the case that the best FCN-MN detector (bolded) improves (or ties) over the

best SW detector (bolded); represented in the table by underlying the one with better metric; with the exception of the two segmentation recalls (for correctly detected and splits) for which the SW case has a better (larger) mean, 98.8 versus 99.9 for correctly detected, and 74.7 versus 78.6 for the split case; and the total split count S, with the best case for FCN-MN being 1 and 0 for the best SW case. These improvements are not statistically significant, however, due to the large standard deviations of the FCN-MN cases, of 3.4 and 8.1, for the correctly detected and split cases, respectively, resulting in (statistically) overlapping values. In some cases the improvements of FCN-MN over SW are overwhelming. For instance, for the detection-precision, the correctly detected segmentation-precision, and the split segmentation-precision, the FCN-MN over SW improvements are 97.7 versus 67.0, 98.1 versus 46.5 and 99.9 versus 67.5, respectively. Also, for NA and ND the FCN-MN versus SW improvements are 0.04 versus 0.22, and 1.1 versus 6.0, respectively.

3.2.1. Detailed analysis of individualization metrics

Graphically one could expect a better combined analysis of the detection-precision and detection-recall than one could obtain by comparing the F1-measure. This is shown as a scatter plot in Figure reffig:detection-scatter-plot, a graphical representation of a non-summarized version of the second and third columns of Table 3. Each dot in the plot is located according to the detection-precision and detection-recall, and the colored black or white whether it corresponds to an FCN-MN or an SW detection model. The graph reinforces the clear and undisputed improvements of FCN-MN over SW already detected in the table, with similar detection-recalls but larger detection-precisions over the majority of scenarios, resulting in a larger area under the PR curve.

Detection-precision and detection-recall are computed over a combination of correctly detected and splitted components. To easily assess the impact of the split cases, we show in Figure 4 the S values, corresponding to the fifth column of a (non-summarized version of) Table 3 in the form of a histogram; with bins representing values of S, and the bars for that bin representing the proportion of models that resulted in that value of S. Black and white bars discriminate the cases for FCN-MN and SW, respectively. For instance, the first bin indicates that approximately 54% of the FCN-MN models and approximately 62% of the

Detector	P_D	R_D	$F1$	S	P_S^{CD}	R_S^{CD}	$Dice^{CD}$	P_S^S	R_S^S	$Dice^S$	NA	ND
FCN-MN$^{0.5}_{8s}$	75.4	98.6	85.4	2	91.0 (11.3)	90.2 (11.7)	**89.6 (10.3)**	96.6 (2.2)	73.1 (17.6)	**82.1 (10.2)**	0.26 (0.69)	3.72 (4.64)
FCN-MN$^{0.9}_{8s}$	90.1	97.1	93.5	8	**98.1 (6.0)**	68.3 (21.1)	77.9 (19.6)	98.7 (3.0)	57.4 (18.4)	70.8 (13.6)	0.24 (0.5)	3.8 (5.66)
FCN-MN$^{0.1}_{16s}$	71.3	**100**	83.2	6	75.7 (13.1)	95.4 (14.7)	83.1 (13.5)	83.1 (8.9)	54.1 (21.9)	61.9 (17.5)	0.12 (0.44)	5.27 (6.53)
FCN-MN$^{0.4}_{16s}$	87.0	96.4	91.5	**1**	87.7 (12.1)	89.8 (18.2)	87.0 (15.6)	96.7 (0.0)	37.0 (0.0)	53.5 (0.0)	**0.04 (0.09)**	3.8 (5.08)
FCN-MN$^{0.6}_{16s}$	95.6	93.6	94.6	3	92.2 (8.7)	88.2 (13.3)	89.1 (10.7)	99.4 (0.6)	16.2 (10.6)	26.6 (16.8)	0.08 (0.11)	**1.1 (0.65)**
FCN-MN$^{0.8}_{16s}$	**97.7**	92.1	**94.9**	4	95.8 (7.0)	81.6 (14.6)	87.0 (10.7)	99.7 (0.3)	34.2 (32.6)	43.9 (33.1)	0.1 (0.12)	1.28 (0.95)
FCN-MN$^{0.9}_{16s}$	**97.7**	91.4	94.5	4	97.6 (5.6)	74.5 (16.5)	83.1 (12.8)	**99.9 (0.1)**	31.8 (27.9)	41.6 (34.0)	0.07 (0.11)	1.33 (0.9)
FCN-MN$^{0.1}_{32s}$	35.4	**100**	52.2	8	67.4 (14.0)	**98.8 (3.4)**	79.1 (11.0)	86.0 (9.4)	73.4 (19.6)	77.1 (10.4)	0.14 (0.66)	4.62 (5.59)
FCN-MN$^{0.2}_{32s}$	50.9	**100**	67.5	10	73.9 (13.6)	98.1 (3.8)	83.5 (10.1)	92.2 (5.4)	53.4 (25.8)	63.6 (19.3)	0.17 (0.55)	4.33 (6.17)
FCN-MN$^{0.3}_{32s}$	49.8	**100**	66.5	10	79.1 (13.2)	95.5 (10.5)	85.2 (11.8)	88.5 (9.7)	61.0 (35.1)	65.8 (28.2)	0.1 (0.39)	3.68 (5.62)
FCN-MN$^{0.6}_{32s}$	68.5	99.3	81.1	16	89.0 (11.5)	89.1 (11.3)	88.1 (9.6)	92.4 (7.7)	**74.7 (28.1)**	78.1 (24.0)	0.11 (0.3)	2.95 (4.36)
SW$^1_{100}$	9.4	**100**	**17.2**	28	24.6 (17.7)	86.7 (19.5)	33.6 (15.1)	57.9 (28.2)	24.8 (16.8)	27.9 (13.8)	1.08 (3.2)	7.68 (6.02)
SW$^3_{100}$	14.6	93.1	25.3	40	42.4 (26.4)	56.8 (29.9)	**39.9 (19.7)**	55.5 (32.2)	24.8 (18.1)	26.0 (15.6)	0.31 (0.96)	6.45 (6.19)
SW$^4_{100}$	19.5	87.4	31.9	49	**46.5 (29.3)**	39.2 (28.9)	33.9 (21.1)	49.0 (29.0)	20.1 (13.7)	24.1 (14.0)	**0.22 (0.57)**	**6.0 (6.56)**
SW$^1_{200}$	20.0	**100**	33.3	12	16.6 (12.5)	94.9 (13.5)	25.9 (14.2)	49.3 (26.4)	40.2 (17.4)	36.8 (11.9)	5.13 (19.3)	7.56 (5.35)
SW$^3_{200}$	26.0	98.6	41.1	19	29.9 (17.0)	74.7 (27.3)	38.5 (17.0)	**67.5 (32.7)**	16.5 (8.9)	24.2 (11.9)	1.69 (3.15)	8.94 (6.22)
SW$^1_{300}$	26.9	**100**	42.4	2	13.7 (13.6)	97.0 (9.6)	21.6 (15.5)	55.0 (11.8)	48.1 (1.1)	**50.8 (4.5)**	7.79 (20.5)	6.83 (4.44)
SW$^1_{400}$	32.7	**100**	49.3	2	10.5 (11.7)	98.7 (9.3)	17.2 (15.3)	42.6 (10.1)	61.9 (11.6)	50.4 (10.9)	11.59 (24.05)	7.12 (4.15)
SW$^2_{400}$	34.6	**100**	51.4	4	15.6 (15.1)	94.5 (13.3)	23.8 (15.6)	48.7 (27.6)	36.0 (4.6)	38.6 (13.1)	9.54 (26.13)	7.88 (4.89)
SW$^1_{500}$	40.2	**100**	57.3	1	8.40 (9.7)	**99.9 (4.9)**	14.2 (13.8)	17.9 (0.0)	**78.6 (0.0)**	29.2 (0.0)	17.39 (30.07)	7.22 (4.04)
SW$^2_{500}$	38.6	**100**	55.7	1	13.5 (14.0)	95.2 (14.5)	21.0 (16.0)	35.2 (0.0)	45.9 (0.0)	39.8 (0.0)	17.19 (39.07)	7.56 (4.42)
SW$^1_{600}$	43.5	**100**	60.6	**0**	6.9 (7.8)	98.5 (10.7)	12.0 (12.0)	nan (nan)	nan (nan)	nan (nan)	25.48 (48.45)	7.72 (4.3)
SW$^2_{600}$	41.7	**100**	58.8	1	10.4 (10.6)	93.7 (18.9)	17.2 (14.4)	19.7 (0.0)	27.2 (0.0)	22.9 (0.0)	20.41 (38.32)	7.92 (4.38)
SW$^1_{700}$	50.6	**100**	67.2	**0**	5.6 (6.5)	98.6 (12.0)	9.9 (10.3)	nan (nan)	nan (nan)	nan (nan)	31.95 (64.36)	7.75 (4.45)
SW$^1_{800}$	56.7	**100**	72.4	**0**	5.1 (6.6)	97.7 (11.0)	9.0 (10.4)	nan (nan)	nan (nan)	nan (nan)	44.53 (71.52)	7.7 (4.06)
SW$^2_{800}$	49.6	99.2	66.1	**0**	8.3 (9.4)	95.0 (15.9)	13.9 (13.2)	nan (nan)	nan (nan)	nan (nan)	30.52 (46.45)	7.82 (4.1)
SW$^1_{900}$	64.3	**100**	78.3	**0**	4.2 (5.7)	94.7 (19.0)	7.5 (9.2)	nan (nan)	nan (nan)	nan (nan)	48.16 (80.31)	7.9 (4.35)
SW$^3_{900}$	42.2	92.4	58.0	**0**	15.0 (14.8)	81.5 (28.9)	22.7 (16.8)	nan (nan)	nan (nan)	nan (nan)	17.97 (29.56)	7.65 (4.67)
SW$^1_{1000}$	**67.0**	**100**	**80.2**	**0**	3.7 (4.7)	95.3 (18.3)	6.8 (7.9)	nan (nan)	nan (nan)	nan (nan)	57.83 (84.87)	7.91 (4.3)
SW$^2_{1000}$	56.7	98.3	71.9	**0**	6.3 (6.9)	93.8 (19.1)	11.1 (10.9)	nan (nan)	nan (nan)	nan (nan)	47.26 (68.92)	7.98 (4.44)

Table 3: Individualization, segmentation and localization metrics for the best FCN-MN and SW detection models. Bolded cells denote the best among all the cells in the column corresponding to the same algorithm (i.e., the best among FCN-MN, and the best among SW). Underlined (bolded) cells denote the best overall FCN-MN and SW detection models.

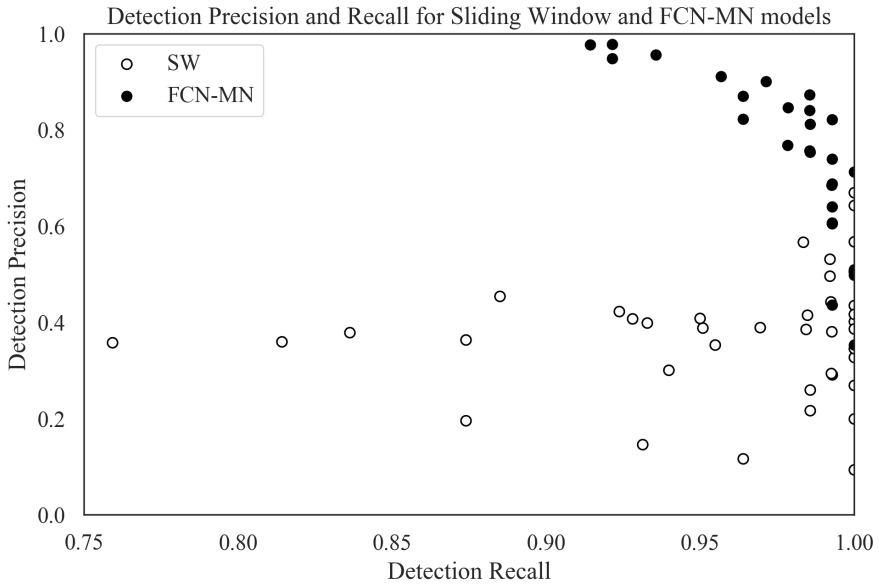


Figure 3: Precision-Recall scatterplots of the second and third columns of Table 3 discriminating the results for FCN-MN and SW with black and white dots, respectively. Each dot then represents the detection-precision and detection-recall computed over all images of the tests, for some particular configurations of hyperparameters. For FCN-MN, these would be the architecture, with values 8s, 16s and 32s, and threshold $\tau = \{0.1, 0.2, \ldots, 0.9\}$, for a total of 27 black dots; while for SW these would be the patch sizes $\{100, 200, \ldots, 1000\}$ and voting thresholds $\{1, 2, 3, 4\}$, for a total of a total of 40 white dots.

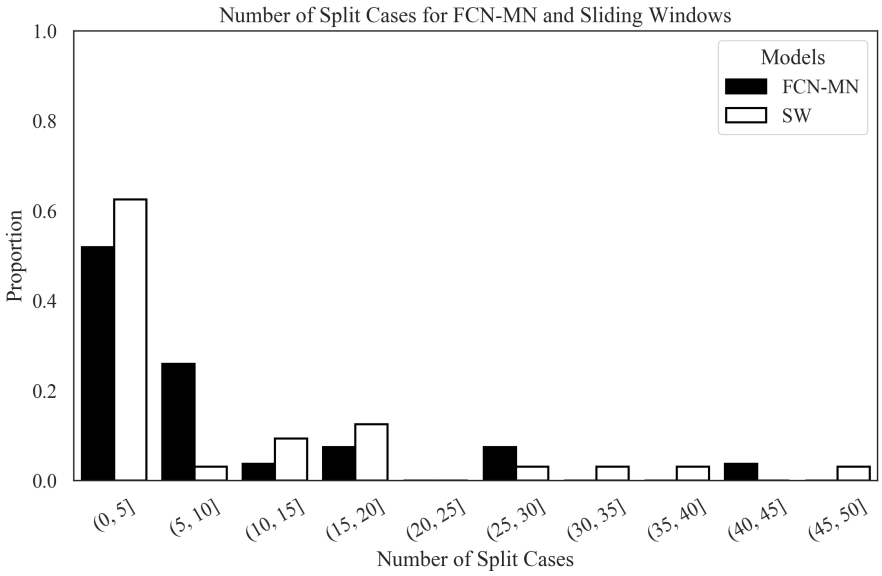
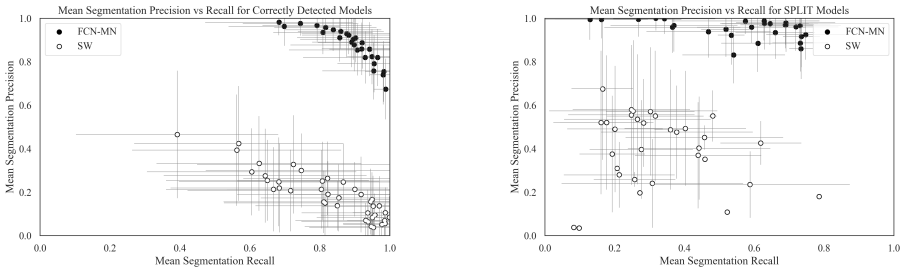


Figure 4: Histogram reporting the distribution of S for FCN-MN and SW in black and white bars, respectively. Each bar represents the proportion among all models (27 for FCN-MN and 40 for SW) that contains the number of splits indicated by the bin's label. For instance, the first (from left to right) white bar indicates that almost 14% out of the 40 SW models contains between 0 to 5 splits.

SW models resulted in a total number splits of less than 5. Overall, the FCN-MN distribution is slightly more concentrated in the lower number of splits than the SW distribution, but in general both algorithms compare fairly, with no clear contender when compared on the average number of splits they produce.

3.2.2. Detailed analysis of segmentation metrics

As for the individualization metrics, we show in Figures 5a and 5b scatter plots for the segmentation precision and segmentation-recall, for the *correct detections* and *splits* cases, respectively. These correspond to their respective columns of (a non-summarized version of) Table 3, with the black and white dots representing the values of FCN-MN and SW detection models, respectively. The position of each dot in the plot corresponds to the mean segmentation-precision and mean segmentation-recall over all images in the test set, computed over the correctly detected components (splitted components, respectively) of the masks produced by the detection model associated to that dot. The standard deviation



(a) (b)

Figure 5: Segmentation Precision-Recall scatterplots reporting the results for FCN-MN and SW in black and white, respectively, with dots representing the average of segmentation precision and segmentation recall over all images in the test set (and bars representing standard deviations), with one dot per configuration of hyperparameters (27 for FCN-MN and 40 for SW). In (a), the averages were computed over the segmentation precision and recall of the correctly detected components, while in (b), the averages were computed over the segmentation precision and recall of the split components. Standar deviations.

of the recall (precision) is shown as a horizontal (vertical) bar. In Figure 5a (correctly detected), one can observe that all black dots (FCN-MN) are clustered on the upper-right corner of the graph, enclosed by a minimum precision of approximately 0.65 and minimum recall of approximately 0.60; while the white dots (SW) are clustered on the lower-right corner of the graph, with maximum precisions of 0.5 and recall ranging from approximately 0.35 to 1.0. Overall, both algorithms show relatively high recalls, but with FCN-MN reaching much larger precisions. We can point to the coarse detection of the SW method as the main cause for the low precision, as this is reduced when extra, false positives are present in the positive mask. In Figure 5b (splits), one can observe again the overwhelming improvements of FCN-MN over SW, with all (but one) SW cases presenting precisions under 60%, with the outlier showing a precision of nearly 70%, and a similar distribution of recall values.

We also report graphically the segmentation results for the false alarm, the NA for each of the 27 models of FCN and each of the 40 models of SW, i.e., for each cell in the one-before-last column of (a non-summarized version of) Table 3

Figure 6 shows these results grouped in the form of two histograms, one for the FCN-MN detection models (black) and one for the SW models (in white). Bars in the histogram represent the proportion of detection models whose mean

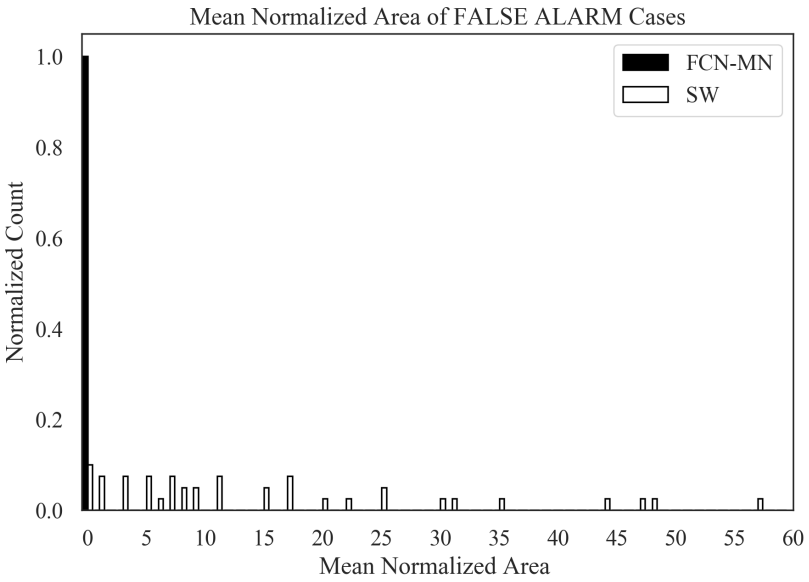


Figure 6: TODO:redactar

NA (over all all false alarm components of all images) falls within the interval of the bin. The more concentrated to the left, the better is the algorithm, as this indicates that more detection models for that algorithm resulted in smaller NA (on average). One can observe the histogram for FCN-MN considerably more concentrated at the left-most part of the histogram than that of SW, with all FCN-MN concentrated in a single bar at the left-most interval of $[0.0, 1.0)$. For SW the situation is rather different, with bars at intervals as far to the right as $[57.0, 58.0)$, that is, detection models with areas as large as 58 times the area of the bud.

3.2.3. Detailed analysis of localization metrics

To conclude, we present in this subsection a graphical representation of the localization results reported in Tab **??**tab:TablaXX), that is, the *normalized distance*(ND) only for false alarms. This assumes that because they overlap the true bud, correctly detected and split cases should be close enough to the true bud to render it unnecessary any analysis on their distance. Instead, a false alarm can be arbitrarily far from the true bud.

Figure 7 summarizes the ND values reported in the corresponding column

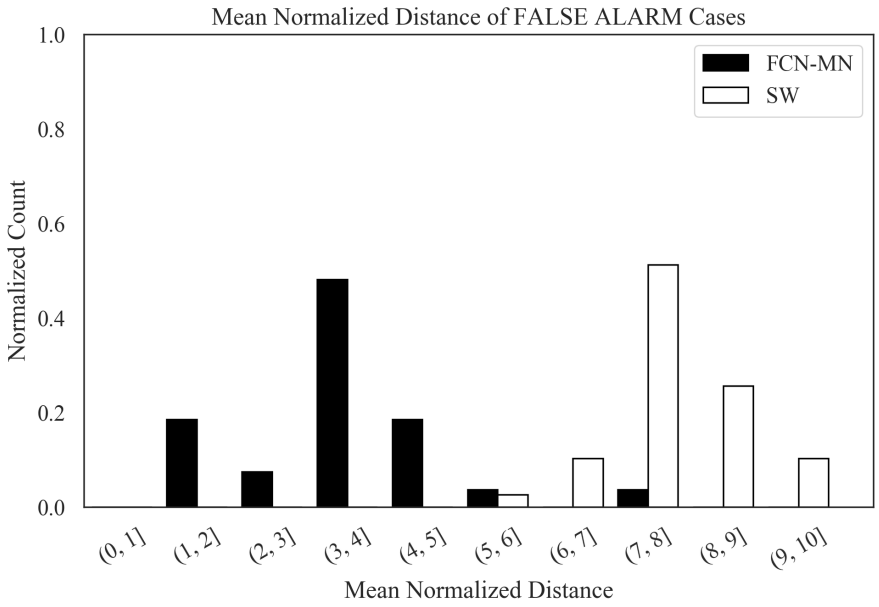


Figure 7: TODO:redactar

of the (non-summarized version) of Tab **??**tab:TablaXX) in the form of two histograms, one for FCN-MN (black) and one for SW (white). Bars in the histogram represent the proportion of detection models (27 for FCN-MN and 40 for SW) whose mean ND (over all all false alarm components of all images) falls within the interval of the bin. The more concentrated to the left, the better is the algorithm, as this indicates that more detection models for that algorithm resulted in smaller ND (on average).

Here again the advantage of FCN-MN over SW is clear, with the histogram for FCN-MN more concentrated to the left-most than that of SW, with the FCN-MN histogram running from the $(0, 1]$ to the $(7, 8]$ bin, whereas the SW histogram running from the $(5, 6]$ towards the $(9, 10]$ bin.

sectionDiscusión

En esta sección se discuten los resultados obtenidos por el enfoque propuesto en el contexto del problema de detección de yemas de vid, su impacto como herramienta para la medición de variables vitícolas de interés y los trabajos futuros.

This work introduces FCN-MN, a fully convolutional network with Mobile Net architecture **?** for the detection of grapevine buds in 2D images captured

in natural field conditions, in winter (i.e., with no leafs nor bunches), and containing a maximum of one bud. The experimental results confirmed our main hypothesis, that the detection quality achieved by FCN-MN improves over the *scanning windows* detector (SW) **?** in all three detection aspects: segmentation, individualization and localization. Being SW the best bud detector known to these authors, one can conclude that FCN-MN is a strong contender in the state-of-the-art for bud detectors.

But even improving over the state-of-the-art bud detectors one can still wonder if it can address the main *quality* and *throughput* requirements of a practical measurement of the bud related variables of Table 1..

Quality performance could be assessed by the metrics reported in Table 3, where in the best case FCN-MN shows a detection-precision and detection-recall of 97.7 and 100, respectively, a mean (and standard deviation) segmentation-precision and segmentation-recall for correctly detected of 98.1(0.6) and 98.8(3.4), respectively; and for splits 99.9(0.1) and 74.7(28.1), respectively. Also, for false alarms, a maximum NA of 0.04(0.09) a maximum ND of 0.04(0.22). However, these maximums correspond each to different FCN-MN detectors. A better assessment must be conducted for one single detector. For that, we picked $\text{FCN-MN}^{0.6}_{16s}$ for showing balanced quality overall. This detector reaches detection precision and recall of 95.6 and 93.6 respectively, meaning than only 4.4% of all the detected connected components over all test images are false alarms, and that only 6.4% of all true buds could not be detected (i.e., resulted in detection failure). Also, $S = 3$, meaning only 3 of all detections were splitted, which on average has a segmentation precision of 99.4(0.6) and segmentation recall of 16.2(10.6). The recall is rather small, suggesting that the split is in fact the result of pixel wise detection of the bud so sparse that it got disconnected. In contrast, all remaining detections were correct (i.e., not splitted), reaching segmentation precisions of 92.2(8.7), a rather similar value to that of splits, but a much larger mean segmentation recall of 88.2(13.3). Overall, this resulted in a mean Dice measure for the correctly detected of 89.1(10.7); demonstrating a considerable (mean) coverage of the true bud, with only 11.8% of the buds pixels missing (on average), and only 7.8% of the detected pixels covering the background (on average). But more promising are the false alarm results, with

$NA = 0.08$ and $ND = 1.1$, showing that these components are rather small, covering only an area that is 8% in size of the total area of a bud (on average), and distant to the true bud by only 1.1(0.65) diameters.

Based on these results, ¿what quality one should expect when the $\text{FCN}_{16s}^{0.6}$ detector takes part in the measurement of the bud related variables? For brevity we discuss this forthree variables from Table 1: *buds number*, *bud area*, and *length between nods*.

El caso del *buds number*, por ejemplo, requiere individualizar las yemas de la escena, por lo que su calidad se verá impactada sólo por la métricas de détection precision and recall (95.6 and 93.6 respectively). Para evaluar este impacto asumimos que una planta tiene aproximadamente en promedio 240 yemas. El número de yemas por planta depende de muchos factores, como ser sistema de conducción, varietal, tipo de tratamiento, época del año, entre otros, por lo que este valor se define a modo indicativo para lograr un análisis aproximado. Para este caso, una detection precision de 95.6 resultaría en 11 yemas contadas en exceso por planta; mientras que la recall de 93.6 resultaría en la omisión del conteo de 15 yemas. Además, este modelo produce 3 splits con dos componentes cada uno, i.e. un error de conteo por exceso del 3% yemas sobre las 140 yemas del testset. Particularmente en este análisis significa que se contarían 6 nuevas yemas de más, dando un total de 17 yemas en exceso, practicamente cancelandose con el error de omisión. Pero además, estos errores podrían en la práctica caracterizarse estadísticamente, permitiendo corregir las mediciones hacia valores más certeros.

La segunda variable de interés considerada es la *bud area*, donde, además de individualizar cada yema de la escena, es necesario segmentarla para estimar su área en píxeles. El análisis de individualización es análogo al del conteo de yemas, por lo que ahora se discuten sólo las métricas de segmentation. Del análisis desarrollado en los párrafos anteriores se puede concluir que los errores de segmentación por splits y false alarm tienen un bajo impacto en los resultados generales, y por ende en la estimación de *bud area*. Por otro lado, si se compensan los errores de segmentación para los correct detected (i.e. 11.8% of the buds pixels missing and 7.8% of the detected pixels covering the background), el error de estimación del área es solo de un 4%. A efectos ilustrativos,

vemos que este error es menor al error de precisión resultante de medir el área de una yema con un calibre. Si asumieramos que la forma de una yema se ajusta a una circunferencia, y que el diámetro típico de una yema es de 5 mm de diámetro, obtenemos un área de $19.63mm^2$. Siendo que un calibre tiene una precisión es $0.1mm$, el error de precisión del área sería de $\pm 1.7mm^2$, equivalente a un 8.6% del área total; un monto que duplica el error del 4% producido por nuestro detector FCN-MN. A está diferencia se le debe además sumar el error de la medición manual resultante de asumir una forma circular de la yema, aproximación innecesaria en el caso de FCN-MN.

Por último, consideremos el caso de la *distance between knots*, estimada por la distancia entre yemas de una misma rama (por la cercanía entre yemas y nudos), la cual involucra las operaciones de individualización y localización. De nuevo, el análisis de individualización es análogo al del conteo de yemas, que en este caso resultará en el reporte de más de una distancia debido a la detección de más de una componente por yema. Entre estas distancias, entendemos que el peor caso puede darse entre los false alarms, siendo estos los más alejados de la true bud, y entre dos yemas ocurre cuando las false alarms están a distancia ND del lado más alejado de la otra yema. En promedio, $ND = 1.1$, que de acuerdo al diámetro típico de las yemas de vid equivale a aprox. 5mm, un valor muy menor a las distancias típicas de yemas de aproximadamente 30cm, i.e., alrededor de un 3.3% de error en la estimación de la distancia entre buds/knots.

Vemos que los errores de mayor impacto ocurren por el exceso u omisión de connected components, con el error de exceso exacerbado por el hecho de asociar buds detectadas con connected components individuales. Una mejora posible para mitigar estos errores consistiría en aplicar algunos post-procesamientos. Uno de ellos es el *spatial clustering* de los connected components que los agrupe por por cercanía. One could expect this to improve the results based on the small areas of split and false alarm components. On one hand, due to the closeness to the true bud of the false alarms (small ND), as well as the splits and correctly detected components (they overlap with it); and the fact that true buds in real plants are typically tens or even hundreds of bud diameters apart, a simple spatial clustering of the components would connect all these components together as one single, and correct, bud detection. Second, due to

their small area, if clustered together, the false alarm components would only slightly reduce the segmentation precision. Otro posible post-procesamiento consistiría en descartar connected components pequeños, por ejemplo, cuya area en pixeles normalizada respecto al area total detectada (suma de las areas de todos los connected components) sea menor a cierto umbral. Podrían esperarse mejoras con este post-procesamiento dado que los resultados en este trabajo muestran que los false alarms presentan areas pequeñas en relacion al true bud. Por último, podrían considerarse filtros de connected components basados en la estructura de la planta, por ejemplo, descartando connected components que estan lejos (o no presentan overlap) con las ramas.

Also, one could consider in future works some improvements that overcome the limitations for a practical use mentioned above: (i) no associations between parts of plants of different images, (ii) distance and area measurements are in pixels, (iii) only 3D geometry, (iv) lack of knowledge of the underlying plant structure, and (v) need of images with no leaves.

One could consider extending to buds the work of Santos et al. (2020) that addresses limitation (i) for grape bunches. Limitation (ii) could be easily addressed by adding to the visual scene some marker with known dimensions. This, however, requires such a marker in every image captured, a problem that could be overcomed by first producing a calibrated 3D reconstruction of the scene, i.e., a 3D reconstruction calibrated with a single marker in one of its frames **?**. This way, every 2D image could be calibrated against the 3D model, omitting the need of a marker. In addition, a 3D reconstruction of the scene could address limitation (iii) by locating the detected buds in 3D space, following, for instance, the approach taken by Díaz et al. (2018).

Finally, a solution to limitations (iv) and (v) would require an integrated solution involving the detection in 3D of branches and leaves, respectively.

4. Conclusions

TODO: Conclusions

Acknowledgments

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